

S #10/782,261 Page 1

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:37 ; Search time 48.2298 seconds  
(without alignments) 666.605 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1277  
Sequence: 1 PMSMLFYTLTAFLAIGTQAE.....FLRIDTACVLSKRAVARA 242

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: A\_Geneseq.101002.\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
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8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
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11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
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13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
24: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1270	99.5	241	12	AA13063
2	1270	99.5	241	12	AA13063
3	1270	99.5	241	12	AA13063
4	1270	99.5	241	16	AA13063
5	1270	99.5	241	16	AA13063
6	1270	99.5	241	18	AA13063
7	1270	99.5	241	19	AA13063
8	1270	99.5	241	20	AA13063
9	1270	99.5	241	22	AA13063
10	1270	99.5	241	23	AA13063

11	1270	99.5	241	23	ABB04994	Human beta nerve g
12	1270	99.5	245	5	AA140038	Sequence encoded b
13	1267	99.2	307	14	AA145241	Human pre-pro nerv
14	1266	99.1	241	22	AA167865	Amino acid sequenc
15	1266	99.1	307	14	AA137799	Human NGF. Homo s
16	1264	99.0	307	19	AA169725	Human beta-nerve g
17	1238	96.9	239	14	AA13910	Nerve growth facto
18	1188.5	93.1	241	12	AA13886	NGF with pro-regio
19	1175	92.0	222	21	AA15084	Human proNGF prote
20	1096	85.8	240	23	AA15084	Sequence encoded b
21	1096	85.8	307	5	AA14003	Sequence encoded b
22	1093	85.6	307	14	AA15240	Cloned mouse pre-p
23	1093	85.6	240	14	AA13937	Sequence of pro re
24	986	78.0	240	15	AA136451	NGF2/NT-3 in pRb13
25	986	78.0	240	15	AA136451	Recombinant beta-N
26	921	77.6	240	13	AA136273	Chimeric neurotroph
27	882	53.4	129	14	AA137539	Human growth hormo
28	882	53.4	129	18	AA14145	Nerve growth facto
29	661	51.8	124	13	AA121851	N-terminal of neut
30	657.5	51.5	154	13	AA122751	NGF-beta amino aci
31	651	51.0	120	20	AA12117	Nerve growth facto
32	651	51.0	120	21	AA12117	Amino acid sequenc
33	651	51.0	120	22	AA12117	Synthetic nerve gr
34	651	51.0	120	22	AA12117	Amino acid sequenc
35	648	50.7	156	23	AA150303	Human nerve growth
36	648	50.7	157	21	AA150303	Human beta-nerve g
37	648	50.7	157	22	AA150303	Parotidic neurotro
38	648	50.7	157	23	AA150303	Human nerve growth
39	647.5	50.7	166	23	AA150303	Sequence encoded b
40	647.5	50.7	167	22	AA150303	
41	647	50.7	167	22	AA150303	
42	647	50.7	262	10	AA150303	
43	647	50.7	262	10	AA150303	
44	642	50.3	118	10	AA150303	
45	642	50.3	119	5	AA140040	

ALIGNMENTS

RESULT 1	AA13063	standard; Protein; 241 AA.
ID	AA13063	
AC	AA13063	
DT	30-SEP-1991	(first entry)
DE	Human NGF Smat-Apai fragment prod.	
XX	Expression vector; human nerve growth factor; yeast;	
XX	senile dementia.	
OS	Homo sapiens.	
XX	JPO3139285-A.	
PN	13-JUN-1991.	
XX	20-DEC-1989; 89JP-0328199.	
XX	27-JUL-1989; 89JP-0192581.	
XX	(TAKE ) TAKEDA CHEMICAL IND KK.	
XX	WPI: 1991-218449/30.	
XX	N-PSDB: AA012638.	
XX	New yeast expression vector - used in produ. of human nerve growth	
XX	factor from corresp. yeast.	
XX	Disclosure: Fig 1(1-2); 14pp; Japanese.	

CC Human NGF is useful as a reagent for study of the nervous system, and  
 CC for treatment of senile dementia. The DNA encoding this fragment was  
 CC derived from the human gene or is synthesized chemically.  
 CC See also AA012639.  
 CC XX

SO Sequence . 241 AA:

Query Match 99.5%: Score 1270; DB 12; Length 241;  
 Best local similarity 100.0%: Pred. No. 1.3e-134;  
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 61  
 DB 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 60  
 OY 62 ARVAGOTRNTITVDPRLFKKRLRSPRVLESTOPPREADTODLDFEYGAAPFNRTHRK 121  
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSPRVLESTOPPREADTODLDFEYGAAPFNRTHRK 120  
 OY 122 RSSHPPIFRGEFSVCDVSVMGDKTTATDIDKEVNVLCGVNINNSVKQYFEETKCR 181  
 DB 121 RSSHPPIFRGEFSVCDVSVMGDKTTATDIDKEVNVLCGVNINNSVKQYFEETKCR 180  
 OY 182 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVRR 241  
 DB 181 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

# RESULT 2

AA01474  
 ID AA01474 standard: Protein; 241 AA.

AC AA01474:  
 XX  
 DT 26-APR-1991 (first entry)  
 XX  
 DE Human nerve growth factor.  
 XX  
 KW NGF; senile dementia.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label- signal sequence  
 FT Protein 19..241  
 FT /label- pro-NGF  
 FT Protein 122..241  
 FT /label- mature NGF  
 FT Disulfide-bond 135..202  
 FT Disulfide-bond 180..230  
 FT Disulfide-bond 190..232  
 XX  
 PN EP414151-A.  
 XX  
 PD 27-FEB-1991.  
 XX  
 PF 17-AUG-1990; 90EP-0115815.  
 XX  
 PR 21-AUG-1989; 89JP-0212980.  
 PR 20-DEC-1989; 89JP-0328198.  
 PR 13-APR-1990; 90JP-0096252.  
 PR 07-JUN-1990; 90JP-0147392.  
 XX  
 PA (TAKE ) TAKEDA CHEMICALS IND KK.  
 XX  
 PI Kakinuma A, Nakahama K, Yoshimura K, Katsuo Y, Iwanai M;  
 XX  
 DR WPI; 1991-059398/09.

DR N-PSDB: AA010620.

XX Human nerve growth factor containing cysteine residues - used as  
 PT reagent and therapeutic drug for senile dementia.  
 XX  
 PS Claim 1: Fig 1; 33pp; English.

CC The sequence was deduced from a clone isolated from a lambda EMBL3  
 CC genomic library prep. from human leukocyte DNA, using a probe  
 CC synthesized based on the sequence of the known human NGF gene (A.  
 CC Ulrich et al., Nature 303, 821 (1983)). The clone, betaLN2113,  
 CC isolated from the library was cleaved with SmaI and ApaI to remove  
 CC a 1kb fragment contg. the gene which was then inserted into plasmid  
 CC pluscript IIK to obtain pNGFp107G. The gene was sequenced from  
 CC this plasmid using Sequase (Biochemical). The sequence of the  
 CC protein coding region was found to be in complete agreement with  
 CC that of Ulrich et al. The sequence was used to produce  
 CC recombinant h-NGF for use in the prodn. of drugs for e.g. senile  
 CC dementia.  
 CC  
 SO Sequence 241 AA:

Query Match 99.5%: Score 1270; DB 12; Length 241;  
 Best local similarity 100.0%: Pred. No. 1.3e-134;  
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 61  
 DB 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 60  
 OY 62 ARVAGOTRNTITVDPRLFKKRLRSPRVLESTOPPREADTODLDFEYGAAPFNRTHRK 121  
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSPRVLESTOPPREADTODLDFEYGAAPFNRTHRK 120  
 OY 122 RSSHPPIFRGEFSVCDVSVMGDKTTATDIDKEVNVLCGVNINNSVKQYFEETKCR 181  
 DB 121 RSSHPPIFRGEFSVCDVSVMGDKTTATDIDKEVNVLCGVNINNSVKQYFEETKCR 180  
 OY 182 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVRR 241  
 DB 181 DPNPVDSCGKIDSKHNSCTTHTFVKALTMQKQAAAFRIIDPACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

# RESULT 3

AA013858  
 ID AA013858 standard: Protein; 241 AA.

AC AA013858:  
 XX  
 DT 21-NOV-1991 (first entry)  
 XX  
 DE Human nerve growth factor.  
 XX  
 KW hNGF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP03175976-A.  
 XX  
 PD 31-JUL-1991.  
 XX  
 PR 12-DEC-1989; 89JP-0320483.  
 PR 30-SEP-1989; 89JP-0253796.  
 PR 15-DEC-1989; 89JP-0314860.  
 PR 12-DEC-1989; 89JP-0320483.  
 XX  
 PA (TAKE ) TAKEDA CHEMICAL IND KK.

DR MPI: 1991-269694/37.  
 DR N-PSDB: AAO13397.  
 XX Secretory prepn. of animal protein - by culturing  
 PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of  
 PS promoter region.  
 XX Disclosure: Fig 3: 12pp; Japanese.  
 XX The amino acid sequence is encoded that of human nerve growth factor  
 CC (NGF). It may be expressed in Schizosaccharomyces pombe using the  
 CC glyceraldehyde-3-phosphate dehydrogenase (Gld) gene promoter.  
 XX Sequence 241 AA:

Query Match 99.5%; Score 1270; DB 12; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;  
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 61  
 DB 1 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 60  
 OY 62 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTQDLDFEYGAAPFNRTHSK 121  
 DB 61 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTQDLDFEYGAAPFNRTHSK 120  
 OY 122 RSSSHPIFRHGEFSYCDVSVMVGDKTATDINKGEVNLGEVINNSVFQYFETCR 181  
 DB 121 RSSSHPIFRHGEFSYCDVSVMVGDKTATDINKGEVNLGEVINNSVFQYFETCR 180  
 OY 182 DPNPVDSCRGIDSKHNSICTTHTFVKALTDGKQAMRIRIDTACVLSRKAARR 241  
 DB 181 DPNPVDSCRGIDSKHNSICTTHTFVKALTDGKQAMRIRIDTACVLSRKAARR 240  
 OY 242 A 242  
 DB 241 A 241

## RESULT 4

ID AAR77419 standard; Protein: 241 AA.  
 XX AAR77419;

XX 10-FEB-1996 (first entry)  
 XX DE Human nerve growth factor.  
 XX KW Nerve growth factor; neurotrophic factor; therapeutic;  
 XX KM protein refolding; NGF.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Protein 123..241  
 FT /note= "mature protein"  
 FT Region 1..121  
 FT /note= "pre-region"

XX PN W09530686-A1.  
 XX PD 16-NOV-1995.  
 XX PR 02-MAY-1995; 95WO-US05423.  
 XX PR 27-JUN-1994; 94US-0266080.  
 XX PR 09-MAY-1994; 94US-0240122.  
 XX PA (SYNT ) SYNTX-SYNERGEN NEUROSCIENCE JOINT VENTU.  
 XX PI Bonam D, Kohno T, Lille J, Rosendahl MS;

XX MPI: 1995-404080/51.  
 DR N-PSDB: AAT05437.  
 XX Process for bacterial expression of recombinant neurotrophic factor  
 PT - useful for promoting the survival and maintaining phenotypic  
 XX differentiation of nerve and glial cells.  
 XX Disclosure: Page 33-34; 57pp; English.

XX The nerve growth factor (NGF) gene is expressed in Escherichia  
 CC coli cells. The recombinant protein is solubilized and  
 CC sulfonated and allowed to refold in the presence of PEG and urea.  
 CC Biologically active NGF, used for promoting the survival of and  
 CC maintaining the phenotypic differentiation of nerve and glial cells,  
 CC is isolated and purified. This method breaks incorrectly formed  
 CC disulfide bonds and allows refolding of the factor into the correct  
 CC tertiary structure required for maximum yield of full active protein.  
 XX Sequence 241 AA:

Query Match 99.5%; Score 1270; DB 16; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;  
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 61  
 DB 1 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPQVHMTKLQHSIDTALRRASAPAAIA 60  
 OY 62 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTQDLDFEYGAAPFNRTHSK 121  
 DB 61 ARVAGOTRNITVDPLFKKRLRSPRYLSTQPPREADTQDLDFEYGAAPFNRTHSK 120  
 OY 122 RSSSHPIFRHGEFSYCDVSVMVGDKTATDINKGEVNLGEVINNSVFQYFETCR 181  
 DB 121 RSSSHPIFRHGEFSYCDVSVMVGDKTATDINKGEVNLGEVINNSVFQYFETCR 180  
 OY 182 DPNPVDSCRGIDSKHNSICTTHTFVKALTDGKQAMRIRIDTACVLSRKAARR 241  
 DB 181 DPNPVDSCRGIDSKHNSICTTHTFVKALTDGKQAMRIRIDTACVLSRKAARR 240  
 OY 242 A 242  
 DB 241 A 241

## RESULT 5

ID AAR66688 standard; Protein: 241 AA.  
 XX AAR66688;

XX 23-AUG-1995 (first entry)  
 XX DE Human nerve growth factor.  
 XX KW Human nerve growth factor; hNGF; polyclonal antibody;  
 XX KM Immunogen; enzyme immunoassay.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= sig\_peptide  
 FT Peptide 19..121  
 FT /label= pro\_peptide

FT MISC-difference 8  
 FT /note= "corresponding codon TCG"  
 FT MISC-difference 59  
 FT /note= "corresponding codon TAT"  
 FT MISC-difference 173  
 FT /note= "corresponding codon TAG"  
 FT Disulfide-bond 136..201

```

FT Disulfide-bond 179..229
XX Disulfide-bond 189..231
XX JPO6317587-A.
XX
XX 15-MOV-1994.
XX
XX 14-FEB-1991: 91CP-0021181.
XX
XX 31-AUG-1990: 90JP-0231317.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI: 1995-033116/05.
XX N-PSDB: AAQ79871.
XX
XX Polyclonal antibody against human nerve growth factor (NGF) -
XX useful to detect human NGF, for diagnosis of disease
XX
XX Example 1: Pages 31-33; 35pp; Japanese.
XX
XX AAQ79871 encodes AAR65688 human nerve growth factor (hNGF), the
XX protein was used as an immunogen to generate a polyclonal
XX antibody against hNGF. The polyclonal antibody can be used
XX to detect and determine hNGF pref. by enzyme immunoassay.
XX
XX Sequence 241 AA:
XX
XX Query Match 99.5%; Score 1270; DB 16; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-134;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHMTKLOHSIDTALRRARSAPAAIA 61
XX 1 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHMTKLOHSIDTALRRARSAPAAIA 60
XX
XX 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRTHRSK 121
XX 61 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRTHRSK 120
XX
XX 122 RSSSHPIFRHGEFSVCDSVYVWGDKTTATDIDKKEVNVLGEVNINSVKOYFEETKCR 181
XX 121 RSSSHPIFRHGEFSVCDSVYVWGDKTTATDIDKKEVNVLGEVNINSVKOYFEETKCR 180
XX
XX 182 DPNPVDGCGRIDSKHMSYCTTHTFVKALTMGKQAAMRFIRIDTACVLSRAVRR 241
XX 181 DPNPVDGCGRIDSKHMSYCTTHTFVKALTMGKQAAMRFIRIDTACVLSRAVRR 240
XX
XX 242 A 242
XX
XX 241 A 241
XX
XX RESULT 6
XX AAQ26237
XX ID AAQ26237 standard; Protein: 241 AA.
XX
XX AAQ26237:
XX
XX 16-MAR-1998 (first entry)
XX
XX Human preproNGF.
XX
XX Fusion protein: hydrophilic spacer: recombinant; expression system:
XX carboxypeptidase; preproNGF.
XX
XX Homo sapiens.
XX
XX WO9728272-A1.
XX
XX 07-AUG-1997.
XX
XX 31-JAN-1997: 97MO-US01470.

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XX
XX 31-JAN-1996: 96US-0595043.
XX
XX (TECH-) TECHNOLOGENE INC.
XX
XX Sgarlato GD;
XX
XX WPI: 1997-402624/37.
XX N-PSDB: AAT80162.
XX
XX Recombinant protein expression system for fusion protein production
XX - useful for high quantity production of authentic recombinant
XX proteins
XX
XX Example 6: Page 140-141; 194pp; English.
XX
XX A novel recombinant vector has been developed which comprises a
XX nucleotide sequence encoding a fusion protein. The fusion protein
XX comprises three domains joined together in order, from N-terminus to
XX C-terminus, of a first domain comprising a protein of interest, a second
XX domain comprising a hydrophilic spacer and an affinity domain, each
XX human preproNGF, used in example 6 of the present invention. The
XX recombinant vector is used for the production of authentic recombinant
XX proteins of interest. The method of the invention is useful for the
XX expression of fusion proteins capable of isolation by affinity
XX chromatography in pro- or eukaryotic cells. This method allows
XX for the efficient cleavage and generation of authentic proteins of
XX interest that do not contain extraneous (i.e. non-naturally occurring)
XX amino acids.
XX
XX Sequence 241 AA:
XX
XX Query Match 99.5%; Score 1270; DB 18; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-134;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHMTKLOHSIDTALRRARSAPAAIA 61
XX 1 MSMLFTLTITAFILGIAOEPHSESNVPAGHTIPQVHMTKLOHSIDTALRRARSAPAAIA 60
XX
XX 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRTHRSK 121
XX 61 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREAADTODLDFEVGGAAPFNRTHRSK 120
XX
XX 122 RSSSHPIFRHGEFSVCDSVYVWGDKTTATDIDKKEVNVLGEVNINSVKOYFEETKCR 181
XX 121 RSSSHPIFRHGEFSVCDSVYVWGDKTTATDIDKKEVNVLGEVNINSVKOYFEETKCR 180
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XX 182 DPNPVDGCGRIDSKHMSYCTTHTFVKALTMGKQAAMRFIRIDTACVLSRAVRR 241
XX 181 DPNPVDGCGRIDSKHMSYCTTHTFVKALTMGKQAAMRFIRIDTACVLSRAVRR 240
XX
XX 242 A 242
XX
XX 241 A 241
XX
XX RESULT 7
XX AAQ48886
XX ID AAQ48886 standard; Protein: 241 AA.
XX
XX AAQ48886:
XX
XX 12-OCT-1998 (first entry)
XX
XX Human prepro-nerve growth factor beta chain.
XX
XX Neurotrophin; nerve growth factor; NGF; human; purification;
XX hydrophobic interaction chromatography.
XX
XX Homo sapiens.
XX

```



Key	Location/Qualifiers
1..121	
Protein	/label= Prepro_region
122..241	
Protein	/label= Mat_protein
167	
Modified-site	/note= "N-glycosylated"
179..189	
Region	/note= "conserved Cys-containing region involved in Cys knot motif"
229..231	
Region	/note= "conserved Cys-containing region involved in Cys knot motif"
MO9821234-A2.	
22-MAY-1998.	
14-NOV-1997.	97MO-US21068.
29-MAY-1997.	97US-0047855.
15-NOV-1996.	96US-0030838.
(GETH ) GENENTECH INC.	
Beck JT, Burton LE, Schmeizler CH;	
WPI: 1998-322333/28.	
Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated variant(s) - using hydrophobic interaction chromatography, optionally in combination with high performance cation exchange chromatography	
Disclosure: Fig 4: 59pp: English.	
This polypeptide comprises the human nerve growth factor (NGF) beta chain precursor. Methods are provided for large-scale purification of neurotrophins, including mature NGF, suitable for clinical use. A claimed method comprises: (1) separating the neurotrophin from the other proteins using a hydrophobic interaction chromatography resin (HICR); and optionally (2) separating the neurotrophin from a chemical variant by high performance cation exchange chromatography (HPEC). The processes can also be used for purification of e.g. mouse NGF (see AAM48887), brain-derived neurotrophic factor (see AAM48888), neurotrophin-4/5 (see AAM48890) and neurotrophin-3 (see AAM48889). The processes allow separation of neurotrophins from various undesirable misprocessed, misfolded, size, glycosylated or charge forms. They allow selective separation from their variants and other molecules, and from other polypeptides with high pI. The processes are applicable to starting materials from various sources, including fermentation broths or lysed bacterial or mammalian cells.	
Sequence 241 AA:	
Query Match 99.5%; Score 1270; DB 19; Length 241;	
Best Local Similarity 100.0%; Pred. No. 1,3e-134;	
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
2 MSMLFYTLIAAFILIGIQAPHSSESNVPAGHITPOVHTKLOHSDTLARASAPAAAT 61	
1 MSMLFYTLIAAFILIGIQAPHSSESNVPAGHITPOVHTKLOHSDTLARASAPAAAT 60	
62 ARVAGORNTVDPRLFKRRRLRSRYLFTSQPPREAADTODLDFEVGAAPFNRTTRSK 121	
61 ARVAGORNTVDPRLFKRRRLRSRYLFTSQPPREAADTODLDFEVGAAPFNRTTRSK 120	
122 RSSSHPIFIRNGEFSYCDYSVWVGDKTATIDIKGEVNLGEVININSVKOFEETKCR 161	
121 RSSSHPIFIRNGEFSYCDYSVWVGDKTATIDIKGEVNLGEVININSVKOFEETKCR 180	
182 DPRVDSGCGIDSKHMNSYCTTTTFYKALTMQKGAARFYTIDTACCVLSRAAVR 241	

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Db      181  DPNPVDSCRCIDSKDHNSYCTTHFVKALTDGCGAAMRIRITDTCVCVLSRAVNR 240
Oy      242  A 242
Db      241  A 241

RESULT 8
AAV07303
ID      AAV07303 standard; Protein; 241 AA.
AC      AAV07303;
XX      06-JUL-1999 (first entry)
DT      XX
DE      Human nerve growth factor beta protein.
XX      XX
XX      Cerebrospinal; axon; growth; mammal; spinal cord injury; lesion; NGF;
KV      expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;
XX      N3; voluntary motor function.
XX      XX
OS      Homo sapiens.
XX      XX
XX      M09900148-A2.
XX      XX
XX      07-JAN-1999.
XX      XX
XX      30-JUN-1998; 98MO-US13778.
XX      XX
XX      30-JUN-1997; 97US-0051255.
XX      XX
XX      (REGC ) UNIV CALIFORNIA.
XX      XX
XX      Gage FH, Grill R, Tuszynski NH;
XX      XX
XX      WPI; 1999-095478/08.
XX      XX
XX      N-PSDB; AAX34366.
XX      XX

PT      Treating spinal cord injuries in a mammal - by inducing growth of
PT      cerebrospinal projection axons using a recombinant vector for
PT      expressing CST neurotrophin
XX      XX
XX      Disclosure: Fig 6; 49pp; English.
XX      XX
XX      The invention relates to a method of inducing cerebrospinal projection
XX      (CST) axon growth in a mammal with a spinal cord injury that involves
XX      a CST lesion by delivering a recombinant expression vector for CST
XX      neurotrophin, such as this sequence - nerve growth factor beta. The
XX      method is used to induce partial recovery of voluntary motor function
XX      in a mammal after disruption of corticospinal projections in the spinal
XX      cord.
XX      XX
XX      Sequence 241 AA:
XX      XX
XX      50

Query Match 99.5%; Score 1270; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,3e-134;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 2 MSMLFTLLTAFLIGIOAEPHSESNNVPAGHITIPQVHMKLOHSDTLRARSAPAAATA 61
1 MSMLFTLLTAFLIGIOAEPHSESNNVPAGHITIPQVHMKLOHSDTLRARSAPAAATA 60
OY 62 ARAVAGTTRNTVDPREFKRRLRSRVLFSTOPPREAADTODLDFEYGGAAPNKRTRSK 121
DB 61 ARAVAGTTRNTVDPREFKRRLRSRVLFSTOPPREAADTODLDFEYGGAAPNKRTRSK 120
OY 122 RSSSHPIEHRGEFSVCDSVVAVGDKTATDIDIKGEVAVLGEVINNSVFKQYFFETKCR 181
DB 121 RSSSHPIEHRGEFSVCDSVVAVGDKTATDIDIKGEVAVLGEVINNSVFKQYFFETKCR 180
OY 182 DPNPVDSCRCIDSKDHNSYCTTHFVKALTDGCGAAMRIRITDTCVCVLSRAVNR 241
DB 181 DPNPVDSCRCIDSKDHNSYCTTHFVKALTDGCGAAMRIRITDTCVCVLSRAVNR 240

```

DB 181 DPNPVDSCGKIDSKHNSYCTTHTFEVKALTMDCQQAAMRFIRIDPACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

RESULT 9  
 AAB66929  
 ID AAB66929 standard; Protein: 241 AA.

AC AAB66929;

DT 17-APR-2001 (first entry)

DE Human NGF.

XX Human: neuroprotective; neuronal factor; NF; neurotrophin-3; NT-3;  
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;  
 KM Huntington's chorea; nerve damage; nerve growth factor; NGF.

OS Homo sapiens.

PN US6174701-B1.

PD 16-JAN-2001.

PE 31-MAY-1995; 95US-0455741.

PR 15-MAR-1990; 90US-0494024.

PR 31-JAN-1995; 95US-0381030.

PR 12-DEC-1989; 89US-0449811.

PA (GETH ) GENENTECH INC.

PI Rosenthal A, Winslow JM;

DR WPI: 2001-201803/20.

XX New nucleic acid encoding a neuronal factor (rat precursor  
 PT neurotrophin-3; NT-3), useful in the recombinant preparation of NT-3,  
 PT which is useful for enhancing the survival of nerve cells and treating  
 PT neurodegenerative diseases -  
 PS Disclosure: Fig 3; 18pp; English.

XX The present invention relates to neuronal factor (NF; also known as  
 CC neurotrophin-3/NT-3; see AAF55829-AAF55830 and AAB66927-AA66928). NF  
 CC is useful in treating neurodegenerative diseases, e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's chorea and other conditions  
 CC characterised by necrosis or loss of neurons. NF is also useful for  
 CC treating damaged nerves, e.g. nerves damaged by traumatic conditions such  
 CC as burns or wounds. The present sequence is human nerve growth factor  
 CC (NGF), which was used in a sequence homology alignment with human NF  
 CC protein.

XX Sequence 241 AA;

Query Match 99.5%; Score 1270; DB 22; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.3e-134; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0;

OY 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLOHSIDTLARRASAPAAATA 61  
 DB 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLOHSIDTLARRASAPAAATA 60  
 OY 62 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 121  
 DB 61 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 120  
 OY 122 RSSSHPIFRGSEFVCDSSVWVGDKTATDIDKEEVNVLGEVAINNSVFKOYFEETKCR 181  
 DB 121 RSSSHPIFRGSEFVCDSSVWVGDKTATDIDKEEVNVLGEVAINNSVFKOYFEETKCR 180

OY 182 DPNPVDSCGKIDSKHNSYCTTHTFEVKALTMDCQQAAMRFIRIDPACVLSRAVRR 241  
 DB 181 DPNPVDSCGKIDSKHNSYCTTHTFEVKALTMDCQQAAMRFIRIDPACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

RESULT 10  
 AAE18904  
 ID AAE18904 standard; Protein: 241 AA.

AC AAE18904;

DT 21-MAY-2002 (first entry)

DE Human beta nerve growth factor (NGF) protein.

XX Human: nerve growth factor; NGF; neurotrophin; cholinergic neuron;  
 KW gene therapy; neuroprotective; Alzheimer's disease; Parkinson's disease;  
 KM neurodegenerative condition; ALS; amyotrophic lateral sclerosis.

OS Homo sapiens.

PN WO200207774-A2.

PD 31-JAN-2002.

PE 17-MAY-2001; 2001WO-US16122.

PR 19-JUL-2000; 2000US-0620174.

PA (REGC ) UNIV CALIFORNIA.

PI Tuszyński MH;

DR WPI: 2002-195846/25.

DR N-PSDB: AAD30144.

XX Delivering therapeutic neurotrophin to targeted defective, diseased or  
 PT damaged cholinergic neurons, useful for treating neurodegenerative  
 PT disease, comprises administering a neurotrophin encoding transgene into  
 PT the brain -  
 PS Example 1; Fig 2; 38pp; English.

XX The invention relates to a method for delivering therapeutic neurotrophin  
 CC to targeted defective, diseased or damaged cholinergic neurons in  
 CC the mammalian brain. The method comprises delivering a neurotrophic  
 CC composition comprising a neurotrophin encoding transgene into one or more  
 CC delivery sites within a region of the brain containing targeted neurons.  
 CC The method is useful for treating neurodegenerative conditions such as  
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis  
 CC (ALS) in primates by stimulating the growth of neurons thus recovering  
 CC neurological function. The present sequence is human nerve growth factor  
 CC (NGF-2) protein which is a neurotrophin.

XX Sequence 241 AA;

Query Match 99.5%; Score 1270; DB 23; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.3e-134; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 0;

OY 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLOHSIDTLARRASAPAAATA 61  
 DB 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLOHSIDTLARRASAPAAATA 60  
 OY 62 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 121  
 DB 61 ARVAGOTRNTITVDPRLFFKKRLRSRVLESTOPPREADTODLDFEYGAAPFNRTHRSK 120

OY 122 RSSHPHFRGSEVCDVSVWVGDKTTATDINGKEVNVLGEVINNSVFKOYFEETKCR 181  
 DB 121 RSSHPHFRGSEVCDVSVWVGDKTTATDINGKEVNVLGEVINNSVFKOYFEETKCR 180  
 OY 182 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARR 241  
 DB 181 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARR 240  
 OY 242 A 242  
 DB 241 A 241

## RESULT 11

ABB04994  
 ID ABB04994 standard; Protein: 241 AA.  
 AC ABB04994;

19-MAR-2002 (first entry)

Human beta nerve growth factor protein.

Human: nerve growth factor 2; beta nerve growth factor; NGF-2; NT-3;  
 neurotrophin-3; nervous system growth factor; neuronal atrophy;  
 aging; brain; axonal growth; neuron; neurotrophic; neuroprotective;  
 anti-aging; cholinergic neuron growth stimulator; gene therapy.

Homo sapiens.

US2001043920-A1.

22-NOV-2001.

05-DEC-2000; 2000US-0730790.

15-APR-1998; 98US-0060543.

(TUSZ/) TUSZYNSKI M H.

(BLES/) BLESCH A.

Tuszyński MH, Blesch A;

WPI: 2002-105567/14.

N-PSDB; ABA92503.

Ameliorating neuronal atrophy and loss of accompanying normal aging

comprises delivering a transgene encoding a growth factor to a

mammalian brain to stimulate axon growth in cholinergic neurons -

Disclosure; Fig 6 1-2; 18pp; English.

The present invention describes a method for ameliorating neuronal

atrophy and loss of accompanying normal aging in the mammalian brain.

The method comprises delivering a growth factor (GF)-encoding transgene

to preselected delivery sites in the brain, so that the encoded GF is

expressed in the brain and stimulates axonal growth in targeted

GF-receptive neurons. The growth factor has neurotrophic, neuroprotective

and anti-aging activities, and can be used as a cholinergic neuron

growth stimulator and in gene therapy. The method is used to

ameliorating neuronal atrophy and loss of accompanying normal aging, in

the human brain. The present sequence represents human beta nerve growth

factor, which is given in the exemplification of the present invention.

Sequence 241 AA.

Query Match

Best Local Similarity 99.5%; Score 1270; DB 23; Length 241;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 61

DB 1 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 60

OY 62 ARVAGOTRNTVDPRLFKRRRLRSRVLSTOPPREADTODLDFEYGAAPFRNRHSR 121  
 DB 61 ARVAGOTRNTVDPRLFKRRRLRSRVLSTOPPREADTODLDFEYGAAPFRNRHSR 120  
 OY 122 RSSHPHFRGSEVCDVSVWVGDKTTATDINGKEVNVLGEVINNSVFKOYFEETKCR 181  
 DB 121 RSSHPHFRGSEVCDVSVWVGDKTTATDINGKEVNVLGEVINNSVFKOYFEETKCR 180  
 OY 182 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARR 241  
 DB 181 DPNPVDSCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRKAARR 240  
 OY 242 A 242  
 DB 241 A 241

## RESULT 12

AAP40038  
 ID AAP40038 standard; Protein: 245 AA.

25-JAN-1992 (first entry)

Sequence encoded by portion of human beta-nerve growth factor

(NGF) chromosomal gene which includes an exon.

Nerve damage; therapy.

Homo sapiens.

EP121338-A.

10-OCT-1984.

02-MAR-1984; 84EP-0301377.

03-MAR-1983; 83US-0471962.

(GEHT) GENENTECH INC.

Gray AM, Ullrich A;

WPI: 1984-251909/41.

N-PSDB; AAN40033.

Human beta-nerve growth factor free from other proteins - obtd.

by recombinant DNA techniques for treating nerve damage

Example; Fig 5; 42pp; English.

The inventors claim human beta-nerve growth factor (NGF) free from

other proteins of human origin. Also claimed are the DNA sequence

encoding human beta-NGF operably linked with a DNA sequence capable

of effecting its expression in a recombinant host cell; a replicable

expression vector contg. the DNA; and host cells transformed with

the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using

the plasmid, larger amounts of pure beta-NGF are obtainable than by

extr. of natural materials, see e.g. EP-2139.

Sequence 245 AA;

Query Match

Best Local Similarity 99.5%; Score 1270; DB 5; Length 245;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 61

DB 5 MSMLFTTLTAFLIGIOAEPRHSESNVPAGHTIPQVHMTKLOHSLDTALRRARSAPAAIA 64

OY 62 ARVAGOTRNTVDPRLFKRRRLRSRVLSTOPPREADTODLDFEYGAAPFRNRHSR 121

```

Db 65 ARVAGOTRNTITVDPRLFKRRRLSPRVLFSTQPPREADTDLDLFEVGAAPFNRTRSK 124
Oy 122 RSSSHPIFHNGEVSVCDSVSWVWGDKTTATDICKKEVNVLGENVINNSVFQYFEETKCR 181
Db 125 RSSSHPIFHNGEVSVCDSVSWVWGDKTTATDICKKEVNVLGENVINNSVFQYFEETKCR 184
Oy 182 DPNPVDSCGCGIDSKHMHNSYCTTHTFEVKALTMDCQKAAAFRIRIDTACVCLSRKAVRR 241
Db 185 DPNPVDSCGCGIDSKHMHNSYCTTHTFEVKALTMDCQKAAAFRIRIDTACVCLSRKAVRR 244
Oy 242 A 242
Db 245 A 245

RESULT 13
AAR45241
ID AAR45241 standard; Protein: 307 AA.
AC AAR45241;
D7 20-JUN-1994 (first entry)
DE Human pre-pro nerve growth factor.
KM Mature: beta-nerve growth factor; pre-pro portion;
KW expression; NGF; hNGF; treatment; Alzheimer's Disease.
OS Homo sapiens.
FH Key
FT Peptide 1..187
FT /note="signal peptide"
FT Peptide 188..307
FT /note="mature peptide"
PN US5272063-A.
PD 21-DEC-1993.
PF 20-JUN-1989; 89US-0383118.
PR 22-NOV-1988; 88US-0274878.
PR 20-JUL-1989; 89US-0383118.
PA (SYNT) SYNTEX USA INC.
PI Baecher PA, Barnett JW, Burszky-n-petlegrew H, Chan HM, Nguyen BT;
PI Ward C;
PI
XX WPI: 1993-413401/51.
XX N-PSDB: AA054283.
XX
PT Prodn. of active mature human beta-nerve growth factor in insect
PT cells - using baculovirus expression system, and potential use of
PT recombinant hNGF in treatment of Alzheimer's disease
XX
PS Disclosure: fig 1: 23pp: English.
XX
CC The sequence is that of human pre-pro nerve growth factor
CC which was used in a method of producing biologically active
CC mature human beta-nerve growth factor in insect cells.
XX
SQ Sequence 307 AA:
Query Match 99.28; Score 1267; DB 14; Length 307;
Best Local Similarity 99.68; Pred. No. 4.2e-134;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 2 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTIPQVHNTKLQSLDTALRARSAPAAIA 61
Db 67 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTIPQVHNTKLQSLDTALRARSAPAAIA 126

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Oy 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLFSTQPPREADTDLDLFEVGAAPFNRTRSK 121
Db 127 ARVAGOTRNTITVDPRLFKRRRLSPRVLFSTQPPREADTDLDLFEVGAAPFNRTRSK 186
Oy 122 RSSSHPIFHNGEVSVCDSVSWVWGDKTTATDICKKEVNVLGENVINNSVFQYFEETKCR 181
Db 187 RSSSHPIFHNGEVSVCDSVSWVWGDKTTATDICKKEVNVLGENVINNSVFQYFEETKCR 246
Oy 182 DPNPVDSCGCGIDSKHMHNSYCTTHTFEVKALTMDCQKAAAFRIRIDTACVCLSRKAVRR 241
Db 247 DPNPVDSCGCGIDSKHMHNSYCTTHTFEVKALTMDCQKAAAFRIRIDTACVCLSRKAVRR 306
Oy 242 A 242
Db 307 A 307

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RESULT 14
AAB67865
ID AAB67865 standard; Protein: 241 AA.
AC AAB67865;
D7 29-JUN-2001 (first entry)
DE Amino acid sequence of a human polypeptide designated PTMA-8.
KM PTMA: immune deficiency; infection; autoimmune disorder; wound closure;
KW connective tissue disease; multiple sclerosis; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer;
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
KW insulin dependent diabetes mellitus; graft-versus-host disease;
KW autoimmune inflammatory eye disease; gut protection; gut regeneration;
KW fibrosis; reperfusion injury; systemic cytokine damage.
XX
OS Homo sapiens.
PN WO200123572-A2.
PD 05-APR-2001.
PF 29-SEP-2000; 2000WO-US41035.
PR 30-SEP-1999; 99US-0156745.
PR 06-OCT-1999; 99US-0158942.
PR 13-OCT-1999; 99US-0158248.
PR 06-DEC-1999; 99US-0169344.
PR 29-JUN-2000; 2000US-0215048.
PA (CURA-) CURAGEN CORP.
PI Prayaga SK, Vernet C, Shinkets RA, Burgess C, Spletak KA;
PI
XX WPI: 2001-273512/28.
XX N-PSDB: AAF80462.
XX
PT Novel polypeptides termed PTMAx, and nucleic acids encoding PTMAx,
PT useful for detecting and treating diseases caused immune deficiencies -
XX
PS Claim 1: Page 20-22: 128pp: English.
XX
CC The present sequence represents a PTMA-8 (not defined) polypeptide. The
CC sequence is derived from clone A1049825. The polypeptide is 26958.5
CC daltons. PTMA polynucleotides and polypeptides are used in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, the disease selected from a pathology associated with
CC PTMA. They may be useful in the treatment of various immune deficiencies
CC and disorders. These immune deficiencies may be genetic or caused by
CC viral as well as bacterial or fungal infections or may result from
CC autoimmune disorders. Autoimmune disorders which may be treated using
CC PTMA include, for example, connective tissue disease, multiple sclerosis,
CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

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CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin  
CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease  
CC and autoimmune inflammatory eye disease. Additionally PTMA may also be  
CC useful to promote better or faster closure of non-healing wounds,  
CC including pressure ulcers, ulcers associated with vascular insufficiency,  
CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for  
CC gut protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissue, and conditions resulting from  
CC systemic cytokine damage.

XX Sequence 241 AA:

Query Match 99.18; Score 1266; DB 22; Length 241;  
Best Local Similarity 99.68; Pred. No. 3.8e-134;  
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIOAEPSSESVPAGHTIPQVHMTKLQHSLODALARASAPAAATA 61  
DB 1 MSMLFTLTITAFILGIOAEPSSESVPAGHTIPQVHMTKLQHSLODALARASAPAAATA 60  
OY 63 ARVAGQTNITVDPRLFKRLRSRVLSTQPPREAAOTQDDLFVCGAAPPNRTNRSK 121  
DB 61 ARVAGQTNITVDPRLFKRLRSRVLSTQPPREAAOTQDDLFVCGAAPPNRTNRSK 120  
OY 122 RSSHPITFRGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFKOYFETKCR 181  
DB 121 RSSHPITFRGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFKOYFETKCR 180  
OY 182 DPNVDSGCRGIDSKHNSCTTHTFVKALTMGKQAAWRIRIDTACVCLSKRAVR 241  
DB 181 DPNVDSGCRGIDSKHNSCTTHTFVKALTMGKQAAWRIRIDTACVCLSKRAVR 240  
OY 242 A 242  
DB 241 A 241

## RESULT 15

AAR37799  
ID AAR37799 standard; Protein: 307 AA.

XX AAR37799;  
XX 29-SEP-1993 (first entry)

XX Human NGF.

XX Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;  
XX BDNF; chimera; fusion; mouse; nerve growth factor; peripheral;  
XX central; precursor; nervous system.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..187

XX Protein 188..307

XX /note="Mature NGF"

XX MO9310150-A.

XX 27-MAY-1993.

XX 13-NOV-1992: 92MO-US09792.

XX 14-NOV-1991: 91US-0792492.

XX (AMGE-) AMGEN.

XX (REG-) REGENERON PHARM INC.

XX Giles D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;

XX WPI: 1993-182492/22.

DR N-PSDB; AAQ42571.

XX Eukaryotic expression of neurotrophins - using prepro region of a  
PT different neurotrophin for more efficient post-translational  
XX processing

PS Disclosure; Fig 4: 80pp; English.

XX This sequence represents human nerve growth factor (NGF). The protein  
CC encoded by this sequence promotes the development of the peripheral  
CC nervous system and also influences the development and maintenance of  
CC specific populations of neurons in the central nervous system. Two  
CC major transcripts from the NGF gene result in a "long" and "short" NGF  
CC prepeptide. The "short" precursor contains a conventional signal  
CC sequence at the N-terminus which flanks the pro-region. The "long"  
CC precursor contains an additional "pro-region" at its N-terminal. No  
CC functional distinction has been elucidated between the "long" and  
CC "short" forms. Characteristics of NGF, such as isoelectric point and  
CC primary structure, are very similar to brain derived neurotrophic  
CC factor (BDNF). The NGF coding sequence may be used in the  
CC construction of a chimeric nucleic acid molecule to encode a prepro-  
CC NGF/BDNF chimera (see also AAQ42568-69).

XX Sequence 307 AA:

Query Match 99.18; Score 1266; DB 14; Length 307;  
Best Local Similarity 99.68; Pred. No. 5.5e-134;  
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIOAEPSSESVPAGHTIPQVHMTKLQHSLODALARASAPAAATA 61  
DB 67 MSMLFTLTITAFILGIOAEPSSESVPAGHTIPQVHMTKLQHSLODALARASAPAAATA 126  
OY 63 ARVAGQTNITVDPRLFKRLRSRVLSTQPPREAAOTQDDLFVCGAAPPNRTNRSK 121  
DB 127 ARVAGQTNITVDPRLFKRLRSRVLSTQPPREAAOTQDDLFVCGAAPPNRTNRSK 186  
OY 122 RSSHPITFRGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFKOYFETKCR 181  
DB 187 RSSHPITFRGEFSVCDVSVMVGDKTTATDINGKENVVLGEVINNSVFKOYFETKCR 246  
OY 182 DPNVDSGCRGIDSKHNSCTTHTFVKALTMGKQAAWRIRIDTACVCLSKRAVR 241  
DB 247 DPNVDSGCRGIDSKHNSCTTHTFVKALTMGKQAAWRIRIDTACVCLSKRAVR 306  
OY 242 A 242  
DB 307 A 307

Search completed: December 2, 2002, 15:08:37  
Job time : 50.2298 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:43 : Search time 19.2919 Seconds  
(Without alignments)  
1205.921 Million cell updates/sec

Title: US-10-072-681-1

Sequence: 1277  
1 PMSMLFTLTATLIGIAQAE.....FIRIDPACVCLSRRAVRA 242

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1370	99.5	286 1	NGHUBM
2	1124	88.0	229 2	I46614
3	1107	86.7	245 2	I56570
4	1096	85.8	307 1	NGMSMG
5	1092	85.5	241 2	JL0097
6	1073	84.0	303 1	NGRTBA
7	788.5	61.7	243 2	A26311
8	773	60.5	235 2	S14481
9	675.5	52.9	243 2	I51193
10	658	51.5	125 2	A26312
11	649	50.8	246 2	A39218
12	484	37.9	117 2	I51709
13	481.5	37.7	194 2	I51709
14	481.5	37.7	257 2	C40304
15	472	37.0	258 2	S09155
16	471.5	36.9	257 2	I50400
17	471	36.9	282 2	A35781
18	455.5	35.4	116 2	NGNXTI
19	446.5	35.1	116 2	A58566
20	426	33.4	286 2	S50855
21	365	28.6	247 2	A40304
22	364	28.5	249 2	B40304
23	360	28.2	249 2	S12555
24	358.5	28.1	252 2	A30361
25	348.5	27.3	248 2	JC6183
26	343	26.9	236 2	JH0400
27	337.5	26.4	210 2	A42587
28	335	26.2	269 2	I51708
29	330.5	25.9	209 2	B42687

30	323.5	25.3	114	2	I84765	brain-derived neur
31	316.5	24.8	114	2	I50606	brain-derived neur
32	307.5	24.1	114	2	I51599	brain-derived neur
33	84.5	6.6	5126	2	S40450	ryanodine receptor
34	83	6.5	397	2	S52783	aspartic proteases
35	80	6.3	835	2	C97322	probable alpha-ara
36	79.5	6.2	749	2	E86774	hypothetical prote
37	79	6.2	807	2	A53225	ecdysone-induced p
38	79	6.2	1095	2	T24061	hypothetical prote
39	78.5	6.1	513	2	A12555	hypothetical prote
40	78.5	6.1	701	2	T52384	hypothetical prote
41	78.5	6.1	742	2	T43520	condensin complex
42	78.5	6.1	1076	2	D82083	carbamoyl phosphat
43	78.5	6.1	1084	2	B64088	hemoglobin-binding
44	78.5	6.1	1609	2	E87243	probable cation tr
45	78	6.1	323	2	S69647	hypothetical prote

## ALIGNMENTS

## RESULT 1

NGHUBM  
nerve growth factor beta chain precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-Feb-1984 #sequence: revision 19-Feb-1984 #text\_change 18-Jun-1999  
C:Accession: A01399; S10253  
R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.  
Nature 303, 821-825, 1983  
A:Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo  
A:Reference number: A93305; M0ID:83244969; PMID:6688123  
A:Accession: A01399  
A:Molecule type: DNA  
A:Residues: 1-286 <B0R>  
R:Berzani, G.; Pizzuti, A.; Ruggeri, E.I.; Fallini, A.; Sillani, V.; Sidoli, A.; Scarla  
Nucleic Acids Res. 18, 4020, 1990  
A:Title: cDNA sequence of human beta-NGF.  
A:Reference number: S10253; M0ID:90326556; PMID:2374737  
A:Accession: S10253  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 46-286 <B0R>  
A:Cross-references: EMBL:X52599; M0D:929476; P0DN:CNA36832.1; P0D:929477  
C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and  
nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels  
C:Genetics:  
A:Gene: GDB:NGFB  
A:Cross-references: GDB:120233; OMIM:162030  
A:Map position: 1p13.1-1p13.1  
C:Complex: nerve growth factor is composed of two alpha chains, two beta chains, and  
C:Keywords: glycoprotein; growth factor; submandibular gland  
F:1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>  
F:167-284/Product: nerve growth factor beta chain #status predicted <MAP>  
F:26,114,159,211/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:181-246,224-274,234-276/Disulfide bonds: #status predicted

Query Match 99.5%; Score 1270; DB 1; Length 286;  
Best Local Similarity 100.0%; Pred. No. 6, 2e-112;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	MSMLFTLTATLIGIAQAEPSHESVNPAGHTIPQVHTKLOHSLDTLRASAPAAATA	61
DB	46	MSMLFTLTATLIGIAQAEPSHESVNPAGHTIPQVHTKLOHSLDTLRASAPAAATA	105
QY	62	ARYAGCTRNITVDPRLEFKRRLSRPVLFSTQPREAADTODLFEVGAAPFNRTNRSK	121
DB	106	ARYAGCTRNITVDPRLEFKRRLSRPVLFSTQPREAADTODLFEVGAAPFNRTNRSK	165
QY	122	RSSSHPIFRGFSVCDSDSVVWGDKTATDINKKEVNVGGEYNNINSVKQFFETKCR	181
DB	166	RSSSHPIFRGFSVCDSDSVVWGDKTATDINKKEVNVGGEYNNINSVKQFFETKCR	225

Oy 182 DPNPVDGCGRGIDSKHNSYCTTHTFVKALITMDGKQAAAFRIIDTACVLSRKAARR 241  
|||  
Db 226 DPNPVDGCGRGIDSKHNSYCTTHTFVKALITMDGKQAAAFRIIDTACVLSRKAARR 285  
Oy 242 A 242  
Db 286 A 286

## RESULT 2

146614  
nerve growth factor B - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: I46614  
R:LabId-Manealis, Y.; Mellink, C.; Yerle, M.; Gellin, J.  
Cytogenet. Cell Genet. 67, 120-125, 1994  
A>Title: A new marker (NGFB) on pig chromosome 4, isolated by using consensus sequence  
A:Reference number: I46614; MUID:94313891; PMID:8039422  
A:Accession: I46614  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-229 <LAH>  
A:Cross-references: GB:U31898; NID:9476732; PIDN:AAA21301.1; PID:9533771  
C:Genetics:  
A:Gene: NGFB  
C:Superfamily: nerve growth factor beta chain

Query Match 88.0%; Score 1124; DB 2; Length 229;  
Best Local Similarity 92.6%; Pred. No. 2,7e-98;  
Matches 212; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Oy 14 LGIOAEPSHESNVPAGHTIPQVHTKLOHSLDTRALRARSAPAAIAARVACQTNITV 73  
|||  
Db 1 LGIOAEPTESNVPAGHAIPQAHHTKLOHSLDTRALRARSAPAGANSARVACQTNITV 60  
Oy 74 DPLFLFKRLRSPRVLFSTOPEAADTODLDFEVGGAAPFNRTNRKSSSHPIRHGE 133  
|||  
Db 61 DPLFLFKRLRSPRVLFSTOPEAADTODLDFEVGGAAPFNRTNRKSSSHPIRHGE 120  
Oy 134 FSVCDVSVMGDKTTATDIDGKEVNVGGEVNNVSFKQFFETKCRDPNPDSCRG 193  
|||  
Db 121 FSVCDVSVMGDKTTATDIDGKEVNVGGEVNNVSFKQFFETKCRDPNPDSCRG 180  
Oy 194 DSKHNSYCTTHTFVKALITMDGKQAAAFRIIDTACVLSRKAARRA 242  
|||  
Db 181 DSKHNSYCTTHTFVKALITMDGKQAAAFRIIDTACVLSRKAARRA 229

## RESULT 3

136570  
beta-nerve growth factor - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I36570  
R:Wittmore, S.R.; Friedman, P.L.; Larhammar, D.G.; Pettersson, H.; Gonzalez-Carvajal, M.;  
J. Neurosci. Res. 20, 403-410, 1988  
A>Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippo  
A:Reference number: I36570; MUID:88037223; PMID:3184206  
A:Accession: I36570  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-245 <RES>  
A:Cross-references: GB:M36589; NID:9205691; PIDN:AAA1697.1; PID:9205692  
C:Superfamily: nerve growth factor beta chain

Query Match 86.7%; Score 1107; DB 2; Length 245;  
Best Local Similarity 85.8%; Pred. No. 1.2e-96;  
Matches 205; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Oy 2 MSMLFTLTATLIGVQAEPTDSNVPEGDSVPEAHMTKLOHSLDTRALRARSAPAAIA 61  
|||  
Db 2 MSMLFTLTATLIGVQAEPTDSNVPEGDSVPEAHMTKLOHSLDTRALRARSAPAAIA 61

Db 5 MSMLFTLTATLIGVQAEPTDSNVPEGDSVPEAHMTKLOHSLDTRALRARSAPAAIA 64  
Oy 62 ARVAGOTRNTVDPRLFKRRRLSPRVLFSTOPEAADTODLDFEVGGAAPFNRTNRK 121  
|||  
Db 65 ARVAGOTRNTVDPRLFKRRRLSPRVLFSTOPEAADTODLDFEVGGAAPFNRTNRK 124  
Oy 122 RSSHPPIFRNGERSVCDVSVMGDKTTATDIDGKEVNVGGEVNNVSFKQFFETKCR 181  
|||  
Db 125 RSSHPPIFRNGERSVCDVSVMGDKTTATDIDGKEVNVGGEVNNVSFKQFFETKCR 184  
Oy 182 DPNPVDGCGRGIDSKHNSYCTTHTFVKALITMDGKQAAAFRIIDTACVLSRKAARR 241  
|||  
Db 185 DPNPVDGCGRGIDSKHNSYCTTHTFVKALITMDGKQAAAFRIIDTACVLSRKAARR 244

## RESULT 4

NGMSMG  
nerve growth factor beta chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Nov-1980 #sequence\_revision 19-Feb-1984 #text\_change 21-Jul-2000  
C:Accession: A93301; A93305; A90366; I49689; I52891; A01400; I49690  
R:Scott, J.; Selby, M.; Urdeda, M.; Quiroga, M.; Bell, G.I.; Rutter, W.J.  
Nature 302, 538-540, 1983  
A>Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse  
A:Reference number: A93301; MUID:83167518; PMID:6336309  
A:Accession: A93301  
A:Molecule type: mRNA  
A:Residues: 1-307 <SCO>  
A:Cross-references: GB:V00836; NID:953364; PIDN:CAA24221.1; PID:953365  
R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.  
Nature 303, 821-825, 1983  
A>Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo  
A:Reference number: A93305; MUID:83244569; PMID:6688123  
A:Accession: A93305  
A:Molecule type: mRNA  
A:Residues: 1-307 <ULN>  
A:Cross-references: GB:K01759; NID:9200051; PIDN:AAA39820.1; PID:9387495  
A>Note: these authors believe that Met-67 is probably the amino-terminal residue and  
R:Angelaki, R.H.; Hermanson, M.A.; Bradshaw, R.A.  
Biochemistry 12, 100-113, 1973  
A>Title: Amino acid sequences of mouse 2.5S nerve growth factor. II. Isolation and ch  
A:Reference number: A90366; MUID:73075048; PMID:4566923  
A:Accession: A90366  
A:Molecule type: protein  
A:Residues: 188-216, 'N', 218-305 <ANG>  
R:Selby, M.J.; Edwards, R.; Sharp, F.; Rutter, W.J.  
Mol. Cell. Biol. 7, 3057-3064, 1987  
A>Title: Mouse nerve growth factor gene: Structure and expression.  
A:Reference number: I49689; MUID:88038855; PMID:3670305  
A:Accession: I49689  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-307 <RES>  
A:Cross-references: GB:M17298; NID:9193493; PIDN:AAA37687.1; PID:9467311  
R:Ullrich, A.; Gray, A.; Berman, C.H.; Consensus, L.; Dull, T.J.  
Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983  
A>Title: Sequence homology of human and mouse beta-NGF subunit genes.  
A:Reference number: I52891; MUID:84206565; PMID:6327169  
A:Accession: I52891  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-307 <RES>  
A:Cross-references: GB:M14805; NID:9200053; PIDN:AAA39821.1; PID:9200054  
C:Comment: The active molecule is a dimer of identical chains associated by noncovalent  
N/C sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels  
C:Genetics:  
A:Gene: NGFB  
A:Introns: 21/2; 62/3  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: glycoprotein; growth factor; homodimer  
F:1-187/Domain: signal sequence and propeptide #status predicted <SIG>  
F:188-305/Product: nerve growth factor beta chain #status experimental <MAT>

F:135,180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:202-267,245-295,255-297/Disulfide bonds: #status experimental  
 F:332/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 85.8%; Score 1096; DB 1; Length 307;  
 Best Local Similarity 85.0%; Pred. No. 1,7e-95;  
 Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAHHTIPQVHMTKLQHSIDTALRRASAPAAATA 61  
 DB 67 MSMLFTLTITAFILGIGIAEPHSESNVPAHHTIPQVHMTKLQHSIDTALRRASAPAAATA 126  
 OY 62 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTPPREAADTODLDFEVGAAPFNRTHRSK 121  
 DB 127 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTPPREAADTODLDFEVGAAPFNRTHRSK 186  
 OY 122 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNLGVEVNNNSVFKOFFETKCR 181  
 DB 187 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNLGVEVNNNSVFKOFFETKCR 246  
 OY 182 DPNPVDSCGRCIDSKHNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAARR 241  
 DB 247 ASNPVESCRCIDSKHNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAARR 306

## RESULT 5

nerve growth factor beta chain precursor - guinea pig  
 C:Species: *Cavia porcellus* (guinea pig)  
 C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 15-Mar-1996  
 C:Accession: J10097

R:Schwarz, M.A.; Fisher, D.; Bradshaw, R.A.; Isackson, P.J.  
 J. Neurochem. 52, 1203-1209, 1989  
 A>Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig  
 A:Reference number: J10097; MUID:89177243; PMID:2926597

A:Accession: J10097  
 A:Molecule type: mRNA  
 A:Residues: 1-241 <SCH>  
 A>Note: the authors translated the codon GCU for residue 214 as Asp  
 C:Gene(s):  
 A:Gene: Beta-MGF  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor; hormone  
 F:1-121/Domain: propeptide #status predicted <PRO>  
 F:122-241/Product: nerve growth factor beta chain #status predicted <MAT>  
 F:146-154/Region: receptor binding #status predicted  
 F:69,114/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.5%; Score 1092; DB 2; Length 241;  
 Best Local Similarity 86.2%; Pred. No. 2,9e-95;  
 Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAHHTIPQVHMTKLQHSIDTALRRASAPAAATA 61  
 DB 1 MSMLFTLTITAFILGIGIAEPHSESNVPAHHTIPQVHMTKLQHSIDTALRRASAPAAATA 60  
 OY 62 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTPPREAADTODLDFEVGAAPFNRTHRSK 121  
 DB 61 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTPPREAADTODLDFEVGAAPFNRTHRSK 120  
 OY 122 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNLGVEVNNNSVFKOFFETKCR 181  
 DB 121 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNLGVEVNNNSVFKOFFETKCR 180  
 OY 182 DPNPVDSCGRCIDSKHNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAARR 241  
 DB 181 DPNPVDSCGRCIDSKHNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAARR 240

## RESULT 6

nerve growth factor beta chain precursor - multimammate rat (*Mastomys natalensis*)  
 C:Species: *Mastomys natalensis*

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 18-Jun-1999  
 C:Accession: J10343

R:Fahnestock, M.; Bell, R.A.  
 Gene 69, 257-264, 1988  
 A>Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from *Rattus norvegicus*  
 A:Reference number: J10343; MUID:89172070; PMID:3234767

A:Accession: J10343  
 A:Molecule type: mRNA  
 A:Residues: 1-303 <FAH>  
 A:Cross-references: GB:M22748; NID:9202514; PIDN:AAA40599.1; PID:9202515  
 A>Note: It is uncertain whether Met-1 or Met-63 is the initiator  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor; homodimer; submaxillary gland  
 F:144-301/Product: nerve growth factor beta chain #status predicted <MAT>  
 F:131,176,241/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:198-263,241-291,251-293/Disulfide bonds: #status predicted

Query Match 84.0%; Score 1073; DB 1; Length 303;  
 Best Local Similarity 83.3%; Pred. No. 2,4e-93;  
 Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAHHTIPQVHMTKLQHSIDTALRRASAPAAATA 61  
 DB 63 MSMLFTLTITAFILGIGIAEPHSESNVPAHHTIPQVHMTKLQHSIDTALRRASAPAAATA 122  
 OY 62 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTPPREAADTODLDFEVGAAPFNRTHRSK 121  
 DB 123 ARVAGOTRNTITVDPRFLFKRRRLSPRYLFTSTPPREAADTODLDFEVGAAPFNRTHRSK 182  
 OY 122 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNLGVEVNNNSVFKOFFETKCR 181  
 DB 183 RSSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVNLGVEVNNNSVFKOFFETKCR 242  
 OY 182 DPNPVDSCGRCIDSKHNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAARR 241  
 DB 243 ARNPVESCRCIDSKHNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAARR 302

## RESULT 7

nerve growth factor beta chain precursor - chicken (fragment)  
 C:Species: *Gallus gallus* (chicken)  
 C>Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 21-Jul-2000  
 C:Accession: A26311; A24857; S00127; S12532

R:Ebdendal, T.; Larhammar, D.; Persson, H.  
 EMBO J. 5, 1483-1487, 1986  
 A>Title: Structure and expression of the chicken beta nerve growth factor gene.  
 A:Reference number: A26311; MUID:86300646; PMID:3017695

A:Accession: A26311  
 A:Molecule type: mRNA  
 A:Residues: 1-243 <EBE>  
 A:Cross-references: GB:X04003; NID:963697; PIDN:CAA27633.1; PID:91334740  
 R:Walon, D.; Perret, C.; Frechlin, N.; Keller, A.; Behar, G.; Brechet, P.; Aufferay, C.  
 FEBS Lett. 203, 82-86, 1986

A>Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription  
 A:Reference number: A24857; MUID:86248129; PMID:3720959  
 A:Accession: A24857  
 A:Molecule type: DNA  
 A:Residues: 118-243 <NIO>

A:Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:9222840; PIDN:BA00008.1; PI  
 R:Walon, D.; Becker-Andre, M.; Goeltz, R.; Heumann, R.; Shaw, A.; Thoenen, H.  
 EMBO J. 5, 1489-1493, 1986  
 A>Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation  
 A:Reference number: A26312; MUID:86300647; PMID:2427334  
 A:Accession: S00127  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA

A:Cross-references: GB:M26810; NID:9212446; PIDN:AAA48984.1; PID:9212447  
 R:Idanez, C.F.; Hallböök, F.; Ebdendal, T.; Persson, H.  
 EMBO J. 9, 1477-1483, 1990  
 A>Title: Structure-function studies of nerve growth factor: functional importance of  
 A:Reference number: S12532; MUID:90228346; PMID:2328722





Qy 178 TRCRDPNPVDSGCGIDSKHNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSRK 237  
Db 61 TRCRDPNPVDSGCGIDAKHNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSRK 120  
Qy 238 AVRA 242  
Db 121 TGORA 125

## RESULT 11

A:Accession: A59218  
C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 31-Mar-2000  
C:Accession: A59218; S13965  
R:Seiby, M.J.; Edwards, R.H.; Rutter, W.J.  
J. Neurosci. Res. 18, 293-298, 1987  
A:Title: Cobra nerve growth factor: structure and evolutionary comparison.  
A:Reference number: A59218; PMID:88090976; PMID:3694712  
A:Accession: A59218  
A:Molecule type: mRNA  
A:Residues: 1-246 <SELS>  
R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.  
FEBS Lett. 279, 38-40, 1991  
A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.  
A:Reference number: S13927; PMID:91138755; PMID:1995338  
A:Accession: S13965  
A:Molecule type: Protein  
A:Residues: 131-246 <IND>  
A:Reference number: 131-246 <IND>  
A:Experimental source: Venom  
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
C:Complex: homodimer  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: growth factor; homodimer; venom  
F:1-23/Domain: signal sequence status predicted <SIG>  
F:131-246/Product: nerve growth factor beta chain status experimental <ANT>  
F:144-208,186-236,196-238/Disulfide bonds: status predicted

Query Match 50.8%; Score 649; DB 2; Length 246;  
Best Local Similarity 50.8%; Pred. No. 1.6e-53;  
Matches 133; Conservative 30; Mismatches 69; Indels 8; Gaps 5;

Qy 2 MSMLTYLTALFLIGIOAEPHSESNVAG---HTIPGVHNTKLDHNSIDTLRRASAPA 57  
Db 6 MSMLTYLTALFLIGIOAEPHSESNVAG---HTIPGVHNTKLDHNSIDTLRRASAPA 57  
Qy 58 AATARVAGOT-RNIVDRLFKRLSPRYLSTOPPREAADTODLDFVGGADPFR 116  
Db 66 POKAEQELTANITIVDFKLFQKRFOSPRYLFSTOPLLSRDESEVF-LDMEDSLNR 124  
Qy 117 THNSKRSSHPITRNGEFSVCSVWVGDKTTATDINGKEVNYLGEVINNSVFKQYFF 176  
Db 125 NIRAAR-EDHPVHNLGEHSCVSAMV-TKTATDINGNTVTVMENVNLDNKKYKQYFF 182  
Qy 177 ETCKRDPNPVDSGCGIDSKHNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSR 236  
Db 183 ETCKRDPNPVDSGCGIDSKHNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSR 242  
Qy 237 K 237  
Db 243 K 243

## RESULT 12

A:Accession: S28161  
C:Species: Vipera russelli (Russell's viper)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S28161  
R:Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.  
Biochim. Biophys. Acta 1160, 287-292, 1992  
A:Title: Purification and amino-acid sequence of a nerve growth factor from the venom of  
A:Reference number: S28161; PMID:93120151; PMID:1477101

A:Accession: S28161  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-117 <KOY>  
C:Superfamily: nerve growth factor beta chain

Query Match 37.9%; Score 484; DB 2; Length 117;  
Best Local Similarity 37.9%; Pred. No. 2.2e-38;  
Matches 63; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

Qy 126 HPFRNGEFSVCSVWVGDKTTATDINGKEVNYLGEVINNSVFKQYFFETKCDPMP 185  
Db 1 HPFRNGEFSVCSVWVGDKTTATDINGKEVNYLGEVINNSVFKQYFFETKCDPMP 60  
Qy 186 VDSGCGIDSKHNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSRK 237  
Db 61 VDSGCGIDAKHNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSRK 112

## RESULT 13

A:Accession: S151709  
C:Species: Xiphophorus maculatus (southern platyfish)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: S151709; S28674  
R:Goetz, R.; Raulf, F.; Scharf, M.  
J. Neurochem. 59, 432-442, 1992  
A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and  
A:Reference number: S151708; PMID:92333301; PMID:1629719  
A:Accession: S151709  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-194 <GON>  
A:Cross-references: EMBL:X59941; NID:965277; PIDN:CAA42566.1; PID:965278  
C:Genetics:  
A:Gene: NGF  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: glycoprotein; growth factor  
F:1-14/Domain: signal sequence status predicted <SIG>  
F:15-79/Domain: signal sequence status predicted <PRO>  
F:80-194/Product: neuropeptide status predicted <PRO>  
F:90-155,133-183,143-185/Disulfide bonds: status predicted  
F:99/Binding site: carbohydrate (asn) (covalent) status predicted

Query Match 37.7%; Score 481.5; DB 2; Length 194;  
Best Local Similarity 37.7%; Pred. No. 7.2e-38;  
Matches 99; Conservative 13; Mismatches 39; Indels 17; Gaps 3;

Qy 72 TVDPRLFKRRLSPRYLSTOPPREAADTODLDFVGGADPFRTRSRKSSHPITFH 130  
Db 40 TVDPRLFKRRLSPRYLSTOPPREAADTODLDFVGGADPFRTRSRKSSHPITFH 83  
Qy 131 NGFVSVDVSVWVGDKTTATDINGKEVNYLGEVINNSVFKQYFFETKCDPMPVDSGC 190  
Db 84 NGFVSVDVSVWVGDKTTATDINGKEVNYLGEVINNSVFKQYFFETKCDPMPVDSGC 143  
Qy 191 RGDSKHNNSYCTTHTFVAKLMDGQQAAMRFRIDFACVLSRKA 238  
Db 144 LGIDARHNSHCTSHFTFVAKLMDGQQAAMRFRIDFACVLSRKS 191

## RESULT 14

A:Accession: C40304  
C:Species: Homo sapiens (man)  
C:Date: 03-Apr-1992 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999  
C:Accession: A36208; J010141; C40304; S10719; C60336  
R:Jones, K.R.; Ketchard, L.F.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990  
A:Title: Molecular cloning of a human gene that is a member of the nerve growth factor  
A:Reference number: A36208; PMID:91045937; PMID:2236018

A:Molecule type: DNA  
 A:Residues: 1-257 <CON>  
 A:Cross-references: GB:M37763; MID:9189300; PIDN:AAA5953.1; PID:9189301  
 R:Kosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nikolic  
 Neuron 4, 767-773, 1990  
 A:Title: Primary structure and biological activity of a novel human neurotrophic factor  
 A:Reference number: JH0141; MUID:90265727; PMID:2344409  
 A:Accession: JH0141  
 A:Molecule type: DNA  
 A:Residues: 1-257 <ROS>  
 R:Malompliere, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la Mc  
 Genomics 10, 558-568, 1991  
 A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struct  
 A:Reference number: A0304; MUID:91365361; PMID:1889806  
 A:Accession: C40304  
 A:Molecule type: DNA  
 A:Residues: 1-257 <MAI>  
 A:Cross-references: GB:M61180; MID:9189302; PIDN:AAA63231.1; PID:9189303  
 R:Kishino, Y.; Yoshimura, K.; Nakahama, K.  
 PNAS Intl. 266, 187-191, 1990  
 A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.  
 A:Reference number: S10719; MUID:90306351; PMID:2365067  
 A:Accession: S10719  
 A:Molecule type: mRNA  
 A:Residues: 1-257 <KAI>  
 A:Cross-references: GB:X53655; MID:9287794; PIDN:CAA37703.1; PID:9287795  
 R:Fanopoulos, G.D.; Malompliere, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton  
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990  
 A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways the  
 A:Reference number: A60536; MUID:9211157; PMID:1966766  
 A:Accession: C60536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-73, 'Q', 75-77, 'R', 79-108, 'T', 110-257 <YAN>  
 C:Genetics:  
 A:Gene: GDB:125917; OMIM:162660  
 A:Cross-references: GDB:125917; OMIM:162660  
 A:Map position: 12p13-12p13  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-138/Domain: propeptide #status predicted <PRO>  
 F:139-257/Product: neurotrophin-3 #status predicted <MAT>  
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 37.7%; Score 481.5; DB 2; Length 257;  
 Best local similarity 40.7%; Pred. No. 1e-37;  
 Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;  
 Oy 2 MSMLFTLTATLIGIOAEPSSESNVPAGHTIPQY-----HMTKIQHSID 46  
 Db 1 MSILFTVITLAIKGIQGNNDORSLEPDSLNLITLQADILKKNLSKQMDVKEHYQ 60  
 Oy 47 TALRNA-----RSAPPAALIAAVAGOTRNITVDPRLFK-KRRLSPRYLSTOPEA 98  
 Db 61 STLPKAEAPREPERGCPAKSAFOV-----IAMDTELLROQRVNSPVLSDSTPLEP 114  
 Oy 99 ADTODLDFEVGGAAPFNFTBRSKRSSHPIFHNGEFSVCDVSWVWGDKTATADIKGEV 158  
 Db 115 PPLYLMEIDYVGSPPVYANTRSRKRIAEHK-SHREYSVCDSESLWTDKSSAIDIRGHQV 173  
 Oy 159 MVLGENVINNSVFKQYFEETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GK 217  
 Db 174 TVLGEIKTGNSPVKQYFEYTRCKEARPVKNGCRGIDKHNNSQCKTSQTYVALTSNNK 233  
 Oy 218 QAAMRFIRIDTACVCLSRKAVR 240  
 Db 234 LVGNRMIRIDTSCVALSRKIGR 256

RESULT 15  
 S09155  
 neurotrophin-3 precursor - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
 A:Accession: S09155; S51179  
 R:Hohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.  
 Nature 344, 339-341, 1990  
 A:Title: Identification and characterization of a novel member of the nerve growth fa  
 A:Reference number: S09155; MUID:90190865; PMID:2314473  
 A:Accession: S09155  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-258 <HOH>  
 A:Cross-references: GB:X53257; MID:953451; PIDN:CAA37348.1; PID:953452  
 R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.  
 Eur. J. Biochem. 225, 995-1003, 1994  
 A:Title: Characterization of neurotrophin dimers and monomers.  
 A:Reference number: S51179; MUID:95045576; PMID:7957235  
 A:Accession: S51179  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:140-258/Product: neurotrophin-3 #status predicted <MAT>  
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 37.0%; Score 472; DB 2; Length 258;  
 Best local similarity 41.9%; Pred. No. 8e-37;  
 Matches 108; Conservative 33; Mismatches 97; Indels 20; Gaps 5;  
 Oy 2 MSMLFTLTATLIGIOAEPSSESNVPAGH-----TIPQYHMTKIQHSIDTAL----- 49  
 Db 1 MSILFTVITLAIKGIQGNNDORSLEPDSLNLITLQADILKKNLSKQMDVKEHYQ 60  
 Oy 50 -----RRASAPPAALIAAVAGOTRNITVDPRLFKRRLSPRYLSTOPEA 104  
 Db 61 STLPKAEAPREPERGCPAKSAFOV-----IAMDTELLROQRVNSPVLSDSTPLEP 120  
 Oy 105 DFEVGAAPNFTBRSKRSSHPIFHNGEFSVCDVSWVWGDKTATADIKGEV 163  
 Db 121 EDYVGNPVYANTRSRKRIAEHK-SHREYSVCDSESLWTDKSSAIDIRGHQV 179  
 Oy 164 VNINNSVFKQYFEETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GK 222  
 Db 180 IKTGNSPVKQYFEYTRCKEARPVKNGCRGIDKHNNSQCKTSQTYVALTSNNKLVGR 239  
 Oy 223 FIRIDTACVCLSRKAVR 240  
 Db 240 WIRIDTSCVALSRKIGR 257

Search completed: December 2, 2002, 15:13:57  
 Job time: 20.2919 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 9.92966 seconds

(without alignments)  
1010.837 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1277

Sequence: 1 PMSMTFTTLTAFLIGIOAE.....FTRIDACVLSRKAVARA 242

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1270	99.5	241	NGF_HUMAN
2	1124	88.0	229	NGF_PIG
3	1107	86.7	241	NGF_RAT
4	1106	86.6	221	NGF_BOVIN
5	1096	85.8	241	NGF_MOUSE
6	1092	85.5	241	NGF_CAVPO
7	1073	84.0	241	NGF_PRANA
8	788.5	61.7	243	NGF_CHICK
9	773	60.5	231	NGF_XENLA
10	675.5	52.9	243	NGF_XENLA
11	484	37.9	117	NGF_DABRR
12	481.5	37.7	194	NGF_XIPMA
13	481.5	37.7	257	NT3_HUMAN
14	474	37.1	260	NT3_XENLA
15	473.5	37.1	257	NT3_FELCA
16	472	37.0	258	NT3_MOUSE
17	471.5	36.9	257	NT3_CHICK
18	471	36.9	258	NT3_RAT
19	459.5	36.0	233	NT3_BRARE
20	449.5	35.2	116	NGF_NAJAT
21	445.5	34.9	116	NGF_NAJAT
22	372.5	29.2	140	NT7_CYPGA
23	365	28.6	247	BDNF_HUMAN
24	365	28.5	249	BDNF_HUMAN
25	363	28.4	255	BDNF_RAT
26	362	28.3	247	BDNF_CAVPO
27	361	28.3	247	BDNF_PROLO
28	361	28.3	247	BDNF_URSAR
29	360	28.2	249	BDNF_URSAR
30	358.5	28.1	252	BDNF_MOUSE
31	350	27.4	247	BDNF_PIG
32	348.5	27.3	248	BDNF_FELCA
33	347.5	27.2	246	BDNF_BOVIN
				BDNF_CHICK

34	343	26.9	236	1	NT4_XENLA	P24727 xenopus lae
35	338.5	26.5	270	1	BDNF_CYPGA	090332 cyprinus ca
36	337.5	26.4	210	1	NT5_HUMAN	P34130 homo sapien
37	335	26.2	269	1	BDNF_XIPMA	002133 xiphophorus
38	330.5	25.9	209	1	NT5_RAT	P34131 ratius norv
39	323.5	25.3	114	1	BDNF_MACMU	006225 macaca mula
40	307.5	24.1	114	1	BDNF_XENLA	P25432 xenopus lae
41	230	18.0	257	1	NT6B_HUMAN	P34133 homo sapien
42	227	17.8	257	1	NT6A_HUMAN	P34132 homo sapien
43	225	17.6	186	1	NT6G_HUMAN	P34134 homo sapien
44	190	14.9	42	1	NGF_VIPLE	P25428 vipera lede
45	136	10.6	154	1	NT3_CEREL	095150 cervus elap

ALIGNMENTS

RESULT 1	ID	NGF_HUMAN	STANDARD	PRT:	241 AA.
AC	P01138:	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Beta-nerve growth factor precursor (Beta-NGF).				
GN	NGF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
NP	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83244969; PubMed=6688123;				
RA	Ullrich A., Gray A., Berman C., Dull T.J.;				
RT	"Human beta-nerve growth factor gene sequence highly homologous to				
RL	that of mouse.";				
RL	Nature 303:821-825(1983).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84206565; PubMed=6327169;				
RA	Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;				
RT	"Sequence homology of human and mouse beta-NGF subunit genes.";				
RL	Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90326556; PubMed=2374737;				
RA	Borsani G., Pizzuti A., Ruggeri E.I., Fallini A., Siliani V.,				
RT	"CDNA sequence of human beta-NGF.";				
RL	Nucleic Acids Res. 18:4020-4020(1990).				
RP	SEQUENCE OF 178-219 FROM N.A.				
RX	TISSUE=Leukocyte;				
RA	MEDLINE=9122573; PubMed=2025430;				
RT	Hallböök F., Ibanez C.F., Persson H.;				
RL	"Evolutionary studies of the nerve growth factor family reveal a				
RL	novel member abundantly expressed in Xenopus ovary.";				
CC	Neuron 6:845-858(1991).				
CC	- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND				
CC	MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT				
CC	STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND				
CC	EMBRYONIC SENSORY NEURONS.				
CC	- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.				
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				

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CC EMBL: V01511; CAA24755.1;
DR EMBL: M21062; AAA59931.1;
DR EMBL: X52595; CAA56832.1;
DR PIR: A01399; NGHUBM.
DR PIR: S10253; S10253.
DR HSSP: P01139; 1BET.
DR Genew: HGNC:7808; NGFB.
DR MIM: 162030;
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD02052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1;
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT SIGNAL 1 18
FT PROPEP 19 121
FT CHAIN 122 241
FT DISULFID 136 201
FT DISULFID 179 229
FT DISULFID 189 231
FT CARBOHYD 69 69
FT CARBOHYD 114 114
SO SEQUENCE 241 AA; 26987 MW; CFIDB4DC6B736B0F CRC64;

Query Match 99.5%; Score 1270; DB 1: Length 241;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 241: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLTATFLGIGIAEPHSESNVPAGHTIPQVHTKQLQHSIDTALRRASAPAAATA 61
DB 1 MSMLFTLTATFLGIGIAEPHSESNVPAGHTIPQVHTKQLQHSIDTALRRASAPAAATA 60
OY 62 ARVAGOTRNTVDPPLFKRRRLSPRVLFSTOPPREAADTODLDFEYGAAPNRTHRSK 121
DB 61 ARVAGOTRNTVDPPLFKRRRLSPRVLFSTOPPREAADTODLDFEYGAAPNRTHRSK 120
OY 122 NSSHPPIHRCGFYSVCSVSWVGDKTTATDIDKGEVNLGEVINNSVFKYFFETKCR 181
DB 121 NSSHPPIHRCGFYSVCSVSWVGDKTTATDIDKGEVNLGEVINNSVFKYFFETKCR 180
OY 182 DNPVDSGCGRIGDSKHNMSYCTTHTTTPVKALTMDSKQAAMRFRTIDACVLSRAVRA 241
DB 181 DNPVDSGCGRIGDSKHNMSYCTTHTTTPVKALTMDSKQAAMRFRTIDACVLSRAVRA 240
OY 242 A 242
DB 241 A 241

RESULT 2
NGF_PIG STANDARD: PRT: 229 AA.
ID NGF_PIG
AC Q29074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RX MEDLINE=94313891; Pubmed=8039422;
RA Lahbib-Manais Y., Mellink C., Yexle M., Gellin J.;
RT "A new marker (NGFB) on pig chromosome 4, isolated by using a
RL cytogenet. Cell Genet. 67:120-125(1994).

```

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSOR NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC
DR EMBL: L31898; AAA21301.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR ProDom: PD02052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1;
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
FT MON_TER 1 1
FT SIGNAL <1 6
FT PROPEP 7 109
FT CHAIN 110 229
FT DISULFID 124 189
FT DISULFID 167 217
FT DISULFID 177 219
FT CARBOHYD 57 57
FT CARBOHYD 102 102
FT CARBOHYD 154 154
SO SEQUENCE 229 AA; 25275 MW; FE8B90771CBA3189 CRC64;

Query Match 88.0%; Score 1124; DB 1: Length 229;
Best Local Similarity 92.6%; Pred. No. 2e-99;
Matches 212: Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 14 LIGIOAEPHSESNVPAGHTIPQVHTKQLQHSIDTALRRASAPAAATAARVAGOTRNTV 73
DB 1 LIGIOAEPHSESNVPAGHTIPQVHTKQLQHSIDTALRRASAPAAATAARVAGOTRNTV 60
OY 74 DPLFKRRRLSPRVLFSTOPPREAADTODLDFEYGAAPNRTHRSSHPPIHRCGE 133
DB 61 DPLFKRRRLSPRVLFSTOPPREAADTODLDFEYGAAPNRTHRSSHPPIHRCGE 120
OY 134 FSVCSVSWVGDKTTATDIDKGEVNLGEVINNSVFKYFFETKCRDNPVDSGCGRI 193
DB 121 FSVCSVSWVGDKTTATDIDKGEVNLGEVINNSVFKYFFETKCRDNPVDSGCGRI 180
OY 194 DSKHNMSYCTTHTTTPVKALTMDSKQAAMRFRTIDACVLSRAVRA 242
DB 181 DSKHNMSYCTTHTTTPVKALTMDSKQAAMRFRTIDACVLSRAVRA 229

RESULT 3
NGF_RAT STANDARD: PRT: 241 AA.
ID NGF_RAT
AC P25427;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; Pubmed=3184206;

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RA Whittemore S.R., Friedman P.L., Lathamar D.G., Persson H.,  
 RA Gonzalez-Carvajal M., Holets V.R.:  
 RT "Rat beta-nerve growth factor sequence and site of synthesis in the  
 RT adult hippocampus.";  
 RL J. Neurosci. Res. 20:403-410(1988).  
 RM (2)  
 RP SEQUENCE OF 178-219 FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Layer;  
 RX MEDLINE-9122573; PubMed-2025430;  
 RA Hallboeok F., Ibanez C.F., Persson H.:  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary.";  
 RL Neuron 6:845-858(1991).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: M35589; AAA41697.1; ALT\_INIT.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KM Growth factor; Signal; 1.  
 FT SIGNAL 1 16  
 FT PROPEP 19 121 POTENTIAL.  
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.  
 FT DISULFID 136 201 BY SIMILARITY.  
 FT DISULFID 179 229 BY SIMILARITY.  
 FT DISULFID 189 231 BY SIMILARITY.  
 FT CARBOHYD 69 69 N-LINKED (GLCNAc... ) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAc... ) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAc... ) (POTENTIAL).  
 SQ SEQUENCE 241 AA; 27009 MW; 665f42371563213D CRC64;  
 Query Match 86.7%; Score 1107; DB 1; Length 241;  
 Best Local Similarity 85.8%; Pred. No. 8.7e-98;  
 Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;  
 Oy 2 MSMLFTLTAFVIGVAPHSSESNVPPGHTIPQVHTKLOHSLDTALRRARSAAPAAIA 61  
 Db 1 MSMLFTLTAFVIGVAPHSSESNVPPGHTIPQVHTKLOHSLDTALRRARSAAPAAIA 60  
 Oy 62 ARVAGOTRNITVDPRLFKRRRLRSRVLFSTOPPREADTODLDFEYGAAPFRTSRK 121  
 Db 61 ARVAGOTRNITVDPRLFKRRRLRSRVLFSTOPPREADTODLDFEYGAAPFRTSRK 120  
 Oy 122 RSSSHPIFRGSEVSCDSVYVWGDKTATDIDKEKENVAGVANNVSKYKOFEEFKR 181  
 Db 121 RSSSHPIFRGSEVSCDSVYVWGDKTATDIDKEKENVAGVANNVSKYKOFEEFKR 180  
 Oy 182 DPPVDSGCGIDSKHMSYCTTHTFVKALTMGQKQANFRIDTACVLSRKAAR 241  
 Db 181 APPVDSGCGIDSKHMSYCTTHTFVKALTMGQKQANFRIDTACVLSRKAAR 240  
 RESULT 4  
 NGF\_BOVIN  
 ID NGF\_BOVIN STANDARD: PRT; 231 AA.

AC P13600; O18969;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF) (fragment).  
 GN NGFB.  
 OS Bos taurus (Bovine).  
 OC Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid-9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood;  
 RX MEDLINE-97430845; PubMed-9284944;  
 RA Eldique C., Laurent P., Hayes H., Rodellar C., Levezuel H.,  
 RT Zaragoza P.;  
 RT "Assignment of the beta-nerve growth factor (NGFB) to bovine  
 RT chromosome 3 band q23 by in situ hybridization.";  
 RL Cytogenet. Cell Genet. 77:306-307(1997).  
 RN (2)  
 RP SEQUENCE OF 107-231 FROM N.A.  
 RX MEDLINE-86300647; PubMed-2427334;  
 RA Meller R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;  
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):  
 RT delineation of conserved and unconserved domains and their  
 RT relationship to the biological activity and antigenicity of NGF.";  
 RL EMBO J. 5:1489-1493(1986).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: Y09566; CA470759.1; -  
 DR EMBL: M26809; AAA30666.1; -  
 DR PIR: A26312; A26312.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KM Growth factor; Signal; 1.  
 FT SIGNAL 1 8  
 FT PROPEP 9 111 POTENTIAL.  
 FT CHAIN 112 231 BETA-NERVE GROWTH FACTOR.  
 FT DISULFID 126 191 BY SIMILARITY.  
 FT DISULFID 169 219 BY SIMILARITY.  
 FT DISULFID 179 221 BY SIMILARITY.  
 FT CARBOHYD 156 156 N-LINKED (GLCNAc... ) (POTENTIAL).  
 FT CARBOHYD 118 118 L -> F (IN REF. 2).  
 FT CONFLICT 161 161 L -> K (IN REF. 2).  
 FT CONFLICT 230 231 AP -> RA (IN REF. 2).  
 SQ SEQUENCE 231 AA; 25437 MW; 01605092931A418C CRC64;  
 Query Match 86.6%; Score 1106; DB 1; Length 231;  
 Best Local Similarity 90.7%; Pred. No. 1e-97;  
 Matches 205; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
 Oy 12 AFIGIOAPHSSESNVPPGHTIPQVHTKLOHSLDTALRRARSAAPAAIAARVAGOTRNT 71  
 Db 11 AFIGIOAPHSSESNVPPGHTIPQVHTKLOHSLDTALRRARSAAPAAIAARVAGOTRNT 70

DB 1 AFLGIOAAPHESNVPAGHAIPOAMRIKLOHSLDTVLRRAHSAPAGIARVAGQTHNI 60  
 OY 72 TVDRLEFKRRRLSPVLESTOPPREADTODLDFEYGGAAPFNTRHRSKSSHPFHR 131  
 DB 61 TVDPKLEFKRRRLSPVLESTOPPREADTODLDFEAGGASSFNTRHRSKSSHPVLHR 120  
 OY 132 GEFVCSDSVWVGDKTTATDINGKREVMYLGSEVNNINSVEFOYFETECRDPNVDGCR 191  
 DB 121 GEFVCSDSVWVGDKTTATDINGKREVMYLGSEVNNINSVEFOYFETECRDPNVDGCR 180  
 OY 192 GIDSKHNSCTTHTFVAKLMDGNOAMRFIRIDTACVCVLSRK 237  
 DB 181 GIDAKHNSCTTHTFVAKLMDGNOAMRFIRIDTACVCVLSRK 226  
 RESULT 5  
 NGF\_MOUSE  
 ID NGF\_MOUSE STANDARD: PRT: 241 AA.  
 AC POL19: 063864.  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83167518; PubMed-6336309;  
 RA Scott J., Selby M.J., Urdan M.S., Quiroga M., Bell G.I., Rutter W.J.;  
 RT "Isolation and nucleotide sequence of a cDNA encoding the precursor  
 of mouse nerve growth factor.";  
 RL Nature 302:538-540(1983).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83244969; PubMed-6688123;  
 RA Ullrich A., Gray A., Berman C., Dull T.J.;  
 RT "Human beta-nerve growth factor gene sequence highly homologous to  
 that of mouse.";  
 RL Nature 303:821-825(1983).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-84206565; PubMed-6327169;  
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;  
 RT "Sequence homology of human and mouse beta-NGF subunit genes.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-Submaxillary gland;  
 RX MEDLINE-88038855; PubMed-3670303;  
 RA Selby M.J., Edwards R., Sharp F., Rutter W.J.;  
 RT "Mouse nerve growth factor gene: structure and expression.";  
 RL Mol. Cell. Biol. 7:3057-3064(1987).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93264918; PubMed-1284621;  
 RA Yamamoto T., Yamakuni T., Okabe N., Amano T.;  
 RT "Production and secretion of nerve growth factor by clonal striated  
 muscle cell line, G8-1.";  
 RL Neurochem. Int. 21:251-258(1992).  
 RN [6]  
 RP SEQUENCE OF 122-239.  
 RX MEDLINE-73075048; PubMed-4566923;  
 RA Angeletti R.H., Hermanson M.A., Bradshaw R.A.;  
 RT "Amino acid sequences of mouse 2.5S nerve growth factor. II.  
 Isolation and characterization of the thermolabile and peptic peptides  
 and the complete covalent structure.";  
 RL Biochemistry 12:100-115(1973).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE-92065986; PubMed-1956407;

RA McDonald N.O., Lapatto R., Murray-Rust J., Gunning J., Wlodawer A.,  
 RA Blundell T.L.;  
 RT "New protein fold revealed by a 2.3-A resolution crystal structure of  
 RT nerve growth factor.";  
 RL Nature 354:411-414(1991).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE-94260545; PubMed-8201620;  
 RA Holland D.R., Coussens L.S., Meng W., Matthews B.W.;  
 RT "Nerve growth factor in different crystal forms displays structural  
 RT flexibility and reveals zinc binding sites.";  
 RL J. Mol. Biol. 239:385-400(1994).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.  
 RC STRAIN-Swiss Webster; TISSUE-Submaxillary gland;  
 RX MEDLINE-98035451; PubMed-9351801;  
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;  
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with  
 RT four binding proteins.";  
 RL Structure 5:1275-1285(1997).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSOR NEUROUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSOR NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC  
 DR EMBL: M35075; AAA39818.1; ALT\_INIT.  
 DR EMBL: V00836; CAA24221.1; ALT\_INIT.  
 DR EMBL: K01759; AAA39820.1; ALT\_INIT.  
 DR EMBL: M14805; AAA39821.1; ALT\_INIT.  
 DR EMBL: M17298; AAA37687.1; ALT\_INIT.  
 DR EMBL: M17296; AAA37687.1; JOINED.  
 DR EMBL: M17297; AAA37687.1; JOINED.  
 DR EMBL: S62089; CAB32081.2; ALT\_SEQ.  
 DR PIR: A01400; NCMSG.  
 DR PDB: 1BET; 31-MAY-94.  
 DR PDB: 1BTG; 08-MAR-96.  
 DR PDB: 1SGF; 27-MAY-98.  
 DR MGD; MGI:97321; NGFB.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS; PR00268; NGF.  
 DR PRODOM; PD002052; NGF; 1.  
 DR SMART; SM00140; NGF; 1.  
 DR PROSITE; PS00248; NGF; 1.  
 DR PROSITE; PS50270; NGF; 2; 1.  
 KW Growth factor; Signal; 3D-structure.  
 FT SIGNAL; 1-18  
 FT PROPEP; 19-121  
 FT CHAIN; 122-241  
 FT DISULFID; 136-201  
 FT DISULFID; 179-229  
 FT DISULFID; 189-231  
 FT CARBOHYD; 69-69  
 FT CARBOHYD; 114-114  
 FT CONFLICT; 233-241  
 SQ SEQUENCE 241 AA; 27076 MW; 164455EDC550081 CRC64;  
 Query Match 85.8%; Score 1096; DB 1; Length 241;  
 Best Local Similarity 85.0%; Pred. No. 9,6e-97;  
 Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;  
 2 MSALFTLTATLFLGIAEPHESNVPAGHAIPOAMRIKLOHSLDTALRARSAPAAIA 61  
 ||||||||||||||||||| : : : |||||||||||||||||||

Db 1 MSMLFTYLTAFILGVAEPYDSNVBGSVPEAHMTKLQNSLDLALRRASAPTA 60  
 QY 62 ARVACQTNITVDPLRFLFKRRRLSPRVLFSTOPPREAATODDPEVGCAPFNRTNRK 121  
 Db 61 ARVTCQTNITVDPLRFLFKRRRLSPRVLFSTOPPREAATODDPEVGCAPFNRTNRK 120  
 QY 122 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFETKCR 181  
 Db 121 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFETKCR 180  
 QY 182 DPNPVDSCGRCIDSKHNSYCTTHTFEVKALTMGKQAAAFRIRIDTACVLSRAVR 241  
 Db 181 ASNPVSCGRCIDSKHNSYCTTHTFEVKALTMGKQAAAFRIRIDTACVLSRAVR 240

## RESULT 6

NGF\_CAVPO STANDARD; PRT: 241 AA.  
 ID NGF\_CAVPO  
 AC P19093;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGFB.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Prestate;  
 RX MEDLINE=89177243; PubMed=2926397;  
 RA Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;  
 RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor  
 from the guinea pig prostate gland."  
 RL J. Neurochem. 52:1203-1209(1989).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 DR PIR: J10097; J10097.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF.  
 DR SMART: SM00140; NGF.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 121  
 FT CHAIN 122 241  
 FT DISULFID 136 201  
 FT DISULFID 179 229  
 FT DISULFID 189 231  
 FT CARBOHYD 69 69  
 FT CARBOHYD 114 114  
 SQ SEQUENCE 241 AA: 26821 MW: 26426B197804B84 CRC64;

Query Match 85.5%; Score 1092; DB 1; Length 241;  
 Best Local Similarity 86.2%; Pred. No. 2,3e-95;  
 Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 2 MSMLFTYLTAFILGVAEPHSESNVPAGHTIPQVHTKLOHSLDIALRRASAPAAIA 61  
 Db 1 MSMLFTYLTAFILGVAEPHSESNVPAGHTIPQVHTKLOHSLDIALRRASAPAAIA 60  
 QY 62 ARVACQTNITVDPLRFLFKRRRLSPRVLFSTOPPREAATODDPEVGCAPFNRTNRK 121  
 Db 61 ARVACQTNITVDPLRFLFKRRRLSPRVLFSTOPPREAATODDPEVGCAPFNRTNRK 120

QY 122 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFETKCR 181  
 Db 121 RSSHPHFHNGEFSVCDVSVMVADKTATDIDKGEVNLGAEVNNINSVFOYFETKCR 180  
 QY 182 DPNPVDSCGRCIDSKHNSYCTTHTFEVKALTMGKQAAAFRIRIDTACVLSRAVR 241  
 Db 181 DPNPVDSCGRCIDSKHNSYCTTHTFEVKALTMGKQAAAFRIRIDTACVLSRAVR 240

## RESULT 7

NGF\_PRANA STANDARD; PRT: 241 AA.  
 ID NGF\_PRANA  
 AC P20675;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGFB.  
 OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 OC Mastomys.  
 OX NCBI\_TaxID=10112;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=89172070; PubMed=3234767;  
 RA Fahnestock M., Bell R.A.;  
 RT "Molecular cloning of a cDNA encoding the nerve growth factor  
 precursor from Mastomys natalensis."  
 RL Gene 69:257-264(1988).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 DR EMBL: M22748; AAA40599.1; ALT\_INIT.  
 DR PIR: J10343; NGFBRA.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF.  
 DR SMART: SM00140; NGF.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 121  
 FT CHAIN 122 241  
 FT DISULFID 136 201  
 FT DISULFID 179 229  
 FT DISULFID 189 231  
 FT CARBOHYD 69 69  
 FT CARBOHYD 114 114  
 SQ SEQUENCE 241 AA: 27035 MW: 88FB8207A1FB287 CRC64;

Query Match 84.0%; Score 1073; DB 1; Length 241;  
 Best Local Similarity 83.3%; Pred. No. 1,5e-94;  
 Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 2 MSMLFTYLTAFILGVAEPHSESNVPAGHTIPQVHTKLOHSLDIALRRASAPAAIA 61



Db	1	MSLFTLTLLTLLICVQAEPTDSDLSNPEGSGVSEAHMTLQSLSLPTALRRARSPAPPIA	60
Qy	62	ARVAGSTNITVDPPLFLFKRRRLSPRLVLESTPPREAPATQOLDPEVGAAPFARTSRK	121
Db	61	ARVATGTRNITVDPPLFLFKRRRLSPRLVLESTPPRSOTLDLDQAHGTSIFENRTSRK	120
Qy	122	RSSSHDIFRGEFSCVDSVWVGDKTTATDINGKGEVWVLGEVNIINSVFQYEFETKCR	181
Db	121	RSTSHVDFOMGEFSCVDSVWVGDKTTATDINGKNEVTVLGEVININSVFQYEFETKCR	180
Qy	182	DPHPVDSGCRGIDSKHNHNSCTTHTTFFVKKLTIDKSGQAAPRTIRIDTACVLSRKKAVR	241
Db	181	ARNPVSQGRGIDSKHNHNSCTTHTTFFVKKLTIDDKQAAPRTIRIDTACVLSRKKAPR	240

RA Hallboeck F., Ibanez C.F., Petsson H.:  
RT "Evolutionary studies of the nerve growth factor family reveal a  
RL novel member abundantly expressed in Xenopus ovary.";  
CC Nucleon 6:845-858(1991).  
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
CC SENSORY NEURONS.  
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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CC -----  
CC EMBL: X55716; CAA39249.1; ALT\_INIT.  
CC PIR: S14481; S14481.  
CC HSSP: P01139; 1BET.  
CC InterPro: IPR02072; NGF.  
CC Pfam: PF00243; NGF; 1.  
CC PRINTS: PR00268; NGF.  
CC PRODOM: PD02052; NGF; 1.  
CC SMART: SM00140; NGF; 1.  
CC PROSITE: PS00248; NGF\_1; 1.  
CC PROSITE: PS50270; NGF\_2; 1.  
CC Growth factor: Signal.  
CC SIGNAL 1 18  
CC PROPEP 19 114 POTENTIAL.  
CC CHAIN 115 231 NERVE GROWTH FACTOR.  
CC DISULFID 128 193 BY SIMILARITY.  
CC DISULFID 171 221 BY SIMILARITY.  
CC DISULFID 181 223 BY SIMILARITY.  
CC CARBOHYD 63 63 N-LINKED (GLCNAc... ) (POTENTIAL).  
CC CARBOHYD 107 107 N-LINKED (GLCNAc... ) (POTENTIAL).  
CC CARBOHYD 158 158 N-LINKED (GLCNAc... ) (POTENTIAL).  
CC SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;  
SQ  
Query Match 60.5%; Score 773; DB 1; Length 231;  
Best Local Similarity 63.6%; Pred. No. 3.9e-66;  
Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;  
OY 2 MSMLFYTLITAFILGIAEPHSESNVPAGHT---IP-QVHWTK-LQHSLSLDTALRRANSA 55  
DB 1 MSMLFYTLITAFILGIAEPHSESNVPAGHT---IP-QVHWTK-LQHSLSLDTALRRANSA 55  
OY 56 PAAIAAVAGOTRNITVDPLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 115  
DB 50 -HGKLEKEPEYFRNVTVDPLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 115  
OY 116 RTHSKSSSSHPFRHGEFVSVDVWVGDKTTATIDIKGEVNVLGSEVNNINSVFOYF 175  
DB 108 KTIKAKR-TVHPVLHKGELSVCSVSMWVGKTKATIDIKGEVTVLGSEVNNINSVFOYF 166  
OY 176 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAMRFIRIDTACVCLSR 236  
DB 167 FETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAMRFIRIDTACVCLSR 236  
OY 236 RK 237  
DB 227 RK 228  
RESULT 10  
NGF\_BUNMU STANDARD: PRT: 243 AA.  
AC P34128;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nerve growth factor precursor (NGF).  
OS Bungarus multicinctus (Many-banded krait).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lophosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Bungarinae; Bungarus.  
OX NCBI\_TaxID=8616;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Venom gland;  
RX MEDLINE=93192074; PubMed=7916740;  
RA Danse J.M., Garnier J.M.;  
RT "Molecular cloning of a cDNA encoding a nerve growth factor precursor  
RT from the krait, Bungarus multicinctus.";  
CC Growth factors 8:77-86(1993).  
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
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CC -1- SUBUNIT: HOMODIMER.  
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: S56212; AAB25729.1; -  
CC HSSP: P01139; 1BET.  
CC InterPro: IPR02072; NGF.  
CC Pfam: PF00243; NGF; 1.  
CC PRINTS: PR00268; NGF.  
CC PRODOM: PD02052; NGF; 1.  
CC SMART: SM00140; NGF; 1.  
CC PROSITE: PS00248; NGF\_1; 1.  
CC PROSITE: PS50270; NGF\_2; 1.  
CC Growth factor: Signal.  
CC SIGNAL 1 18 POTENTIAL.  
CC PROPEP 19 125 NERVE GROWTH FACTOR.  
CC CHAIN 126 243 BY SIMILARITY.  
CC DISULFID 139 204 BY SIMILARITY.  
CC DISULFID 182 232 BY SIMILARITY.  
CC DISULFID 192 234 BY SIMILARITY.  
CC SEQUENCE 243 AA; 27514 MW; E3F64B142179A08 CRC64;  
SQ  
Query Match 52.9%; Score 675.5; DB 1; Length 243;  
Best Local Similarity 56.8%; Pred. No. 7.4e-57;  
Matches 137; Conservative 30; Mismatches 67; Indels 7; Gaps 4;  
OY 2 MSMLFYTLITAFILGIAEPHSESNVPAG---HTIPQVHWTKLQHSLSLDTALRRANSA 57  
DB 1 MSMLFYTLITAFILGIAEPHSESNVPAGSDSDTNCAGTSGELTSSNTDQHPPT 60  
OY 58 AAIAA-RVAGOTRNITVDPLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 116  
DB 61 PKKSDDELGAANITVDPLFKRRRLSPRYLSTOPPREAADTODLDFEYGAAPFN 116  
OY 117 THRSKSSSSHPFRHGEFVSVDVWVGDKTTATIDIKGEVNVLGSEVNNINSVFOYF 176  
DB 120 NIWA-NNENHNVHNGEHSVCSVSMWVGKTKATIDIKGEVTVLGSEVNNINSVFOYF 178  
OY 177 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAMRFIRIDTACVCLSR 236  
DB 179 EETKCRDPNVDSCGRGIDSKHNSYCTTTFVKALTDGKQAMRFIRIDTACVCLSR 238  
OY 237 K 237  
DB 239 K 239

```

RESULT 11
NGF_DABRR STANDARD: PRT: 117 AA.
ID NGF_DABRR
AC P30894:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Viperidae; Viperinae; Daboia.
NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC Tissue-Venom:
RA MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
RT the venom of Viper russelli russelli."
RL Blochim. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC PIR: S28161; S28161.
CC HSSP: P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF.1.
CC PRINTS: PR00268; NGF.
CC PRODOM: PD002052; NGF.1.
CC SMART: SM00140; NGF.1.
CC PROSITE: PS00248; NGF.1.
CC PROSITE: PS0270; NGF.2; 1.
CC Glycoprotein: Growth factor.
KM DISULFID 12 77 BY SIMILARITY.
FT DISULFID 55 105 BY SIMILARITY.
FT DISULFID 65 107 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC...)
SQ SEQUENCE 117 AA: 13283 MW: A6359GCFECILIF66 CRC64:

Query Match 37.9%: Score 484; DB 1; Length 117;
Best Local Similarity 74.1%: Pred. No. 4,4e-39;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 126 HRFHGESEVCDVSVWVGDKTTATDIDKGEVAVLGEVNNINSVFQYFEETKCRDPNP 185
DB 1 HPHMGGEFVCDVSVWVANKTTATDIDKGVAVVAVDYNINNVYQYFEETKCRNP 60

QY 186 VDSGCGIDSKHNNSTCTTHTFVKALTMQKQAMRFIRIDTACVCLSRK 237
DB 61 VPSGCGIDAKHNNSTCTTDTFVRLTMRNQASMRIRINACVCLSRK 112

RESULT 12
NGF_XIPMA STANDARD: PRT: 194 AA.
ID NGF_XIPMA
AC P34129:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF)
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=92333301; PubMed=1629719;
RA Gotz R., Raulf F., Scharlt M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
RT structure and function than nerve growth factor during vertebrate
RT evolution."
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC or send an email to license@isb-sdb.ch).
CC EMBL: X59941; CAA42566.1;
CC HSSP: P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF.1.
CC PRINTS: PR00268; NGF.
CC PRODOM: PD002052; NGF.1.
CC SMART: SM00140; NGF.1.
CC PROSITE: PS00248; NGF.1. FALSE_NEG.
CC PROSITE: PS0270; NGF.2; 1.
CC Growth factor: Signal.
KM SIGNAL 1 30 POTENTIAL.
FT PROPEP 31 79 NERVE GROWTH FACTOR.
FT CHAIN 80 194 BY SIMILARITY.
FT DISULFID 90 155 BY SIMILARITY.
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 143 185 BY SIMILARITY.
SQ SEQUENCE 194 AA: 21596 MW: 0369E0FA51147AE CRC64:

Query Match 37.7%: Score 481.5; DB 1; Length 194;
Best Local Similarity 58.9%: Pred. No. 1,4e-38;
Matches 99; Conservative 13; Mismatches 39; Indels 17; Gaps 3;

QY 72 TVDPRLEKRRRLSPVLESTQPPREADYDOLDFE-VGGAAPNRHRRSSSHIFM 130
DB 40 TVDPLKRRRLSPVLESTQPPREADYDOLDFE-VGGAAPNRHRRSSSHIFM 83

QY 131 RGEFVCDVSVWVGDKTTATDIDKGEVAVLGEVNNINSVFQYFEETKCRDPNPVDSG 190
DB 84 RGVSVCDVSVWVGDKTTATDIDKGEVAVLGEVNNINSVFQYFEETKCRDPNPVDSG 143

QY 191 RGISKNNSTCTTHTFVKALTMQKQAMRFIRIDTACVCLSRK 238
DB 144 LGIDARRHNSHCTSHTEFVALTSENQVAKRLIRINACVCLSRK 191

RESULT 13
NT3_HUMAN STANDARD: PRT: 257 AA.
ID NT3_HUMAN
AC P20783:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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OX NCBI_TaxID=8355;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97252639; PubMed=9096131;
RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
RT "Activity-dependent expression of NT-3 in muscle cells in culture:
RL implications in the development of neuromuscular junctions.";
RN 12
RP SEQUENCE OF 197-217 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9122573; PubMed=2025430;
RA Hallboeek F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.";
RX Neuron 6:845-858(1991).
-1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: U27576; AAB17723.1; -
DR HSP: P20783; 188K.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS0270; NCF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP 17 141
FT CHAIN 142 260
FT DISULFID 155 220
FT DISULFID 198 249
FT DISULFID 208 251
FT CARBOHYD 134 134
SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5EA93CC5 CRC64;

Query Match 37.1%; Score 474; DB 1; Length 260;
Best Local Similarity 41.5%; Pred. No. 1e-37;
Matches 108; Conservative 36; Mismatches 94; Indels 22; Gaps 7;

OY 2 MSMLFTLLTAFLIGIOAEPHSESNVPAQH-----TIPOVHMTK---LDHSLDTALRRA 52
DB 1 MSILFTVMEFLPYCGIHATNMKRLNPENSNLSFIKLIQADLKNKISKQVDTKENHQ 60
OY 53 RSAPAAAIARVAGOTRN-----ITVDPRLF---KRRRLSRPVLFSOTOPREAADTQ 102
DB 61 STLPKQIILLDDGDDNMKQDPVIVSLAEVLKQKQNRKSPRVLLSDLPLEPPPLX 120
OY 103 DLDFEYGCAPF-NRTHRSKRSSHPHFHGEFSVCDVSVVWGDKTATADIKGEVAVL 161
DB 121 LMDVYGHSTVNNKTSRRKRAEHK-GHREYSVCDSESLAVTDKMAIDIRGHQVTVL 179
OY 162 GEVNNINSVKQYFFETKCRDPNPVDSGCGRIDSKHNSYCTTHTFVKALIND-GQAA 220
DB 180 GEIKTGSPPVKYFETTRCKEAPVKNCGRIDKHNMSCKTSOTYVRAITDSNNKNMG 229
OY 221 WRIRIDTACVCLSKRAVR 240

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DB 240 WRIRIDTSCVCLSKRIKR 259

RESULT 15
NT3_FELICA STANDARD: PRT: 257 AA.
AC 09TST2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20211727; PubMed=10745216;
RA Iain E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system
RL development.";
RX J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF192538; AAF03424.1; -
DR HSP: P20783; 188K.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS0270; NCF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHYD 131 131
SQ SEQUENCE 257 AA; 29403 MW; EB53F7E5951138A CRC64;

Query Match 37.1%; Score 473.5; DB 1; Length 257;
Best Local Similarity 40.1%; Pred. No. 1e-37;
Matches 103; Conservative 40; Mismatches 95; Indels 19; Gaps 5;

OY 2 MSMLFTLLTAFLIGIOAEPHSESNVPAQHITPOV-----HMTKIQHSLD 46
DB 1 MSILFTVFLVFLAYLIGNMMQDRSLPDSLSLFIKLIQADLKNKLSKQMDVLEKNYQ 60
OY 47 TALRRASAPAAAIARVAGOTRNIT-VDPRLF-KRRRLSRPVLFSOTOPREAADTQ 104
DB 61 STLPKAEPRPEEGEPKASEPOTVAMDLELRQQRISRPVLLSDLPLEPPPLX 120
OY 105 DFEVGAAPFKRTHRSKRSSHPHFHGEFSVCDVSVVWGDKTATADIKGEVAVLGEV 164
DB 121 EDVYGSPVAANKRTSRRKRAEHK-SHREYSVCDSESLAVTDKSSAIDIRGHQVTVLGEI 179
OY 165 NINNSVKQYFFETKCRDPNPVDSGCGRIDSKHNSYCTTHTFVKALIND-GQAA 223

```

Db 180 KSGNSPVKQYFETRCKEAPYKNGCRGIDKHNSOCTSOITYRALTSNNKLYGRN 239  
QY 224 IRIDTACVCVLSRAVR 240  
Db 240 IRIDTSCVICALSRKIGR 256

Search completed: December 2, 2002, 15:12:42  
Job time : 10.9297 secs

GenCore version 5.1.3  
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OW protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 37.449 Seconds  
(without alignments)  
1331.501 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1377

Sequence: 1 PMSMLFTTLTFLTFLGIGIQA.....FTRIDTACVCVLSKRAVRA 242

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPRMBL\_21:\*  
1: sp\_archae:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1365	99.1	241	4	09UKL8
2	1365	99.1	241	4	09P208
3	1358	98.5	241	4	08P650
4	1349	97.8	241	6	09N2F0
5	1348	97.7	241	6	09N2F1
6	1347	97.7	241	6	09N2E9
7	1332	88.6	217	6	09N183
8	1038	81.3	294	11	091XB4
9	713	55.8	241	13	09DE29
10	709	55.5	241	13	090W38
11	462	36.2	87	6	09TTC3
12	459	35.9	87	4	09P224
13	449.5	35.2	132	11	09WU15
14	426.5	33.4	241	6	09N182
15	426	33.4	286	13	091988
16	363	28.4	247	6	097759

17	360	28.2	249	11	08VNH4	08vnh4 mus musculus
18	342.5	26.8	246	13	08OC74	08qg74 cyclophilops
19	341.5	26.7	246	13	08OC76	08qg76 japalura sp
20	339.5	26.6	270	13	09YH42	09yha42 brachydania
21	335.5	26.3	246	13	08OC75	08qg75 phrynoceph
22	334.5	26.2	153	11	09CYL3	09cy13 mus musculus
23	331.5	26.0	177	13	091BL2	091bl2 poephille gu
24	319	25.0	247	13	08OC77	08qg77 tylocottito
25	294.5	23.1	101	6	09T732	09t732 macaca fusc
26	293	22.9	324	13	09X795	09x795 lampetra fl
27	291	22.8	186	11	09S5D9	09s5d9 lewipox vir
28	282	19.0	52	6	09N1V4	09n1v4 equus caball
29	226	17.7	85	6	002790	002790 macropus fu
30	224	17.5	42	6	002802	002802 trichosaurus
31	220	17.2	85	6	013114	013114 isodon mac
32	220	17.2	85	6	013122	013122 tarsipes ro
33	220	17.2	85	6	002795	002795 orlithorbyn
34	220	17.2	85	6	002798	002798 petaurus br
35	220	17.2	85	6	013104	013104 cercartetus
36	220	17.2	85	6	002792	002792 notoryctes
37	220	17.2	85	6	013105	013105 daayuides
38	220	17.2	85	6	002801	002801 techylosau
39	219	17.1	85	6	002803	002803 trichosaurus
40	211	16.5	42	6	002794	002794 orlithorbyn
41	209	16.4	42	6	002800	002800 tachylosau
42	178.5	14.0	186	6	09BF74	09bf74 lemur catra
43	178.5	14.0	186	11	09XW11	09xw11 castor cana
44	176.5	13.8	186	6	09BF77	09bf77 ochotona hy
45	175	13.7	185	6	09BFK6	09bfk6 talpa alai

#### ALIGNMENTS

##### RESULT 1

09UKL8 ID 09UKL8 PRELIMINARY; PRT; 241 AA.

AC 09UKL8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)

DE Nerve growth factor B.

OS NGFB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-9925629; PubMed-10322959;

RA Tong Y., Wang H., Chen W.,

RT Cloning and sequencing of the gene for premature beta nerve growth

factor.

RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Tong Y., Wang H.,

RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF15960; AAD5975.1; -.

DR HSSP; P01139; 1BE7.

DR InterPro; IPR02072; NGF.

DR Pfam; PF00243; NGF; 1.

DR PRINTS; PR00268; NGF.

DR ProDom; PD002052; NGF; 1.

DR SMART; SM00148; NGF; 1.

DR PROSITE; PS00240; NGF; 1.

DR PROSITE; PS00270; NGF; 2; 1.

SO SEQUENCE

241 AA; 26959 MW; 619DFC65EB3BD671 CRC64;

Query Match

Best Local Similarity 99.1%; Score 1365; DB 4; Length 241;

Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPVHMTKLQHSIDTALRRARSAPAAATA 61
DB 1 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPVHMTKLQHSIDTALRRARSAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHSK 121
DB 61 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHSK 120
OY 122 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKGEVNWLGCVNINNSVFQYFFETKCR 181
DB 121 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKGEVNWLGCVNINNSVFQYFFETKCR 180
OY 182 DPNPVDGCGIGIDSKHNSYCTTHTFVKALITMDGKQAAMRFIRIDTACVLSRKAARR 241
DB 181 DPNPVDGCGIGIDSKHNSYCTTHTFVKALITMDGKQAAMRFIRIDTACVLSRKAARR 240
OY 242 A 242
DB 241 A 241

```

## RESULT 2

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O9P208 PRELIMINARY: PRT: 241 AA.
AC O9P208:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitanu T., Kobayakawa H., Saitou N.;
RT "Silver Project";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037519; BAA90437.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA: 26998 MW: D5531ED825D96C14 CRC64:

```

Query Match 99.1%; Score 1265; DB 4; Length 241;  
 Best Local Similarity 99.6%; Pred. No. 8,3e-117;  
 Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPVHMTKLQHSIDTALRRARSAPAAATA 61
DB 1 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPVHMTKLQHSIDTALRRARSAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHSK 121
DB 61 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHSK 120
OY 122 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKGEVNWLGCVNINNSVFQYFFETKCR 181
DB 121 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKGEVNWLGCVNINNSVFQYFFETKCR 180
OY 182 DPNPVDGCGIGIDSKHNSYCTTHTFVKALITMDGKQAAMRFIRIDTACVLSRKAARR 241
DB 181 DPNPVDGCGIGIDSKHNSYCTTHTFVKALITMDGKQAAMRFIRIDTACVLSRKAARR 240
OY 242 A 242
DB 241 A 241

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DB 241 A 241

## RESULT 3

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O96P60 PRELIMINARY: PRT: 241 AA.
AC O96P60:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Nerve growth factor beta.
GN NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF11526; AAI05874.1; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS0270; NGF_2; 1.
SQ SEQUENCE 241 AA: 26964 MW: 745216485C21E558 CRC64:

```

Query Match 98.5%; Score 1258; DB 4; Length 241;  
 Best Local Similarity 98.8%; Pred. No. 4.1e-116;  
 Matches 238; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 2 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPVHMTKLQHSIDTALRRARSAPAAATA 61
DB 1 MSMLFTLTITAFILGIGIAEPHSESNVPAGHTIPVHMTKLQHSIDTALRRARSAPAAATA 60
OY 62 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHSK 121
DB 61 ARVAGOTRNTITVDPRLFKKRLRSLPRVLFSTQPREAADTODLDFEYVGAAPFNRTHSK 120
OY 122 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKGEVNWLGCVNINNSVFQYFFETKCR 181
DB 121 RSSSHPIFRHGEFSCVDSVSWVWGDKTTATDIDKGEVNWLGCVNINNSVFQYFFETKCR 180
OY 182 DPNPVDGCGIGIDSKHNSYCTTHTFVKALITMDGKQAAMRFIRIDTACVLSRKAARR 241
DB 181 DPNPVDGCGIGIDSKHNSYCTTHTFVKALITMDGKQAAMRFIRIDTACVLSRKAARR 240
OY 242 A 242
DB 241 A 241

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## RESULT 4

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O9N2F0 PRELIMINARY: PRT: 241 AA.
AC O9N2F0:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-GORILLA-01;
RA Kitanu T., Kobayakawa H., Saitou N.;
RT "Silver Project";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037519; BAA90439.1; -.

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DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF; 1.  
 DR PRINTS: PR00268; NCF.  
 DR PRODOM: PD002052; NCF; 1.  
 DR SMART: SM00140; NCF; 1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS50270; NCF\_2; 1.  
 DR NON\_TER 241 241  
 FT  
 SQ SEQUENCE 241 AA; 26915 MW; 6F5AD163C384BB34 CRC64;

Query Match 97.8%; Score 1249; DB 6; Length 241;  
 Best Local Similarity 98.8%; Pred. No. 3.1e-115;  
 Matches 238; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAATA 61  
 DB 1 MSMLFTLTATLTAFLIGIOAEHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60  
 OY 62 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEYGAAPFNRTHRSK 121  
 DB 61 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEYGAAPFNRTHRSK 120  
 OY 122 RSSHPHFHGFSEVCDSSVWVGDKTTATDIDKGEVWVLEVINNSVFOYFFETKCR 181  
 DB 121 RSSHPHFHGFSEVCDSSVWVGDKTTATDIDKGEVWVLEVINNSVFOYFFETKCR 180  
 OY 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241  
 DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

## RESULT 5

ID 09N2F1 PRELIMINARY; PRT; 241 AA.  
 AC 09N2F1.  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Beta-nerve growth factor (Fragment).  
 GN BETA-NGF.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CHMP-220;  
 RA Kitano T., Kobayakawa H., Saitou N.;  
 RT "Silver Project."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB037518; BAA90438.1;  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF; 1.  
 DR PRINTS: PR00268; NCF.  
 DR PRODOM: PD002052; NCF; 1.  
 DR SMART: SM00140; NCF; 1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS50270; NCF\_2; 1.  
 DR NON\_TER 241 241  
 FT  
 SQ SEQUENCE 241 AA; 26868 MW; B39FA8912C00A08 CRC64;

Query Match 97.7%; Score 1248; DB 6; Length 241;  
 Best Local Similarity 98.3%; Pred. No. 3.9e-115;  
 Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAATA 61  
 DB 1 MSMLFTLTATLTAFLIGIOAEHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60

DB 1 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60  
 OY 62 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEYGAAPFNRTHRSK 121  
 DB 61 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEYGAAPFNRTHRSK 120  
 OY 122 RSSHPHFHGFSEVCDSSVWVGDKTTATDIDKGEVWVLEVINNSVFOYFFETKCR 181  
 DB 121 RSSHPHFHGFSEVCDSSVWVGDKTTATDIDKGEVWVLEVINNSVFOYFFETKCR 180  
 OY 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241  
 DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

## RESULT 6

ID 09N2E9 PRELIMINARY; PRT; 241 AA.  
 AC 09N2E9.  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Beta-nerve growth factor (Fragment).  
 GN BETA-NGF.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ORAN-01;  
 RA Kitano T., Kobayakawa H., Saitou N.;  
 RT "Silver Project."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB037520; BAA90440.1;  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF; 1.  
 DR PRINTS: PR00268; NCF; 1.  
 DR PRODOM: PD002052; NCF; 1.  
 DR SMART: SM00140; NCF; 1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS50270; NCF\_2; 1.  
 DR NON\_TER 241 241  
 FT  
 SQ SEQUENCE 241 AA; 26876 MW; DEC168E74E01F15 CRC64;

Query Match 97.7%; Score 1247; DB 6; Length 241;  
 Best Local Similarity 98.3%; Pred. No. 4.9e-115;  
 Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 MSMLFTLTATLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAATA 61  
 DB 1 MSMLFTLTATLTAFLIGIOAEHSESNVPAGHTIPQAHMTKLOHSLDTALRRASAPAAATA 60  
 OY 62 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEYGAAPFNRTHRSK 121  
 DB 61 ARVAGOTRNITVDPRLEFKRRRLSPRVLESTOPPREAADTODLDFEYGAAPFNRTHRSK 120  
 OY 122 RSSHPHFHGFSEVCDSSVWVGDKTTATDIDKGEVWVLEVINNSVFOYFFETKCR 181  
 DB 121 RSSHPHFHGFSEVCDSSVWVGDKTTATDIDKGEVWVLEVINNSVFOYFFETKCR 180  
 OY 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 241  
 DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMGKQAAAFRIRIDTACVLSRAVRR 240  
 OY 242 A 242  
 DB 241 A 241

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RESULT 7
ID 09N183 PRELIMINARY: PRT: 217 AA.
AC 09N183:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Beta nerve growth factor (Fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Macaca.
NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=9270338; PubMed=10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys."
RL J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF222682; AAF33790.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
FT NON_TER 1
FT SEQUENCE 217
SQ SEQUENCE 217 AA: 24240 MM: 36A5A2D1DFCD8D5C CRC64;

Query Match 88.6%; Score 1132; DB 6; Length 217;
Best Local Similarity 98.2%; Pred. No. 9.8e-104;
Matches 213; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 APLIGIOAEPHSESNVPAGHTIPQVHMTKLQHSIDLRLRARSAPAAIAARYAGOTRNT 71
DB 1 APLIGIOAEPHSESNVPAGHTIPQVHMTKLQHSIDLRLRARSAPAAIAARYAGOTRNT 60
QY 72 TVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVGGAAPFNRHSKRSSHPIFHR 131
DB 61 TVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVGGAAPFNRHSKRSSHPIFHR 120
QY 132 GEFSSVCDSSVWVGDKTTATDIDKGEVNLGEVINNSVFEKQYFEFKCDPVPDSCGR 191
DB 121 GEFSSVCDSSVWVGDKTTATDIDKGEVNLGEVINNSVFEKQYFEFKCDPVPDSCGR 180
QY 192 GIDSKHNSYCTTATFVALTMDGKQAAWRFIRDT 228
DB 181 GIDSKHNSYCTTATFVALTMDGKQAAWRFIRDT 217

RESULT 8
ID 091X84 PRELIMINARY: PRT: 294 AA.
AC 091X84:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Similar to nerve growth factor, beta.
OS NCFB.
NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=9270338; PubMed=10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys."
RL J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF222682; AAF33790.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
FT NON_TER 1
FT SEQUENCE 217
SQ SEQUENCE 217 AA: 24240 MM: 36A5A2D1DFCD8D5C CRC64;

Query Match 88.6%; Score 1132; DB 6; Length 217;
Best Local Similarity 98.2%; Pred. No. 9.8e-104;
Matches 213; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC011123; AAH11123.1; -.
DR MGI: 97321; N91D.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
FT NON_TER 1
FT SEQUENCE 294 AA: 32336 MM: 9E27402DAC89229 CRC64;

Query Match 81.3%; Score 1038; DB 11; Length 294;
Best Local Similarity 84.6%; Pred. No. 2.7e-94;
Matches 193; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 2 NSMLFTLLTAFLIGIOAEPHSESNVPAGHTIPQVHMTKLQHSIDLRLRARSAPAAIA 61
DB 67 NSMLFTLLTAFLIGIOAEPHSESNVPAGHTIPQVHMTKLQHSIDLRLRARSAPAAIA 126
QY 62 ARVAGOTRNTVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVGGAAPFNRHSKR 121
DB 127 ARVAGOTRNTVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVGGAAPFNRHSKR 186
QY 122 RSSSHPIFHRGFEVCDSSVWVGDKTTATDIDKGEVNLGEVINNSVFEKQYFEFKCR 181
DB 187 RSSSHPIFHRGFEVCDSSVWVGDKTTATDIDKGEVNLGEVINNSVFEKQYFEFKCR 246
QY 182 DPNVDSGCRGIDSKHNSYCTTATFVALTMDGKQAAWRFIRDTA 229
DB 247 ASNPVDSGCRGIDSKHNSYCTTATFVALTMDGKQAAWRFIRDTA 294

RESULT 9
ID 09DEZ9 PRELIMINARY: PRT: 241 AA.
AC 09DEZ9:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Nerve growth factor.
OS Crotales duisus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Crotalus.
NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Hayashi M.A.F., Radis-Baptista G., Yamane T., Camargo A.C.M.;
RT "Cloning and sequence of a cDNA coding for a rattlesnake (Crotalus
RT terrificus terrificus) nerve growth factor."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF306533; MAG30924.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF.1.
DR PRODOM: PD002052; NCF.1.
DR SMART: SM00140; NCF.1.
DR PROSITE: PS00248; NCF_1; 1.
DR PROSITE: PS50270; NCF_2; 1.
FT NON_TER 1
FT SEQUENCE 241 AA: 27118 MM: 4A261F42C5D6FF3F CRC64;

Query Match 55.8%; Score 713; DB 13; Length 241;
Best Local Similarity 59.8%; Pred. No. 2.6e-62;
Matches 144; Conservative 29; Mismatches 58; Indels 10; Gaps 4;

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DR ProDom: PD002052; NCF: 1.  
 DR SMART: SM00140; NCF: 1.  
 DR PROSITE: PS50270; NCF\_2: 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 87 AA; 9729 MW; 4539227388FDEE27 CRC64;

Query Match 35.9%; Score 459; DB 4; Length 87;  
 Best Local Similarity 94.3%; Pred. No. 8.6e-38;  
 Matches 82; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 123 SSSHPFRHGEFSVCSVWVGDTTATIDIKGEVNLGVNINNSVFOYFEETKCRD 182  
 DB 1 SSSHPFRHGEFSVCSVWVGDTTATIDIKGEVNLGVNINNSVFOYFEETKCRD 60

OY 183 PNPVDSGCGIDSKHNNSCTTHTREV 209  
 DB 61 PNPVDSGCGIDSKHNNSCTTHTREV 87

RESULT 13  
 OY09N182 PRELIMINARY: PRT: 132 AA.

AC 09N182  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Nerve growth factor (Fragment).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus  
 OX NCBI\_TaxID=10036;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Jensen H.T., Lehman M.N., Stevens P.J.;  
 RL "Golden Hamster Neurotrophin and Neurotrophin Receptor cDNA."  
 DR EMBL: AF104239; AAD21010.1; -

FT NON\_TER 1 132  
 FT SEQUENCE 132 AA; 14649 MW; 0C36B6283225DA6 CRC64;

Query Match 35.2%; Score 449.5; DB 11; Length 132;  
 Best Local Similarity 75.4%; Pred. No. 1.3e-36;  
 Matches 89; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

OY 2 MSMLFYTLTFLAFLIGIOAEPHSESNYPACHTIPQVHTKRLQHSIDPTALRRASAPAAIA 61  
 DB 16 MSMLFYTLTFLAFLIGIOAEPHSESNYPACHTIPQVHTKRLQHSIDPTALRRASAPAAIA 75  
 OY 62 ARVAGOTRNTVDPRLFKKRLRSPVLFSTQPPREAADTODDFEVGGAAPFKRTR 119  
 DB 76 ARVAGOTRNTVDPRLFKKRLRSPVLFSTQPPREAADTODDFEVGGAAPFKRTR 132

RESULT 14  
 OY09N182 PRELIMINARY: PRT: 241 AA.

AC 09N182  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Neurotrophin-3 (Fragment).  
 OS Macaca fasciata (Japanese macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9542;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Tissue-Blood;  
 RL MEDLINE=99270338; PubMed=10340513;  
 RX OKuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in  
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway  
 RT in adult macaque monkeys."  
 RL J. Comp. Neurol. 408:378-398(1999).

RM 12  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood.  
 RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;  
 RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and  
 RT their receptor messenger RNAs in monkey rhinal cortex."  
 RL Neuroscience 0:0-0(2000).  
 DR EMBL: AF222683; AAF33791.1; -  
 DR HSSP: P20783; 1B8K.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.  
 DR PRINTS: PR00268; NGF.  
 DR ProDom: PD002052; NCF: 1.  
 DR SMART: SM00140; NCF: 1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS50270; NCF\_2; 1.  
 FT NON\_TER 1 241  
 FT SEQUENCE 241 AA; 27803 MW; AB95E457C7B07113 CRC64;

Query Match 33.4%; Score 426.5; DB 6; Length 241;  
 Best Local Similarity 39.1%; Pred. No. 5.1e-34;  
 Matches 97; Conservative 35; Mismatches 85; Indels 31; Gaps 6;

OY 5 LFYTLTFLAFLIGIOAEPHSESNYPACHTIPQV-----HWTKLQHSIDPTAL 49  
 DB 1 LFYTLTFLAFLIGIOAEPHSESNYPACHTIPQV-----HWTKLQHSIDPTAL 60  
 OY 50 RRA-----RSAPAAIAARVAGOTRNTVDPRLFK-KRLRSRVLFSTQPPREAADT 101  
 DB 61 PKAEPREPERGQPAKSEFQPV-----IAMDTELRQRRRNSRVVLSSTPLEPPPL 114  
 OY 102 QDLDFEVGGAAPFKRTRSRKSSHPFRHGEFSVCSVWVGDTTATIDIKGEVNL 161  
 DB 115 YLMEYVGNPVPANRTSRKRYAEHK-SRGEYSVCSSESLAVTQSSAIDIRGHQTVL 173  
 OY 162 GEVNNNSVFOYFEETKCRDPPVDSGCGIDSKHNNSCTTHTREVKALTNQ-GQMA 220  
 DB 174 GEITGNSPVQYFETKCEARPVKNGCRGIDKHNNSCTTHTREVKALTNQ 233  
 OY 221 WRFIRIDT 228  
 DB 234 WRFIRIDT 241

RESULT 15  
 OY091988 PRELIMINARY: PRT: 286 AA.

AC 091988  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Neurotrophin-6 precursor.  
 OS Xiphophorus maculatus (Southern platyfish), and  
 OS Xiphophorus helleri.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;  
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.  
 OX NCBI\_TaxID=8083, 8084;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95059452; PubMed=7969471;  
 RX Goetz R., Koster R., Winkler C., Raulf F., Lottspeich F., Scharf M.,  
 RA Thoenen H.;  
 RT "Neurotrophin-6 is a new member of the nerve growth factor family."  
 RL Nature 372:266-269(1994).  
 RX EMBL: L36942; AAA61923.1; -  
 DR EMBL: L36925; AAA61922.1; -

DR EMBL: L36326: AAA61921.1; -  
DR HSSP: P01139: 1BET; NGF.  
DR InterPro: IPR002072: NGF.  
DR Pfam: PF00243: NGF; 1.  
DR PRINTS: PR00268: NGF.  
DR ProDom: PD002052: NGF; 1.  
DR SMART: SM00140: NGF; 1.  
DR PROSITE: PS00248: NGF\_1; 1.  
DR PROSITE: PS50270: NGF\_2; 1.  
KW Signal.  
FT SIGNAL 1 142  
FT CHAIN 143 286 NEUROTROPHIN-6.  
SQ SEQUENCE 286 AA: 3142 MW: 5607 DBA6792E12D CRC64;  
  
Query Match 33.4%; Score 426; DB 13; Length 286;  
Best Local Similarity 38.6%; Pred. No. 78-34;  
Matches 110; Conservative 31; Mismatches 84; Indels 60; Gaps 10;  
  
QY 9 LITAFLLIGIOAEHPHSESNTV-----PAGHTIPQVH-----WTKLQHSIDTALRA 52  
DB 6 LVLLLLIGVQAVLNMGGGLARNPGAAHNSAGQDETAARGQLSDQSTSTQQRHTTHRTK 65  
QY 53 RSAPAA-----IAARVAGQT--RNITVDERLFKKRLR--SPVLEFS--TOPPREAA 99  
DB 66 RTOSAAASNMQRNRTPIVIGSPSPAGSSPDSPVDPKLFSSKRHYRSPRVYSEVYIPSHDYL 125  
QY 100 DTODDFFE-VGGAAPFNRTHRSSKSSHPITFHGEFSVCDVSVMYGDKTATADIKGEY 158  
DB 126 DDEGIDFERVRKGL-----RYRKAAVSHTHNGEYSVCDSTNTWV--NKTIRATDMGNEY 177  
QY 159 NVLGEVNINNSVFNOYFEETKCRDP-----NPDSCGRCIDSK 196  
DB 178 TVLSHYTVNNKVKKOLFETTCRSPTHRSSGIYIGRSGRGKQSGKSGNSGCRGIDSR 237  
QY 197 HNNSYCTTHTFVKALTFMDGKQAAARIRIDTACVCLSKAVRR 241  
DB 238 YNNSHCTNTDIYSALTYFKQZARFIRINACVCLSRNSWR 282

Search completed: December 2, 2002, 15:12:00  
Job time : 38.449 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 16.7386 Seconds  
(without alignments) 425.386 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1 PMSMLFTLITAFLLGIGLAE.....FIRIDTACVCLSRKAVRRA 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/laa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/laa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/laa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/laa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/laa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/laa/Deckfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	242	4	US-09-675-503-1
2	1270	99.5	241	1	US-08-266-080B-4
3	1270	99.5	241	1	US-08-451-947-5
4	1270	99.5	241	2	US-08-424-826A-5
5	1270	99.5	241	2	US-08-595-043A-75
6	1270	99.5	241	3	US-08-970-865-1
7	1270	99.5	241	3	US-08-928-694-5
8	1270	99.5	241	4	US-09-363-573-1
9	1270	99.5	241	4	US-09-447-356-3
10	1270	99.5	241	5	PCR-US91-06950-5
11	1270	99.5	241	5	PCR-US95-05423-4
12	996	78.0	240	3	US-08-910-691-11
13	651	51.0	120	1	US-08-440-049-3
14	651	51.0	120	2	US-08-441-513A-3
15	651	51.0	120	3	US-08-581-662-31
16	651	51.0	120	4	US-08-845-541B-1
17	651	51.0	120	4	US-09-066-065A-1
18	651	51.0	120	4	US-09-447-356-1
19	651	51.0	120	4	US-09-664-295-31
20	651	51.0	120	5	PCR-US95-06918-3
21	648	50.7	120	4	US-08-970-865-2
22	648	50.7	120	4	US-09-363-573-2
23	648	50.7	121	4	US-09-675-503-2
24	648	50.7	127	4	US-09-675-922-4
25	647.5	50.7	167	4	US-09-675-922-8
26	642	50.3	119	3	US-08-753-642-2
27	642	50.3	153	4	US-09-675-922-2

28	642	50.3	163	4	US-09-675-922-6	Sequence 6, Appl 1
29	637	49.9	120	4	US-08-845-541B-3	Sequence 3, Appl 1
30	637	49.9	120	4	US-09-066-065A-3	Sequence 3, Appl 1
31	634	49.6	120	4	US-08-845-541B-4	Sequence 4, Appl 1
32	634	49.6	120	4	US-09-066-065A-4	Sequence 4, Appl 1
33	629	49.3	120	4	US-08-845-541B-12	Sequence 12, Appl 1
34	629	49.3	120	4	US-09-066-065A-12	Sequence 12, Appl 1
35	628	49.2	120	4	US-08-845-541B-17	Sequence 17, Appl 1
36	628	49.2	120	4	US-08-845-541B-20	Sequence 20, Appl 1
37	628	49.2	120	4	US-09-066-065A-17	Sequence 17, Appl 1
38	628	49.2	120	4	US-09-066-065A-20	Sequence 20, Appl 1
39	626	49.0	120	4	US-08-845-541B-18	Sequence 18, Appl 1
40	626	49.0	120	4	US-08-845-541B-21	Sequence 21, Appl 1
41	626	49.0	120	4	US-09-066-065A-18	Sequence 18, Appl 1
42	626	49.0	120	4	US-09-066-065A-21	Sequence 21, Appl 1
43	623	48.8	120	4	US-08-845-541B-13	Sequence 13, Appl 1
44	623	48.8	120	4	US-08-845-541B-19	Sequence 19, Appl 1
45	623	48.8	120	4	US-09-066-065A-13	Sequence 13, Appl 1

#### ALIGNMENTS

Result 1  
US-09-675-503-1  
Sequence 1, Application US/09675503  
Patent No. 6423831  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmelzer, Charles H.  
TITLE OF INVENTION: ISOLATION OF NEUTROPHILS FROM A  
TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUTROPHIL VARIANTS  
FILE REFERENCE: GENE 037C2  
CURRENT APPLICATION NUMBER: US/09/675,503  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-675-503-1

Query Match 100.0%; Score 1277; DB 4; Length 242;

Best Local Similarity 100.0%; Pred. No. 1.7e-143; Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 PMSMLFTLITAFLLGIGLAE...FIRIDTACVCLSRKAVRRA 60  
1 PMSMLFTLITAFLLGIGLAE...FIRIDTACVCLSRKAVRRA 60  
61 AARVAGOTRNTIVDRLEKRRRLSPVLESTOPREADOTDLEFVGCAAPFRHTRS 120  
61 AARVAGOTRNTIVDRLEKRRRLSPVLESTOPREADOTDLEFVGCAAPFRHTRS 120  
121 KRSSHPIFRHGEFVCSVSWVGDITATDVGKGVVLGEVNIINSVFQYFETKC 180  
121 KRSSHPIFRHGEFVCSVSWVGDITATDVGKGVVLGEVNIINSVFQYFETKC 180  
181 RDPNVDSCRGIDSKHNSYCTTHTFVKALTDGQAAAPRIRIDTACVCLSRKAVR 240  
181 RDPNVDSCRGIDSKHNSYCTTHTFVKALTDGQAAAPRIRIRIDTACVCLSRKAVR 240  
181 RDPNVDSCRGIDSKHNSYCTTHTFVKALTDGQAAAPRIRIRIDTACVCLSRKAVR 240

OY 241 RA 242  
DB 241 RA 242

RESULT 2  
US-08-266-080B-4  
Sequence 4, Application US/08266080B  
Patent No. 5606031  
GENERAL INFORMATION:  
APPLICANT: Jack Lille  
APPLICANT: Tadahiko Kohno  
APPLICANT: Duane Bonham  
APPLICANT: Mary S. Rosenbahl  
TITLE OF INVENTION: Production of Biologically Active  
TITLE OF INVENTION: Recombinant Neurotrophic Protein  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 Inch, 360 Kb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/266,080B  
FILING DATE: 27-JUNE-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,122  
FILING DATE: 09-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/087,912  
FILING DATE: 06-JULY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/660,681  
FILING DATE: 04-APRIL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/594,126  
FILING DATE: 09-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/547,750  
FILING DATE: 02-JULY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/505,441  
FILING DATE: 06-APRIL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: SYNE200C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Inferred amino acid sequence of human NGF  
US-08-266-080B-4

Query Match 99.5%; Score 1270; DB 1; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1,1e-142;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSNLTFLITAFIGIOAEPHSESNVPAGHTIPQVHTKLOHSDTALRRARSAPAAIA 61  
DB 1 MSNLTFLITAFIGIOAEPHSESNVPAGHTIPQVHTKLOHSDTALRRARSAPAAIA 60

OY 62 ARVAGOTRNTTVPRLFKKRLRLSPVLFSTQPPREADDTQDLODFEYGAAPFNRTRSK 121  
DB 61 ARVAGOTRNTTVPRLFKKRLRLSPVLFSTQPPREADDTQDLODFEYGAAPFNRTRSK 120  
OY 122 RSSHPLEFRNGEFSVCDSSVWVGDKTTATDITKEEVAVLGEVNIINSVFRQFFETKCR 181  
DB 121 RSSHPLEFRNGEFSVCDSSVWVGDKTTATDITKEEVAVLGEVNIINSVFRQFFETKCR 180  
OY 182 DPNPVDSCGCGISKIHNSYCTTHTFVKALTMDCQAAARFTRIDTACVCLSRKAVRR 241  
DB 181 DPNPVDSCGCGISKIHNSYCTTHTFVKALTMDCQAAARFTRIDTACVCLSRKAVRR 240  
OY 242 A 242  
DB 241 A 241

RESULT 3  
US-08-451-947-5  
Sequence 5, Application US/08451947  
Patent No. 5702906  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,947  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-947-5

Query Match 99.5%; Score 1270; DB 1; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1,1e-142;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	MSLFTLTATLTDIGIOAEPSSESNAWGHTIOVWHTLOHSLOIAPRAASAAAAIA	61
Db	1	MSLFTLTATLTDIGIOAEPSSESNAWGHTIOVWHTLOHSLOIAPRAASAAAAIA	60
QY	62	ARAGCGRTITVDPLPFKKRRRLASRVLFSTOPPREALDODLDEEVGGAAPFNKTRRSK	121
Db	61	ARAGGRTITVDPLPFKKRRRLASRVLFSTOPPREALDODLDEEVGGAAPFNKTRRSK	120
QY	122	RSSSHLFTIRGEFSYCDSDSYVWAGDKTTATDIDGKEVMVLGEVMTINSVFKQYFEETKCR	181
Db	121	RSSSHLFTIRGEFSYCDSDSYVWAGDKTTATDIDGKEVMVLGEVMTINSVFKQYFEETKCR	180
QY	182	DPNPVDSGCRGIDSKRHMSYCTTHTYVKALATMDGKOAAAREFRIIDTACVCLSKAVRR	241
Db	181	DPNPVDSGCRGIDSKRHMSYCTTHTYVKALATMDGKOAAAREFRIIDTACVCLSKAVRR	240
QY	242	A 242	
Db	241	A 241	

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: RESULT 4
: US-08-424-826A-5
: Sequence 5, Application US/08424826A
: Patent No. 5830858
: GENERAL INFORMATION:
: APPLICANT: Rosenthal, Arnon
: TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
: NUMBER OF SEQUENCES: 98
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/424,826A
: FILING DATE: 19-Apr-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/240387
: FILING DATE: 10-May-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/648482
: FILING DATE: 31-JAN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/587707
: FILING DATE: 25-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, PhD., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P0666P1C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-8674
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 241 amino acids
: TYPE: Amino acid
: TOPOLOGY: Linear
:
: US-08-424-826A-5
:
: Query Match 99.5%; Score 1270; DB 2; Length 241;
: Best Local Similarity 100.0%; Pred. No. 1,1e-142;
: Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2	MSMFEFLTAFLIGIOAPEHSSESVNPGCHTIOVHMTLQHSLSLTALRRRSPAAIA	61
Db	1	MSMFEFLTAFLIGIOAPEHSSESVNPGCHTIOVHMTLQHSLSLTALRRRSPAAIA	60
QY	62	ARVAGGTNRNTYDPLFFKRRRLRSRYLVESTOPRPAADTODLDFNGCAAPFNRTRSK	121
Db	61	ARVAGGTNRNTYDPLFFKRRRLRSRYLVESTOPRPAADTODLDFVGGAAFPNRTRSK	120
QY	122	RSSHPLFRGCFSEVCDYSVWVGDKTTAIDIGKEVMVLGEVAINNSVFQFFETKCR	181
Db	121	RSSHPLFRHGFSEVCDYSVWVGDKTTAIDIGKEVMVLGEVAINNSVFQFFETKCR	180
QY	182	DPNPVDSGCRGIDSKHMNSYCTTTHFPKALIMDGKQAAARRFIRIDTACVCLSRKAVRR	241
Db	181	DPNPVDSGCRGIDSKHMNSYCTTTHFPKALIMDGKQAAARRFIRIDTACVCLSRKAVRR	240
QY	242	A 242	
Db	241	A 241	

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RESULT 5
US-08-595-043A-75
Sequence 75: Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEO ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-75

Query Match          99.5%; Score 1270; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSMLFYTLIAFLIGIOAEPHSESNVPAAGHTIPQVHTKLIQHSIDLTALRAARSAPAAATA 61
Db 1 MSMLFYTLIAFLIGIOAEPHSESNVPAAGHTIPQVHTKLIQHSIDLTALRAARSAPAAATA 60
QY 62 ARVAGGGRNTITVPRLEFKRRRLRSRYLSTQPRREAAODDDLFEGVGAAPRNTRHSK 121
Db 61 ARVAGGGRNTITVPRLEFKRRRLRSRYLSTQPRREAAODDDLFEGVGAAPRNTRHSK 120

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OY 122 RSSHPIFRHGEFSVCDSSVWVGDKTATDINKGEVWVGEVNNINSVKOYFETKCR 181  
121 RSSHPIFRHGEFSVCDSSVWVGDKTATDINKGEVWVGEVNNINSVKOYFETKCR 180  
OY 182 DPNPVDSCGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVJSRAVNR 241  
181 DPNPVDSCGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVJSRAVNR 240  
OY 242 A 242  
241 A 241

Db 241 A 241

RESULT 6  
US-08-970-865-1  
Sequence 1, Application US/08970865  
Patent No. 6005081  
GENERAL INFORMATION:  
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck  
TITLE OF INVENTION: Purification of NGF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970-865  
FILING DATE: 14-MAY-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030838  
FILING DATE: 11/15/1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P106332  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/225-8674  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-970-865-1

Query Match 99.5%; Score 1270; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1,1e-142;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLITAFILGIAEPHSESNVPAGHTTPOVHTKLOHSLDTALRRARSAPAAIA 61  
1 MSMLFTLITAFILGIAEPHSESNVPAGHTTPOVHTKLOHSLDTALRRARSAPAAIA 60  
Db 1 MSMLFTLITAFILGIAEPHSESNVPAGHTTPOVHTKLOHSLDTALRRARSAPAAIA 60  
OY 62 ARVAGOTRNTIVDPRLFKKRLRSPVLFSTOPPREADTODLDEEVGGAAPFNTRHSK 121  
61 ARVAGOTRNTIVDPRLFKKRLRSPVLFSTOPPREADTODLDEEVGGAAPFNTRHSK 120  
Db 61 ARVAGOTRNTIVDPRLFKKRLRSPVLFSTOPPREADTODLDEEVGGAAPFNTRHSK 120  
OY 122 RSSHPIFRHGEFSVCDSSVWVGDKTATDINKGEVWVGEVNNINSVKOYFETKCR 181  
121 RSSHPIFRHGEFSVCDSSVWVGDKTATDINKGEVWVGEVNNINSVKOYFETKCR 180  
Db 121 RSSHPIFRHGEFSVCDSSVWVGDKTATDINKGEVWVGEVNNINSVKOYFETKCR 180

OY 182 DPNPVDSCGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVJSRAVNR 241  
181 DPNPVDSCGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVJSRAVNR 240  
OY 242 A 242  
241 A 241

Db 241 A 241

RESULT 7  
US-08-928-694-5  
Sequence 5, Application US/08928694  
Patent No. 6037320  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUTROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,694  
FILING DATE: 12-SEP-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/451947  
FILING DATE: 26-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P06662C1D2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/225-8674  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-928-694-5

Query Match 99.5%; Score 1270; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1,1e-142;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFTLITAFILGIAEPHSESNVPAGHTTPOVHTKLOHSLDTALRRARSAPAAIA 61  
1 MSMLFTLITAFILGIAEPHSESNVPAGHTTPOVHTKLOHSLDTALRRARSAPAAIA 60  
Db 1 MSMLFTLITAFILGIAEPHSESNVPAGHTTPOVHTKLOHSLDTALRRARSAPAAIA 60  
OY 62 ARVAGOTRNTIVDPRLFKKRLRSPVLFSTOPPREADTODLDEEVGGAAPFNTRHSK 121  
61 ARVAGOTRNTIVDPRLFKKRLRSPVLFSTOPPREADTODLDEEVGGAAPFNTRHSK 120  
Db 61 ARVAGOTRNTIVDPRLFKKRLRSPVLFSTOPPREADTODLDEEVGGAAPFNTRHSK 120

Qy	Db	Qy	Db
122	121	182	181
RSSSHIFPFRGEFVSCDVSVMWDKTTARDINGKEVMVLGEVININSPKQFFPENTCR	RSSSHDIFPRGEFVSCDVSVMWDKTTARDINGKEVMVLGEVININSPKQFFPENTCR	DRPVPDGGCRGIDSKHNHNSYCTTHTFVKALITMDGQAAHFRITDZACVYLSKAVRR	DRPVPDGGCRGIDSKHNHNSYCTTHTFVKALITMDGQAAHFRITDZACVYLSKAVRR
182	181	242	241
DRPVPDGGCRGIDSKHNHNSYCTTHTFVKALITMDGQAAHFRITDZACVYLSKAVRR	DRPVPDGGCRGIDSKHNHNSYCTTHTFVKALITMDGQAAHFRITDZACVYLSKAVRR	242 A 242	241 A 241

**RESULT 8**  
**US-09-363-573-1**

```

1 Sequence 1, Application US/09363573
2 Patent No. 6184360
3
4 GENERAL INFORMATION:
5 APPLICANT: Louis E. Burton, Charles H. Schmea
6 TITLE OF INVENTION: Purification of NGF
7 NUMBER OF SEQUENCES: 6
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Genentech, Inc.
10 STREET: 1 DNA Way
11 CITY: South San Francisco
12 STATE: California
13 COUNTRY: USA
14 ZIP: 94080
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Mumpalin (Genentech)
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/363,573
23 FILING DATE:
24
25 CLASSIFICATION:
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US/08/970,865
29 FILING DATE: 14-No. 6184360-1997
30 APPLICATION NUMBER: 60/030838
31 FILING DATE: 11/15/1996
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: 60/047855
34 FILING DATE: 5/29/1997
35
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Torchia, PhD., Timothy E.
38 REGISTRATION NUMBER: 36,700
39 REFERENCE/DOCKET NUMBER: P106382
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: 650/225-8674
42 TELEFAX: 650/952-9881
43
44 INFORMATION FOR SEQ ID NO: 1:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 241 amino acids
47 TYPE: Amino Acid
48 TOPOLOGY: Linear
49
50 US-09-363-573-1

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Query Match	99.5%	Score 1270	DB 4	Length 241
Best Local Similarity	100.0%	Pred. No. 1.1e-142		
Matches 241	Conservative	0	Mismatches 0	Indels 0
			Gaps	0
QY	2 MSMLFTYLTIAFLIGIOAEPHSESNVPAQHTTIPQVHMTKLOHSDLTALRRASAPATA	61		
Db	1 MSMLFTYLTIAFLIGIOAEPHSESNVPAQHTTIPQVHMTKLOHSDLTALRRASAPATA	60		
QY	62 ARVAGGTQNTITVDPRLFKRRRLRSPPVLESTQPREADTDODLFEWGGAAPFRTIRSK	121		
Db	61 ARVAGGTQNTITVDPRLFKRRRLRSPPVLESTQPREADTDODLFEWGGAAPFRTIRSK	120		
QY	122 RSSSHPIFHNGEESVQDSVYVWGDKTATLTDKKGAEVNVLDENVINNSYEQIYFEETKCR	181		

D6	121	RSSSHPIFRNGEFSYCDSDSYVWVGDKTATDINGKEVMVLGEVINNSVFQGYFFETKCR	180
Q7	182	DPNPVDSGCGRIDSKHMSYCCTHTFYKALITMDGKOAAARFIRIDPACVCYLSEKAAYR	241
D6	181	DPNPVDSGCGRIDSKHMSYCCTHTFYKALITMDGKOAAARFIRIDPACVCYLSEKAAYR	240
Q7	242	A 242	
D6	241	A 241	

**RESULT 9**  
**US-09-447-356-3**

Sequence 3 Application US/09447356  
Patent No. 6395513  
GENERAL INFORMATION:  
APPLICANT: POSTER, KEITH ALAN  
APPLICANT: DUGGAN, MICHAEL JOHN  
APPLICANT: SHONE, CLIFFORD CHARLES  
TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL  
TITLE OF INVENTION: SENSORY AFFERENT FUNCTIONS  
FILE REFERENCE: 023223/0104  
CURRENT APPLICATION NUMBER: US/09/447,356  
CURRENT FILING DATE: 1999-11-22  
PRIOR APPLICATION NUMBER: 08/945,037  
PRIOR FILING DATE: 1998-01-12  
PRIOR APPLICATION NUMBER: GB 9508204.6  
PRIOR FILING DATE: 1995-04-21  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 241  
TYPE: PR1  
ORGANISM: Murline sp.  
IS-09-447-356-3

Query Match	99.5%	Score 1270:	DB 4:	Length 241:
Best Local Similarity	100.0%	Pred. No. 1:	je-142:	
Matches 241:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY	2	MSMLFTLTATLTAFLIGTQAEPHSESNVPACHTTPQVHMTKLQHSIDLTALRRARSAPAAATA	61	
Db	1	MSMLFTLTATLTAFLIGTQAEPHSESNVPACHTTPQVHMTKLQHSIDLTALRRARSAPAAATA	60	
QY	62	ARVAGCGRATITVDPRLFFKKRRLRSPVLESTQPREADTDODLDFEYGAAPFNRTRRSK	121	
Db	61	ARVAGCGRATITVDPRLFFKKRRLRSPVLESTQPREADTDODLDFEYGAAPFNRTRRSK	120	
QY	122	RSSSHPLFMHGEESVCDSDSVVWVGDKTTATDIDKGEVNAVLCSEVININNSVFKQYFEETKCR	181	
Db	121	RSSSHPLFMHGEESVCDSDSVVWVGDKTTATDIDKGEVNAVLCSEVININNSVFKQYFEETKCR	180	
QY	182	DPNPVDSGCGRIDSKHMNSYCTTTHTFVVALTMDCKQAAMFIRIDPACCVLSRRAVR	241	
Db	181	DPNPVDSGCGRIDSKHMNSYCTTTHTFVVALTMDCKQAAMFIRIDPACCVLSRRAVR	240	
QY	242	A 242		
Db	241	A 241		

RESULT 10  
PCT-11S91-

Sequence 5 Application PC/TUS9106550  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06950  
FILING DATE: 19910924  
CLASSIFICATION: 436  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/644862  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
ATTORNEY/AGENT INFORMATION:  
NAME: Hensley, Max D.  
REGISTRATION NUMBER: 27,043  
REFERENCE/DOCKET NUMBER: 666P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US91-06950-5

Query Match 99.5%; Score 1270; DB 5; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1,1e-142;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLQHSIDTLARRASAPAAIA 61  
DB 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLQHSIDTLARRASAPAAIA 60  
QY 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVCGAAPFRRTIRSK 121  
DB 61 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVCGAAPFRRTIRSK 120  
QY 122 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDQKGEVAVLGEVINNSVFEQYFEETKCR 181  
DB 121 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDQKGEVAVLGEVINNSVFEQYFEETKCR 180  
QY 182 DPNPVDSCRCIGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVCVLSRKAARR 241  
DB 181 DPNPVDSCRCIGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVCVLSRKAARR 240  
QY 242 A 242  
DB 241 A 241

RESULT 11  
PCT-US95-05423-4  
Sequence 4, Application PC/TUS9505423  
GENERAL INFORMATION:  
APPLICANT: Jack Lille  
APPLICANT: Tadahiko Kohno  
APPLICANT: Duane Bonham  
APPLICANT: Mary S. Rosendahl  
TITLE OF INVENTION: Production of Biologically Active  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado

COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05423  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/266, 090  
FILING DATE: 27-JUNE-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/240, 122  
FILING DATE: 09-MAY-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/087, 912  
FILING DATE: 06-JULY-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/680, 681  
FILING DATE: 04-APRIL-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/594, 126  
FILING DATE: 09-OCT-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/547, 750  
FILING DATE: 02-JULY-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/505, 441  
FILING DATE: 06-APRIL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: STINE200/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Inferred amino acid sequence of human NGF  
PCT-US95-05423-4

Query Match 99.5%; Score 1270; DB 5; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1,1e-142;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLQHSIDTLARRASAPAAIA 61  
DB 1 MSMLFTLTITAFILGIAEPHSESNVPAGHTIPVHMTKLQHSIDTLARRASAPAAIA 60  
QY 62 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVCGAAPFRRTIRSK 121  
DB 61 ARVAGOTRNTITVDPRLFKRRRLSPRVLESTOPPREADTODLDFEVCGAAPFRRTIRSK 120  
QY 122 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDQKGEVAVLGEVINNSVFEQYFEETKCR 181  
DB 121 RSSHPHFHRRGEFSVCDVSVMVGDKTTATDQKGEVAVLGEVINNSVFEQYFEETKCR 180  
QY 182 DPNPVDSCRCIGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVCVLSRKAARR 241  
DB 181 DPNPVDSCRCIGIDSKHNSCTTHTFVKALTDGKQAMRFIRIDTACVCVLSRKAARR 240  
QY 242 A 242  
DB 241 A 241

RESULT 12

US-08-910-691-11  
; Sequence 11, Application US/08910691  
; Patent No. 6015552  
; GENERAL INFORMATION:  
; APPLICANT: MATSANBE, Tatsuya  
; APPLICANT: YOSHITOMI, Sumie  
; APPLICANT: SASADA, Reiko  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPHILIA  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,691  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/074,969  
; FILING DATE: 19930604  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NEUNER, George W  
; REGISTRATION NUMBER: 26964  
; REFERENCE/DOCKET NUMBER: 12345  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-910-691-11

Query Match 78.0%; Score 966; DB 3; Length 240;  
Best Local Similarity 79.2%; Pred. No. 3.9e-110;  
Matches 190; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

QY 2 MSMLFYTLITAFILGIAQPHSESNVPAHTIPOVHWIKLQNSLDTALRRASAPAAIA 61  
DB 1 MSMLFYTLITAFILGIAQPHSESNVPAHTIPOVHWIKLQNSLDTALRRASAPAAIA 60  
QY 62 ARVAGQTNITVDRLFKRRRLRSRYLFTSTPPREAAOTDLDFFVCGAAPPNTHTRSK 121  
DB 61 ARVAGQTNITVDRLFKRRRLRSRYLFTSTPPREAAOTDLDFFVCGAAPPNTHTRSK 120  
QY 122 BSSHPFHRGEEVCDVSVMVGDKTATDIDKKEVMVLCGVNINSVFQYFEETCR 181  
DB 121 RIAEIK-SHROEIVCDSESLMVTDKSSAIDINGHOYTVLGEIKTNSPVKQFFETCR 179  
QY 183 DPNVDSGCRGIDSKHNSYCTTHTFVKALJMD-GKQAAWPIRIDTACVLSRAKAVR 240  
DB 180 EAPVKNCGCRGIDSKHNSYCTTHTFVKALJMD-GKQAAWPIRIDTACVLSRAKAVR 239

RESULT 13  
US-08-440-049-3  
; Sequence 3, Application US/08440049  
; Patent No. 5728803  
; GENERAL INFORMATION:  
; APPLICANT: Uifer, Roman  
; APPLICANT: Presta, Leonard G.

APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: PANTROPIC NEUTROTROPIC FACTORS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,049  
; FILING DATE: 12-May-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/253937  
; FILING DATE: 03-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P0905C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8674  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-440-049-3

Query Match 51.0%; Score 651; DB 1; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 SSSHPFHRGEEVCDVSVMVGDKTATDIDKKEVMVLCGVNINSVFQYFEETCRD 182  
DB 1 SSSHPFHRGEEVCDVSVMVGDKTATDIDKKEVMVLCGVNINSVFQYFEETCRD 60  
QY 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALJMDGKQAAWPIRIDTACVLSRAKAVR 242  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALJMDGKQAAWPIRIDTACVLSRAKAVR 120

RESULT 14  
US-08-441-513A-3  
; Sequence 3, Application US/08441513A  
; Patent No. 5981480  
; GENERAL INFORMATION:  
; APPLICANT: Uifer, Roman  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: Pantropic Neutrotrophic Factors  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,513A  
FILING DATE: 15-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/953-3881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-441-513A-3

Query Match 51.0%; Score 651; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPHFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNIINSVFQYFEETKCRD 182  
|||||  
DB 1 SSSHPHFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNIINSVFQYFEETKCRD 60  
OY 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 242  
|||||  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 120

RESULT 15  
US-08-581-662-31  
Sequence 31, Application US/08581662  
Patent No. 6121235  
GENERAL INFORMATION:  
APPLICANT: Gao, Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments  
FILE REFERENCE: P0981  
CURRENT APPLICATION NUMBER: US/08/581,662  
CURRENT FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 36  
SEQ ID NO 31  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-581-662-31

Query Match 51.0%; Score 651; DB 3; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.3e-69;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPHFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNIINSVFQYFEETKCRD 182  
|||||  
DB 1 SSSHPHFHRCGEFVCDVSVMWGDKTTATDINGKEVWVLGEVNIINSVFQYFEETKCRD 60  
OY 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 242  
|||||  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTDGKQAAAFRIRIDTACVLSKRAVRA 120

Search completed: December 2, 2002, 15:09:42  
Job time: 17.7386 secs

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 8.5114 Seconds  
(without alignments)  
453.778 Million cell updates/sec

Title: US-10-072-681-1

Perfect score: 1277

Sequence: 1 PMSMLFYLITFLAFLIGIQAE.....FIRIDYACVLSRAVRA 242

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

## Database :

Published Applications -AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	242	12	US-10-072-681-1
2	1270	99.5	241	8	US-08-450-842-5
3	1266	99.1	241	10	US-09-872-263-16
4	648	50.7	121	12	US-10-072-681-2
5	648	50.7	157	10	US-09-798-338-4
6	647.5	50.7	167	10	US-09-798-338-8
7	642	50.3	153	10	US-09-798-338-2
8	621	48.6	121	9	US-09-813-398-9
9	584	45.7	121	12	US-10-072-681-3
10	481.5	37.7	257	8	US-08-450-842-4
11	452	35.4	142	8	US-08-450-842-52
12	390	30.5	172	10	US-09-848-664-21
13	388.5	30.4	119	10	US-09-745-032-6
14	388.5	30.4	119	10	US-09-742-600-6
15	388.5	30.4	119	10	US-09-872-090-6
16	388.5	30.4	120	10	US-09-745-032-3
17	388.5	30.4	120	10	US-09-742-600-3
18	388.5	30.4	120	10	US-09-872-090-3
19	388.5	30.4	120	10	US-09-872-090-3

20	387.5	30.3	117	10	US-09-745-032-7	Sequence 7, Appl1
21	387.5	30.3	117	10	US-09-742-600-7	Sequence 7, Appl1
22	387.5	30.3	117	10	US-09-872-090-7	Sequence 7, Appl1
23	387.5	30.3	118	10	US-09-745-032-5	Sequence 5, Appl1
24	387.5	30.3	118	10	US-09-742-600-5	Sequence 5, Appl1
25	387.5	30.3	118	10	US-09-872-090-5	Sequence 5, Appl1
26	383.5	30.0	120	10	US-09-745-032-1	Sequence 1, Appl1
27	383.5	30.0	120	10	US-09-742-600-1	Sequence 1, Appl1
28	383.5	30.0	120	10	US-09-872-090-1	Sequence 1, Appl1
29	376.5	29.5	120	9	US-09-813-398-11	Sequence 11, Appl1
30	373.5	29.2	120	12	US-10-072-681-5	Sequence 5, Appl1
31	363	28.4	247	8	US-08-450-842-3	Sequence 3, Appl1
32	337.5	26.4	120	10	US-09-745-032-10	Sequence 10, Appl1
33	337.5	26.4	120	10	US-09-742-600-10	Sequence 10, Appl1
34	337.5	26.4	210	8	US-08-450-842-2	Sequence 2, Appl1
35	333.5	26.1	120	10	US-09-745-032-9	Sequence 9, Appl1
36	333.5	26.1	120	10	US-09-742-600-9	Sequence 9, Appl1
37	329.5	25.8	168	8	US-08-450-842-6	Sequence 6, Appl1
38	327.5	25.6	120	10	US-09-745-032-8	Sequence 8, Appl1
39	327.5	25.6	120	10	US-09-742-600-8	Sequence 8, Appl1
40	323.5	25.3	130	8	US-08-450-842-47	Sequence 47, Appl1
41	311.5	24.4	119	12	US-10-072-681-4	Sequence 4, Appl1
42	310	24.3	132	8	US-08-450-842-51	Sequence 51, Appl1
43	309.5	24.2	120	9	US-09-813-398-10	Sequence 10, Appl1
44	306.5	24.0	130	8	US-08-450-842-23	Sequence 23, Appl1
45	304.5	23.8	130	8	US-08-450-842-22	Sequence 22, Appl1

## ALIGNMENTS

RESULT 1  
US-10-072-681-1  
Sequence 1, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmeizer, Charles H.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: PURIFICATION OF NGF  
FILE REFERENCE: GEMNET.037C3  
CURRENT APPLICATION NUMBER: US/10/072.681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675,503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-072-681-1  
Query Match 100.0%; Score 1277; DB 12; Length 242;  
Best local similarity 100.0%; Pred. No. 1.8e-127;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 PMSMLFYLITFLAFLIGIQAEPSSESNVAGTITQVMTKLQSLDTALRRASAPAAI 60  
QY AAVVACQTNTINIVDRLFLFKRLRSRVLFTSTPPREAAVDYDLDLFEVGAAPFNTTHS 120  
DB 61 AAVVACQTNTINIVDRLFLFKRLRSRVLFTSTPPREAAVDYDLDLFEVGAAPFNTTHS 120

OY 121 RSSSHPIFHGSESVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQFEETKCR 180  
DB 121 RSSSHPIFHGSESVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQFEETKCR 180  
OY 181 RDPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVR 240  
DB 181 RDPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVR 240  
OY 241 RA 242  
DB 241 RA 242

## RESULT 2

US-08-450-842-5  
Sequence 5, Application US/08450842  
Patent No. US20020045576A1

## GENERAL INFORMATION:

APPLICANT: GENE TECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842

## FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419

## FILING DATE: 19-APR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013

## FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707

## FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-450-842-5

## Query Match

Best Local Similarity 99.5%; Score 1270; DB 8; Length 241;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MSMLFYTLITAFGLIGIAEPHSESNYPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 61  
DB 1 MSMLFYTLITAFGLIGIAEPHSESNYPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 60

OY 62 ARVAGOTRNTIVDPRLFKRRRLRSRVLFSQPREAADTODLDFEYGAAPFNRTNRK 121  
DB 61 ARVAGOTRNTIVDPRLFKRRRLRSRVLFSQPREAADTODLDFEYGAAPFNRTNRK 120  
OY 122 RSSSHPIFHGSESVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQFEETKCR 181  
DB 121 RSSSHPIFHGSESVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQFEETKCR 180  
OY 182 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVR 241  
DB 181 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVR 240  
OY 242 A 242  
DB 241 A 241

## RESULT 3

US-09-822-263-16  
Sequence 16, Application US/09822263  
Patent No. US20020036598A1

## GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas  
APPLICANT: Verneel, Corine  
APPLICANT: Shimketa, Richard A  
APPLICANT: Burgess, Catherine  
APPLICANT: Spylek, Kimberly  
APPLICANT: Tchernev, Velizar T  
TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded

## FILE REFERENCE: 15966-572 CIP1

CURRENT APPLICATION NUMBER: US/09/822,263  
CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 09/672,665  
PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/156,745  
PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/158,942  
PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: 60/159,248  
PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/169,344  
PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/215,048  
PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 241  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-822-263-16

## Query Match

Best Local Similarity 99.1%; Score 1266; DB 10; Length 241;  
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 MSMLFYTLITAFGLIGIAEPHSESNYPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 61  
DB 1 MSMLFYTLITAFGLIGIAEPHSESNYPAGHTIPQVHMTKLQHSIDTALRRARSAPAAIA 60  
OY 62 ARVAGOTRNTIVDPRLFKRRRLRSRVLFSQPREAADTODLDFEYGAAPFNRTNRK 121  
DB 61 ARVAGOTRNTIVDPRLFKRRRLRSRVLFSQPREAADTODLDFEYGAAPFNRTNRK 120  
OY 122 RSSSHPIFHGSESVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQFEETKCR 181  
DB 121 RSSSHPIFHGSESVCDVSVWVGDKTTATDIDKKEVNVLGSEVNIINSVFKQFEETKCR 180  
OY 182 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVR 241  
DB 181 DPNPDSCGCGIDSKHNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVR 240  
OY 242 A 242





PRIOR APPLICATION NUMBER: 09/141.153  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 153  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Artificial  
US-09-798-338-2

Query Match 50.3%; Score 642; DB 10; Length 153;  
Best Local Similarity 100.0%; Pred. No. 1,3e-60;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 182  
DB 35 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 94  
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 240  
DB 95 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 152

## RESULT 8

US-09-798-338-6  
Sequence 6, Application US/09798338  
Patent No. US20010020086A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schenae, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798.338  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141.153  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6  
LENGTH: 163  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Artificial  
OTHER INFORMATION: Protein Sequence  
US-09-798-338-6

Query Match 50.3%; Score 642; DB 10; Length 163;  
Best Local Similarity 100.0%; Pred. No. 1,3e-60;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 182  
DB 45 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 104  
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 240  
DB 105 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 162

## RESULT 9

US-09-813-398-9  
Sequence 9, Application US/09813398  
Patent No. US20020169292A1  
GENERAL INFORMATION:  
APPLICANT: Bruce D. Weintraub  
APPLICANT: Mariusz W. Szklinski  
APPLICANT: University of Maryland

TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: USFMD.003C1  
CURRENT APPLICATION NUMBER: US/09/813.398  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US98/19772  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 121  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-09-813-398-9

Query Match 48.6%; Score 621; DB 9; Length 121;  
Best Local Similarity 95.8%; Pred. No. 1,4e-58;  
Matches 115; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 123 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 182  
DB 2 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 61  
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 242  
DB 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 121

## RESULT 10

US-10-072-681-3  
Sequence 3, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmelzer, Charles H.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: PURIFICATION OF NGR  
FILE REFERENCE: GENENT.037C3  
CURRENT APPLICATION NUMBER: US/10/072.681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675.503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 121  
TYPE: PRT  
ORGANISM: mouse  
US-10-072-681-3

Query Match 45.7%; Score 584; DB 12; Length 121;  
Best Local Similarity 89.9%; Pred. No. 1,2e-54;  
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 123 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 182  
DB 2 SSSHPIFRGEFSVCDVSVMWGDKTATDIDKGEVNLGEVNNINSVFKOYFEETKCD 61  
OY 183 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 241  
DB 62 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRAVR 120

## RESULT 11



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US-09-848-664-21
: Sequence 21, Application US/09848664
: Patent No. US20020146414A1
: GENERAL INFORMATION:
: APPLICANT: Sakiyama-Elbert, Shelly E.
: APPLICANT: Hubbard, Jeffrey A.
: TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth
: TITLE OF INVENTION: Factors from Heparin Containing Matrices
: FILE REFERENCE: ETH 108
: CURRENT APPLICATION NUMBER: US/09/848,664
: PRIOR FILING DATE: 2001-05-03
: PRIOR APPLICATION NUMBER: 09/298,084
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 21
: LENGTH: 72
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-848-664-21
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Query Match          30.4%; Score 390; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SSSHPFHRGEFVSVDVSVVGDKTATDIDKKEVNLGEVININSVFKEFFETKCRD 182
DB 1 SSSHPFHRGEFVSVDVSVVGDKTATDIDKKEVNLGEVININSVFKEFFETKCRD 60
OY 183 PNPVDSGCRGID 194
DB 61 PNPVDSGCRGID 72
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```
RESULT 14
US-09-745-032-6
: Sequence 6, Application US/09745032
: Patent No. US20010027179A1
: GENERAL INFORMATION:
: APPLICANT: Boone, Thomas C.
: APPLICANT: Cheung, Ellen N.
: APPLICANT: Herhenson, Susan I.
: APPLICANT: Young, John D.
: TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
: FILE REFERENCE: A-411A US Revised073100
: CURRENT APPLICATION NUMBER: US/09/745,032
: PRIOR FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: 09/214,214
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 08/684,353
: PRIOR FILING DATE: 1996-07-19
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 119
: TYPE: PRT
: ORGANISM: Human
US-09-745-032-6
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Query Match          30.4%; Score 388.5; DB 10; Length 119;
Best Local Similarity 61.6%; Pred. No. 5.2e-34;
Matches 69; Conservative 18; Mismatches 24; Indels 1; Gaps 1;
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OY 130 HRGEFVSVDVSVVGDKTATDIDKKEVNLGEVININSVFKEFFETKCRDPNPVDSG 189
DB 7 HRGEFVSVDVSVVGDKTATDIDKKEVNLGEVININSVFKEFFETKCRDPNPVDSG 66
OY 190 CRGIDSKHNSYCTTHTFEKALTM-D-CROAMRFIRIDTACVLSRKA VR 240
DB 67 CRGIDSKHNSYCTTHTFEKALTM-D-CROAMRFIRIDTACVLSRKA VR 118
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RESULT 15

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US-09-742-600-6
: Sequence 6, Application US/09742600
: Patent No. US20020010135A1
: GENERAL INFORMATION:
: APPLICANT: Boone, Thomas C.
: APPLICANT: Cheung, Ellen N.
: APPLICANT: Herhenson, Susan I.
: APPLICANT: Young, John D.
: TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
: FILE REFERENCE: A-411A US Revised073100
: CURRENT APPLICATION NUMBER: US/09/742,600
: PRIOR FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: 09/214,214
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 08/684,353
: PRIOR FILING DATE: 1996-07-19
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 119
: TYPE: PRT
: ORGANISM: Human
US-09-742-600-6
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Query Match          30.4%; Score 388.5; DB 10; Length 119;
Best Local Similarity 61.6%; Pred. No. 5.2e-34;
Matches 69; Conservative 18; Mismatches 24; Indels 1; Gaps 1;

OY 130 HRGEFVSVDVSVVGDKTATDIDKKEVNLGEVININSVFKEFFETKCRDPNPVDSG 189
DB 7 HRGEFVSVDVSVVGDKTATDIDKKEVNLGEVININSVFKEFFETKCRDPNPVDSG 66
OY 190 CRGIDSKHNSYCTTHTFEKALTM-D-CROAMRFIRIDTACVLSRKA VR 240
DB 67 CRGIDSKHNSYCTTHTFEKALTM-D-CROAMRFIRIDTACVLSRKA VR 118
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Job time : 9.51114 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002. CompuGen Ltd.

OK protein - protein search, using sw model

Run on: December 2, 2002, 15:05:37 ; Search time 24.1149 Seconds

(Without alignments)  
668.605 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
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8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	648	98.5	120 20	AA081117
2	648	98.5	120 21	AA029141
3	648	98.5	120 22	AA064994
4	648	98.5	120 22	AA035944
5	648	98.5	124 13	AA021851
6	648	98.5	241 12	AA013063
7	648	98.5	241 12	AA011474
8	648	98.5	241 12	AA013858
9	648	98.5	241 12	AA013886
10	648	98.5	241 16	AA074119

11	648	98.5	241 16	AA066588	Human nerve growth
12	648	98.5	241 18	AA026237	Human preproNGF
13	648	98.5	241 19	AA048886	Human prepro-nerve
14	648	98.5	241 20	AA070303	Human nerve growth
15	648	98.5	241 22	AA067865	Amino acid sequenc
16	648	98.5	241 22	AA066939	Human NGF. Homo s
17	648	98.5	241 23	AA018904	Human beta nerve g
18	648	98.5	241 23	AA004994	Sequence encoded b
19	648	98.5	245 5	AA040038	Human pre-pro nerve
20	648	98.5	307 14	AA052411	Human beta-nerve g
21	648	98.5	307 19	AA069725	Human NGF. Homo s
22	648	97.9	307 14	AA037799	Human NGF. Homo s
23	640	97.3	120 17	AA090511	Paratropic neurotro
24	639	97.1	118 10	AA091034	Human nerve growth
25	639	97.1	119 5	AA040040	Sequence encoded b
26	639	97.1	119 12	AA013064	Human NGF. HindIII-
27	639	97.1	119 16	AA077420	Nerve growth facto
28	639	97.1	119 21	AA080327	Human beta-nerve g
29	639	97.1	129 14	AA037539	Recombinant beta-N
30	639	97.1	129 18	AA024145	Factor XIIIa subst
31	639	97.1	152 23	AA050302	Amino acid sequenc
32	639	97.1	153 22	AA067676	Human growth hormo
33	639	97.1	154 13	AA022751	Nerve growth facto
34	639	97.1	155 23	AA050303	Nerve growth facto
35	639	97.1	157 21	AA015896	Nerve growth facto
36	639	97.1	157 22	AA067677	Amino acid sequenc
37	639	97.1	157 23	AA085725	Synthetic nerve gr
38	639	97.1	162 23	AA050300	Factor XIIIa subst
39	639	97.1	163 23	AA067678	Amino acid sequenc
40	639	97.1	166 23	AA050301	Nerve growth facto
41	639	97.1	167 22	AA067679	Amino acid sequenc
42	639	97.1	222 21	AA090884	Human proNGF prote
43	639	97.1	261 10	AA091299	Human nerve growth
44	639	97.1	262 7	AA061033	Human beta-nerve g
45	634	96.4	120 20	AA081119	Nerve growth facto

#### ALIGNMENTS

RESULT 1  
AA081117  
ID: AA081117 standard; protein: 120 AA.  
AC: AA081117;  
DT: 01-MAR-1999 (first entry)  
DE: Nerve growth factor wild type.  
XX: Nerve growth factor: tkc; neuron; neural disease; animal feed;  
XX: neurotrophin assay; nerve cell culture media; neurotrophic factor; NT-3;  
XX: tkc; tkb.  
OS: Homo sapiens.  
XX: WO9849308-A1.  
XX: PD 05-NOV-1998.  
XX: PF 23-APR-1998; 98WO-US08242.  
XX: PR 29-APR-1997; 97US-0841045.  
XX: PR 25-APR-1997; 97US-0845541.  
XX: PA (GETH ) GENENTECH INC.  
XX: PI Presta LG, Ufer R, Winslow JW;  
XX: WPI: 1999-009429/01.  
XX: PT New variants of nerve growth factor able to bind tkc - contain  
specified mutations and have multiple neurotrophic activities in a



CC sclerotics, Bell's palsy, and various conditions involving spinal muscular  
 CC atrophy, or paralysis. They are also useful for treating other human  
 CC neurodegenerative disorders, such as Alzheimer's disease, Parkinson's  
 CC disease, epilepsy, multiple sclerosis, Huntington's disease, Down's  
 CC Syndrome, nerve deafness, Meniere's disease and other conditions  
 CC characterized by necrosis or loss of neurones, whether central,  
 CC peripheral, or motor neurones.

XX Sequence 120 AA:

Query Match 98.5% Score 648: DB 22: Length 120:  
 Best Local Similarity 99.2% Pred. No. 2.3e-69;  
 Matches 119: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

0Y 2 SSSHPFHRGFEFVSVDVSVWVGDKTATDIDKGEVWVLGEVWLNNSVFRQYFFETKCRD 61  
 Db 1 SSSHPFHRGFEFVSVDVSVWVGDKTATDIDKGEVWVLGEVWLNNSVFRQYFFETKCRD 60  
 0Y 62 PNPVDSGCGIDSKHNSYCTTHTFFVKALTMDSKQAMRIRIDTACVCLSRKAVRRA 121  
 Db 61 PNPVDSGCGIDSKHNSYCTTHTFFVKALTMDSKQAMRIRIDTACVCLSRKAVRRA 120

RESULT 4  
 AAB35944 standard: protein: 120 AA.

XX AAB35944:

XX 26-FEB-2001 (first entry)

XX NGF-beta amino acid sequence.

XX Heparin binding: vascular graft; matrix; cell adhesion; growth factor;  
 XX wound healing; dermal wound; wound healing; NGF-beta.

XX Unidentified.

XX WO200064481-A1.

XX 02-NOV-2000.

XX 22-APR-1999: 99MO-IB00800.

XX 22-APR-1999: 99MO-IB00800.

XX (ETHZ-) ETH ZURICH & UNIV ZURICH.

XX Sakiyama SE, Hubbard JA:

XX WPI: 2001-024627/03.

XX Matrix for controlled release of growth factor for wound healing, has  
 XX substrate that attaches heparin binding peptide, protein growth factor  
 XX that bind heparin with low affinity, and heparin or heparin-like  
 XX polymer.

XX Example 5: Page 21: 48pp: English.

XX This invention relates to a matrix comprising a substrate capable of  
 CC providing attachment of a heparin binding peptide (HBP), a peptide  
 CC comprising a binding domain which binds heparin with high affinity,  
 CC heparin or heparin-like polymer, and a protein growth factor or peptide  
 CC fragment which has a domain that binds heparin with low affinity.  
 CC Included in the invention is a vascular graft comprising the matrix,  
 CC which is capable of supporting cell adhesion. The matrix is used for  
 CC delivering low heparin binding affinity growth factor proteins or  
 CC peptides in a controlled manner suitable for wound healing. The matrix  
 CC can be used in an article for treating dermal wounds, and in an  
 CC implantable sterilized composition capable of supporting cell adhesion.  
 CC The present sequence represents a growth factor protein. The protein is  
 CC used in an example illustrating that non-heparin binding growth factors  
 CC can be released in a controlled manner from heparin-based drug delivery

CC systems based on their low affinity for heparin.

XX Sequence 120 AA:

Query Match 98.5% Score 648: DB 22: Length 120:  
 Best Local Similarity 99.2% Pred. No. 2.3e-69;  
 Matches 119: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

0Y 2 SSSHPFHRGFEFVSVDVSVWVGDKTATDIDKGEVWVLGEVWLNNSVFRQYFFETKCRD 61  
 Db 1 SSSHPFHRGFEFVSVDVSVWVGDKTATDIDKGEVWVLGEVWLNNSVFRQYFFETKCRD 60  
 0Y 62 PNPVDSGCGIDSKHNSYCTTHTFFVKALTMDSKQAMRIRIDTACVCLSRKAVRRA 121  
 Db 61 PNPVDSGCGIDSKHNSYCTTHTFFVKALTMDSKQAMRIRIDTACVCLSRKAVRRA 120

RESULT 5

XX AAR21851 standard: protein: 124 AA.

XX AAR21851:

XX 10-JUN-1992 (first entry)

XX Chimeric neurotrophic factor R1.

XX Human BDNF: brain derived neurotrophic factor; NGF;

XX neurotrophic growth factor; Alzheimer's disease; ageing; peripheral;

XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;

XX amyotrophic lateral sclerosis; nervous system disorders.

XX Homo sapiens.

XX Key

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

CC diseased cells, e.g. virus infected cells or tumours of nervous system  
 CC orlin. It may also be used to treat patients whose nervous system has  
 CC been damaged by trauma, surgery, ischemia, infection (e.g. polio or  
 CC AIDS), metabolic disease, nutritional deficiency, malignancy or toxic  
 CC agents. Also to treat e.g. Alzheimer's disease, aging, peripheral  
 CC neuropathies, Parkinson's disease, Huntington's chorea or amyotrophic  
 CC lateral sclerosis. The NF or antibodies to it can also be used in the  
 CC diagnosis and study of nervous system disorders. See also  
 CC AAR21857-R21874 and AAQ2080-022131.

XX Sequence 124 AA:

Query Match 98.5%; Score 648; DB 13; Length 124;  
 Best Local Similarity 99.2%; Pred. No. 2,4e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGRFSCDSVSWVWGDITATDIDKKEVNLGEVNLNINSVFROFFETKCRD 61  
 DB 5 SSSHPFIRHGRFSCDSVSWVWGDITATDIDKKEVNLGEVNLNINSVFROFFETKCRD 64  
 OY 62 PNPVDSGCGIDSKHNSYCTTHFFVKALTMDSKQAAMRFIRIDTACVLSRKAARRA 121  
 DB 65 PNPVDSGCGIDSKHNSYCTTHFFVKALTMDSKQAAMRFIRIDTACVLSRKAARRA 124

# RESULT 6

AAR3063  
 ID AAR3063 standard; Protein: 241 AA.

XX AAR3063:

XX 30-SEP-1991 (first entry)

XX Human NGF SmaI-ApaI fragment prod.

XX Expression vector: human nerve growth factor; yeast;

XX senile dementia.

XX Homo sapiens.

XX JF03139285-A.

XX 13-JUN-1991.

XX 20-DEC-1989; 89JP-0328199.

XX 27-JUL-1989; 89JP-0192581.

XX (TAKE ) TAKEDA CHEMICAL IND KK.

XX WPI: 1991-218449/30.

XX N-PSDB: AAQ12638.

XX New yeast expression vector - used in prodn. of human nerve growth

XX factor from corresp. yeast.

XX Disclosure: Fig 1(1-2); 14pp; Japanese.

XX Human NGF is useful as a reagent for study of the nervous system, and

XX for treatment of senile dementia. The DNA encoding this fragment was

XX See also AAQ12639.

XX Sequence 241 AA:

Query Match 98.5%; Score 648; DB 13; Length 241;  
 Best Local Similarity 99.2%; Pred. No. 5,9e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGRFSCDSVSWVWGDITATDIDKKEVNLGEVNLNINSVFROFFETKCRD 61  
 DB 122 SSSHPFIRHGRFSCDSVSWVWGDITATDIDKKEVNLGEVNLNINSVFROFFETKCRD 181

OY 62 PNPVDSGCGIDSKHNSYCTTHFFVKALTMDSKQAAMRFIRIDTACVLSRKAARRA 121  
 DB 182 PNPVDSGCGIDSKHNSYCTTHFFVKALTMDSKQAAMRFIRIDTACVLSRKAARRA 241

# RESULT 7

AAR1474  
 ID AAR1474 standard; Protein: 241 AA.

XX AAR1474:

XX 26-APR-1991 (first entry)

XX Human nerve growth factor.

XX NGF; senile dementia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18 /label- signal sequence

FT Protein 19..241 /label- pro-NGF

FT Protein 122..241 /label- mature NGF

FT Disulfide-bond 135..202

FT Disulfide-bond 180..230

FT Disulfide-bond 190..232

XX EP414151-A.

XX 27-FEB-1991.

XX 17-AUG-1990; 90EP-0115815.

XX 21-AUG-1989; 89JP-0212980.

XX 20-DEC-1989; 89JP-0328198.

XX 13-APR-1980; 90JP-0096252.

XX 07-JUN-1990; 90JP-0147392.

XX (TAKE ) TAKEDA CHEMICALS IND KK.

XX Kakinuma A, Nakahama K, Yoshimura K, Katsuo Y, Iwan M;

XX WPI: 1991-059398/09.

XX N-PSDB: AAQ10620.

XX Human nerve growth factor containing cysteine residues - used as

XX reagent and therapeutic drug for senile dementia.

XX Claim 1: Fig 1: 33pp; English.

XX The sequence was deduced from a clone isolated from a lambda EMBL3

XX genomic library prepd. from human leukocyte DNA, using a probe

XX synthesized based on the sequence of the known human NGF gene [A.

XX Ullrich et al., Nature 303: 821 (1983)]. The clone, betaLN2113,

XX isolated from the library was cleaved with SmaI and ApaI to remove

XX a 1kb fragment contg. the gene which was then inserted into plasmid

XX pUC19 using BamHI to obtain pNGF1076. The gene was sequenced from

XX this plasmid using Sequenase (Biochemical). The sequence of the

XX protein coding region was found to be in complete agreement with

XX that of Ullrich et al. The sequence was used to produce

XX recombinant h-NGF for use in the prodn. of drugs for e.g. senile

XX dementia.

XX Sequence 241 AA:

Query Match 98.5%; Score 648; DB 12; Length 241;  
 Best Local Similarity 99.2%; Pred. No. 5,9e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFIRHGRFSCDSVSWVWGDITATDIDKKEVNLGEVNLNINSVFROFFETKCRD 61

DB 122 SSSHPIFRHGFESVCDVSVMVGDKTTATDICKGEVAVLGEVINNSVFRQYFFETKCRD 181  
 OY 62 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFIRIDTACVLSRAKAVRRA 121  
 DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFIRIDTACVLSRAKAVRRA 241

## RESULT 8

AAR13858  
 ID AAR13858 standard; Protein: 241 AA.

AC AAR13858;

DT 21-NOV-1991 (first entry)

DE Human nerve growth factor.

KM hNGF.

OS Homo sapiens.

PN JP03175976-A.

PD 31-JUL-1991.

PF 12-DEC-1989; 89JP-0320483.

PR 30-SEP-1989; 89JP-0253796.

PR 15-DEC-1988; 88JP-0314860.

PR 12-DEC-1989; 89JP-0320483.

PA (TAKE ) TAKEDA CHEMICAL IND KK.

DR WP1; 1991-269694/37.

DR N-PSDB; AAQ13397.

PT Secretory prepn. of animal protein - by culturing

PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of

PT promoter region.

PS Disclousure: Fig 3; 12pp; Japanese.

CC The amino acid sequence is encoded that of human nerve growth factor

CC (NGF). It may be expressed in Schizosaccharomyces pombe using the

CC glyceraldehyde-3-phosphate dehydrogenase (GPD) gene promoter.

CC Sequence 241 AA;

SO

Query Match 98.5%; Score 648; DB 12; Length 241;

Best Local Similarity 99.2%; Pred. No. 5.9e-69;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRHGFESVCDVSVMVGDKTTATDICKGEVAVLGEVINNSVFRQYFFETKCRD 61

DB 122 SSSHPIFRHGFESVCDVSVMVGDKTTATDICKGEVAVLGEVINNSVFRQYFFETKCRD 181

OY 62 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFIRIDTACVLSRAKAVRRA 121

DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFIRIDTACVLSRAKAVRRA 241

## RESULT 9

AAR13886

ID AAR13886 standard; Protein: 241 AA.

AC AAR13886;

DT 04-DEC-1991 (first entry)

DE NGF with pro-region and signal sequence.

XX NGF with pro-region and signal sequence.

XX Nerve growth factor; cerebral nerve system; senile dementia;

KM vector; expression.

FX Key

FT Region

FT Region

FT Region

FT Protein

FT Protein

PN JP03183485-A.

PD 09-AUG-1991.

PF 26-JUL-1990; 90JP-0196270.

PR 26-JUL-1990; 90JP-0196270.

PR 27-JUL-1989; 89JP-0192581.

PR 30-SEP-1989; 89JP-0253796.

PA (TAKE ) TAKEDA CHEMICAL IND KK.

DR WP1; 1991-27586/38.

DR N-PSDB; AAQ13592.

PT Human nerve growth factor for treating senile dementia - obtd. by

PT culturing yeast transformed by yeast expression vector contg. NGF

PT encoding DNA.

PS Disclousure: Fig 1+3; 11pp; Japanese.

CC A human NGF gene (obtd. from PNGF107G) or its chemically synthesised

CC DNA were used; opt. cleaved by restriction enzymes. In the human NGF,

CC arginine and alanine may added to the C-terminal. A fragment of

CC PNGF107G was ligated into pGUD906-1 contg. a GPD promoter to obtain

CC pGCM228. DNA comprising nucleotides 1-99 of this sequence and a

CC partial sequence of pGCM228 and pGUD906-1 were ligated to obtain

CC pGCM301.

CC S. cerevisiae NA74-3A(cho-)/pGCM301 (FERM-P2532) contains the

CC expression vector and is useful for the prodn. of human NGF.

CC The NGF is used as a reagent to study the cerebral nerve system

CC and to treat senile dementia.

CC Sequence 241 AA;

SO

Query Match 98.5%; Score 648; DB 12; Length 241;

Best Local Similarity 99.2%; Pred. No. 5.9e-69;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRHGFESVCDVSVMVGDKTTATDICKGEVAVLGEVINNSVFRQYFFETKCRD 61

DB 122 SSSHPIFRHGFESVCDVSVMVGDKTTATDICKGEVAVLGEVINNSVFRQYFFETKCRD 181

OY 62 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFIRIDTACVLSRAKAVRRA 121

DB 182 PNPVDSGCRGIDSKHMNSYCTTHTFVKALTMGKQAAAFIRIDTACVLSRAKAVRRA 241

## RESULT 10

AAR77419

ID AAR77419 standard; Protein: 241 AA.

AC AAR77419;

DT 10-FEB-1996 (first entry)

DE Human nerve growth factor.

XX Human nerve growth factor.

XX Nerve growth factor; neurotrophic factor; therapeutic;

XX protein refolding; NGF.

XX Homo sapiens.

XX



FH Key Location/Qualifiers  
 FT Protein 122..241  
 FT /note- "mature protein"  
 FT Region 1..121  
 FT /note- "pre-region"  
 XX W0530686-A1.  
 XX 16-NOV-1995.  
 PD  
 XX  
 XX 02-MAY-1995; 95MO-US05423.  
 XX  
 XX 27-JUN-1994; 94US-0266080.  
 PR 09-MAY-1994; 94US-0240122.  
 XX  
 XX (SYNT ) SYNTAX-SYNERGEN NEUROSCIENCE JOINT VENTU.  
 PA  
 PI Bonam D, Kohno T, Lille J, Rosendahl MS;  
 XX  
 XX WPI: 1995-404080/51.  
 DR N-PSDB; AAT05437.  
 DR  
 XX  
 XX Process for bacterial expression of recombinant neurotrophic factor  
 PT - useful for promoting the survival and maintaining phenotypic  
 PT differentiation of nerve and glial cells.  
 PS  
 PS Disclosure: Page 33-34; 57pp: English.  
 XX  
 XX The nerve growth factor (NGF) gene is expressed in Escherichia  
 CC coli cells. The recombinant protein is solubilized and  
 CC sulfonyletally active NGF, used for promoting the survival of and  
 CC biologically active NGF, used for promoting the survival of and  
 CC maintaining the phenotypic differentiation of nerve and glial cells.  
 CC is isolated and purified. This method breaks incorrectly formed  
 CC disulphide bonds and allows refolding of the factor into the correct  
 CC tertiary structure required for maximum yield of full active protein.  
 XX  
 SO Sequence 241 AA:  
 Query Match 98.5%; Score 648; DB 16; Length 241;  
 Best Local Similarity 99.2%; Pred. No. 5.9e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SSSHPIFHGRGEFVSVDVSVWVGDKTTATDIDKKEVNLGEVININSVFROYFEETKCRD 61  
 DB 122 SSSHPIFHGRGEFVSVDVSVWVGDKTTATDIDKKEVNLGEVININSVFROYFEETKCRD 181  
 QY 62 PNPVDSGCRGIDSKHNSCTTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 121  
 DB 182 PNPVDSGCRGIDSKHNSCTTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 241  
 RESULT 11  
 AAR66688  
 ID AAR66688 standard; Protein: 241 AA.  
 XX  
 XX AAR66688;  
 XX  
 XX 23-AUG-1995 (first entry)  
 DE Human nerve growth factor.  
 DE Human nerve growth factor.  
 XX  
 XX Human nerve growth factor; hNGF; polyclonal antibody;  
 KW Immunogen; enzyme immunoassay.  
 XX  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label- sig-peptide  
 FT Peptide 19..121  
 FT /label- pro-peptide  
 FT Misc-difference 8

FT /note- "corresponding codon TCG"  
 FT Misc-difference 59  
 FT /note- "corresponding codon TAT"  
 FT Misc-difference 173  
 FT /note- "corresponding codon TAG"  
 FT Disulfide-bond 136..201  
 FT Disulfide-bond 179..229  
 FT Disulfide-bond 189..231  
 XX  
 XX JP06317587-A.  
 XX  
 XX 15-NOV-1994.  
 PD  
 XX  
 XX 14-FEB-1991; 91JP-0021181.  
 XX  
 XX 31-AUG-1990; 90JP-0231317.  
 PR  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 PI WPI: 1995-033116/05.  
 DR N-PSDB; AAQ79871.  
 DR  
 XX  
 XX Polyclonal antibody against human nerve growth factor (NGF) -  
 PT useful to detect human NGF, for diagnosis of disease  
 PT  
 XX Example 1; Pages 31-33; 35pp: Japanese.  
 PS  
 XX AAQ79871 encodes AAR66688 human nerve growth factor (hNGF), the  
 CC protein was used as an immunogen to generate a polyclonal  
 CC antibody against hNGF. The polyclonal antibody can be used  
 CC to detect and determine hNGF pref. by enzyme immunoassay.  
 XX  
 SO Sequence 241 AA:  
 Query Match 98.5%; Score 648; DB 16; Length 241;  
 Best Local Similarity 99.2%; Pred. No. 5.9e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SSSHPIFHGRGEFVSVDVSVWVGDKTTATDIDKKEVNLGEVININSVFROYFEETKCRD 61  
 DB 122 SSSHPIFHGRGEFVSVDVSVWVGDKTTATDIDKKEVNLGEVININSVFROYFEETKCRD 181  
 QY 62 PNPVDSGCRGIDSKHNSCTTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 121  
 DB 182 PNPVDSGCRGIDSKHNSCTTTHTFVKALTMDSGQAAMRFIRIDTACVLSKAVRRA 241  
 RESULT 12  
 AAW26237  
 ID AAW26237 standard; Protein: 241 AA.  
 XX  
 XX AAW26237;  
 XX  
 XX 16-MAR-1998 (first entry)  
 DE Human preproNGF.  
 DE Fusion protein; hydrophilic spacer; recombinant; expression system;  
 KW carboxypeptidase; preproNGF.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W09728272-A1.  
 PM  
 PD 07-AUG-1997.  
 XX  
 XX 31-JAN-1997; 97MO-US01470.  
 XX  
 XX 31-JAN-1996; 96US-03595043.  
 PR (TECH-) TECHNOLOGENE INC.  
 PA  
 XX Sgarlato GD;

XX WPI: 1997-402624/37.  
 DR N-PSDB: AAT80162.  
 XX  
 XX Recombinant protein expression system for fusion protein production  
 PT - useful for high quantity production of authentic recombinant  
 PT proteins  
 XX  
 PS Example 6; Page 140-141; 194pp: English.  
 XX  
 XX A novel recombinant vector has been developed which comprises a  
 CC nucleotide sequence encoding a fusion protein. The fusion protein  
 CC comprises three domains joined together in order, from N-terminus to  
 CC C-terminus, of a first domain comprising a protein of interest, a second  
 CC domain comprising a hydrophilic spacer and an affinity domain, each  
 CC domain comprising a hydrophilic spacer and an affinity domain, each  
 CC human preproNGF, used in example 6 of the present invention. The  
 CC recombinant vector is used for the production of authentic recombinant  
 CC proteins of interest. The method of the invention is useful for the  
 CC expression of fusion proteins capable of isolation by affinity  
 CC chromatography in pro- or eukaryotic cells. This method allows  
 CC for the efficient cleavage and generation of authentic proteins of  
 CC interest that do not contain extraneous (i.e. non-naturally occurring)  
 CC amino acids.  
 CC  
 XX Sequence 241 AA:  
 S0  
 Query Match 98.5%; Score 648; DB 18; Length 241;  
 Best Local Similarity 99.2%; Pred. No. 5.9e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 SSSHPHFHGEFSVCSVSWVGDKTTATDINGKENVVLGEVNNINSVROFFETKCD 61  
 DB 122 SSSHPHFHGEFSVCSVSWVGDKTTATDINGKENVVLGEVNNINSVROFFETKCD 181  
 OY 62 PNPVDSGCGIDSKHNSYCTTHTFEVKALTDGKQAAAFRIRIDACVLSRAVRRA 121  
 DB 182 PNPVDSGCGIDSKHNSYCTTHTFEVKALTDGKQAAAFRIRIDACVLSRAVRRA 241  
 RESULT 13  
 AAM48886  
 ID AAM48886 standard; Protein: 241 AA.  
 XX  
 AC AAM48886;  
 XX  
 DT 12-OCT-1998 (first entry)  
 XX  
 DE Human prepro-nerve growth factor beta chain.  
 XX  
 KW Neurotrophin: nerve growth factor; NGF: human; purification;  
 KW hydrophobic interaction chromatography.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..121  
 FT Protein /label= Prepro-region  
 FT 122..241  
 FT Protein /label= Mat\_protein  
 FT 167  
 FT Modified-site /note= "N-glycosylated"  
 FT 179..189  
 FT Region /note= "conserved Cys-containing region involved in  
 FT 229..231  
 FT Region Cys knot motif"  
 FT /note= "conserved Cys-containing region involved in  
 FT Cys knot motif"  
 XX  
 XX W09821234-A2.  
 XX  
 XX 22-MAY-1998.

PF 14-NOV-1997; 97WO-US21068.  
 XX  
 XX 29-MAY-1997; 97US-0047855.  
 PR 15-NOV-1996; 96US-0030838.  
 XX  
 XX (GERTH ) GENENTECH INC.  
 XX  
 PI Beck JT, Burton LE, Schmelzer CH;  
 XX  
 DR WPI: 1998-32233/28.  
 XX  
 XX Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated  
 PT variant(s) - using hydrophobic interaction chromatography,  
 PT optionally in combination with high performance cation exchange  
 PT chromatography  
 XX  
 PS Disclosure; Fig 4; 59pp: English.  
 XX  
 XX This polypeptide comprises the human nerve growth factor (NGF)  
 CC beta chain precursor. Methods are provided for large-scale  
 CC purification of neurotrophins, including mature NGF, suitable for  
 CC clinical use. A claimed method comprises: (1) separating the  
 CC neurotrophin from the other proteins using a hydrophobic  
 CC interaction chromatography resin (HICR); and optionally (2)  
 CC separating the neurotrophin from a chemical variant by high  
 CC performance cation exchange chromatography (HPEC). The processes  
 CC can also be used for purification of e.g. mouse NGF (see AAM48887),  
 CC brain-derived neurotrophic factor (see AAM48888), neurotrophin-4/5  
 CC (see AAM48890) and neurotrophin-3 (see AAM48889). The processes allow  
 CC separation of neurotrophins from various undesirable misprocessed,  
 CC misfolded, size, glycosylated or charge forms. They allow selective  
 CC separation from their variants and other molecules, and from other  
 CC polypeptides with high pI. The processes are applicable to  
 CC starting materials from various sources, including fermentation  
 CC broths or lysed bacterial or mammalian cells.  
 XX  
 S0 Sequence 241 AA:  
 Query Match 98.5%; Score 648; DB 19; Length 241;  
 Best Local Similarity 99.2%; Pred. No. 5.9e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 SSSHPHFHGEFSVCSVSWVGDKTTATDINGKENVVLGEVNNINSVROFFETKCD 61  
 DB 122 SSSHPHFHGEFSVCSVSWVGDKTTATDINGKENVVLGEVNNINSVROFFETKCD 181  
 OY 62 PNPVDSGCGIDSKHNSYCTTHTFEVKALTDGKQAAAFRIRIDACVLSRAVRRA 121  
 DB 182 PNPVDSGCGIDSKHNSYCTTHTFEVKALTDGKQAAAFRIRIDACVLSRAVRRA 241  
 RESULT 14  
 AAT07303  
 ID AAT07303 standard; Protein: 241 AA.  
 XX  
 AC AAT07303;  
 XX  
 DT 06-JUL-1999 (first entry)  
 XX  
 DE Human nerve growth factor beta protein.  
 XX  
 KW Cerebrospinal; axon; growth; mamma; spinal cord injury; lesion; NGF2;  
 KW expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;  
 KW NT3; voluntary motor function.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09900148-A2.  
 XX  
 XX 07-JAN-1999.  
 XX  
 XX 30-JUN-1998; 98WO-US13778.  
 XX  
 XX

PR 30-JUN-1997: 97US-0051255.  
 XX (RECG) UNITV CALIFORNIA.  
 PA Gage FH, Grill R, Tuszyński MH:  
 PI MPI: 1999-095478/08.  
 XX N-PSDB: AAX34366.  
 DR  
 XX Treating spinal cord injuries in a mammal - by inducing growth of  
 PT cerebrospinal projection axons using a recombinant vector for  
 PS expressing CST neurotrophin  
 XX Disclosure: Fig 6: 49pp: English.  
 XX The invention relates to a method of inducing cerebrospinal projection  
 CC (CST) axon growth in a mammal with a spinal cord injury that involves  
 CC a CST lesion by delivering a recombinant expression vector for CST  
 CC neurotrophin, such as this sequence - nerve growth factor beta. The  
 CC method is used to induce partial recovery of voluntary motor function  
 CC in a mammal after disruption of corticospinal projections in the spinal  
 CC cord.  
 CC  
 XX Sequence 241 AA:  
 SQ  
 Query Match 98.5%: Score 648: DB 20: Length 241;  
 Best Local Similarity 99.2%: Pred. No. 5.9e-69;  
 Matches 119: Conservative 1: Mismatches 0: Indels 0: Gaps 0:  
 OY 2 SSSHPFRHGEFSVCDVSVMVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETCRD 61  
 DB 122 SSSHPFRHGEFSVCDVSVMVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETCRD 181  
 OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRKAARRA 121  
 DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRKAARRA 241

RESULT 15  
 AAB67865  
 ID AAB67865 standard: Protein: 241 AA.  
 AC AAB67865:  
 XX  
 XX 29-JUN-2001 (first entry)  
 DE Amino acid sequence of a human polypeptide designated PTMA-8.  
 XX  
 XX PTMA: Immune deficiency; infection; autoimmune disorder; wound closure;  
 KW connective tissue disease; multiple sclerosis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer;  
 KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;  
 KW insulin dependent diabetes mellitus; graft-versus-host disease;  
 KW autoimmune inflammatory eye disease; gut protection; gut regeneration;  
 KW fibrosis; reperfusion injury; systemic cytokine damage.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO200123572-A2.  
 PN  
 XX  
 XX 05-APR-2001.  
 PD  
 XX  
 XX 29-SEP-2000: 2000MO-US41035.  
 PF  
 XX 30-SEP-1999: 99US-0156745.  
 PR 06-OCT-1999: 99US-0158942.  
 PR 13-OCT-1999: 99US-0159248.  
 PR 06-DEC-1999: 99US-0169344.  
 PR 29-JUN-2000: 2000US-0215048.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Prayaga SK, Vernet C, Shinkets RA, Burgess C, Spytek KA.  
 PI

XX MPI: 2001-273512/28.  
 DR N-PSDB: AAF80462.  
 DR  
 XX Novel polypeptides termed PTMAX, and nucleic acids encoding PTMAX,  
 PT useful for detecting and treating diseases caused immune deficiencies -  
 PS Claim 1: Page 20-22: 128pp: English.  
 XX  
 XX The present sequence represents a PTMA-8 (not defined) polypeptide. The  
 CC sequence is derived from clone AL049825. The polypeptide is 26938.5  
 CC daltons. PTMA polynucleotides and polypeptides are used in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, the disease selected from a pathology associated with  
 CC PTMA. They may be useful in the treatment of various immune deficiencies  
 CC and disorders. These immune deficiencies may be genetic or caused by  
 CC viral as well as bacterial or fungal infections or may result from  
 CC autoimmune disorders. Autoimmune disorders which may be treated using  
 CC PTMA include, for example, connective tissue disease, multiple sclerosis,  
 CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary  
 CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin  
 CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease  
 CC and autoimmune inflammatory eye disease. Additionally PTMA may also be  
 CC useful to promote better or faster closure of non-healing wounds,  
 CC including pressure ulcers, ulcers associated with vascular insufficiency,  
 CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for  
 CC gut protection or regeneration and treatment of lung or liver fibrosis,  
 CC systemic cytokine damage.  
 CC  
 XX Sequence 241 AA:  
 SQ  
 Query Match 98.5%: Score 648: DB 22: Length 241;  
 Best Local Similarity 99.2%: Pred. No. 5.9e-69;  
 Matches 119: Conservative 1: Mismatches 0: Indels 0: Gaps 0:  
 OY 2 SSSHPFRHGEFSVCDVSVMVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETCRD 61  
 DB 122 SSSHPFRHGEFSVCDVSVMVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETCRD 181  
 OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRKAARRA 121  
 DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAAFRIRIDTACVLSRKAARRA 241

Search completed: December 2, 2002, 15:08:37  
 Job time : 24.1149 secs

GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 : Search time 9.64596 Seconds  
(without alignments)  
1205.921 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 658

Sequence: 1 PSSSHPIFRNGEFSVCDYSV.....FIRIDTACVLSRKAVRRA 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR-73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	648	98.5	286	1 NGHUBM
2	640	97.3	229	2 I46614
3	628	95.4	125	2 A26312
4	599	91.0	245	2 I56570
5	587	89.2	307	1 NGMSMG
6	581	88.3	243	2 A26311
7	580	88.1	241	2 JI0097
8	569	86.5	303	1 NGMRBA
9	568	85.6	235	2 S14481
10	488	74.2	243	2 I51193
11	481	73.1	117	2 S28161
12	449.5	68.3	116	1 NGNXXI
13	445.5	67.7	116	2 A58566
14	445.5	67.7	246	2 A59218
15	388	59.0	194	2 I51709
16	380.5	57.8	257	2 C40304
17	380.5	57.8	257	2 I50400
18	380.5	57.8	258	2 S09155
19	380.5	57.8	282	2 A35781
20	348	52.9	286	2 S50855
21	324.5	49.3	247	2 A40304
22	324.5	49.3	249	2 S12555
23	324.5	49.3	249	2 B40361
24	324.5	49.3	252	2 A30361
25	320.5	48.7	114	2 I84765
26	318.5	48.4	248	2 JC6183
27	313.5	47.6	114	2 I50606
28	310.5	47.2	269	2 I51708
29	308.5	46.9	236	2 JH0400

30	307.5	46.7	210	2 A42687	neurotrophin-4 pre
31	305.5	46.4	209	2 B42687	neurotrophin-4 pre
32	304.5	46.3	114	2 I51599	brain-derived neur
33	76.5	11.6	835	2 C97332	probable alpha-ara
34	74.5	11.3	365	2 T08577	hypothetical prote
35	73	11.1	229	2 C69806	hypothetical prote
36	71.5	10.9	499	2 S53637	protein kinase clk
37	69.5	10.6	481	2 T27655	hypothetical prote
38	68.5	10.4	1254	2 E82064	conserved hypothet
39	68.5	10.4	4544	1 S02392	alpha-2-macroglobu
40	68.5	10.4	4545	1 S25111	alpha-2-macroglobu
41	68	10.3	518	2 B48088	beta-transducin re
42	67.5	10.3	361	2 T48029	hypothetical prote
43	67.5	10.3	554	2 T48029	hypothetical prote
44	67.5	10.3	1155	2 T40532	hypothetical prote
45	67.5	10.3	4543	1 A53102	alpha-2-macroglobu

## ALIGNMENTS

### RESULT 1

NGHUBM  
nerve growth factor beta chain precursor - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 19-Feb-1984  
C:Accession: A01399; S10253

R:Ulrich, A.; Gray, A.; Berman, C.; Dull, T.J.  
Nucleic Acids Res. 18, 4020, 1990

A:Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo  
A:Reference number: A93305; MUID:83244969; PMID:6688123

A:Accession: A01399

A:Molecule type: DNA  
A:Residues: 1-286 <BOR>  
R:Bozsan, G.; Pizutti, A.; Rugaril, E.T.; Falini, A.; Silani, V.; Sidoli, A.; Scarla  
Nucleic Acids Res. 18, 4020, 1990

A:Title: CDNA sequence of human beta-NGF.

A:Reference number: S10253; MUID:90326556; PMID:2374737

A:Accession: S10253

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 46-286 <BOR>  
A:Cross-references: EXBL:X52599; NID:929476; PIDN:CA56832.1; PID:929477

C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and  
nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels

C:Genetics:

A:Gene: GDB:NGF8

A:Map position: 1p13.1-1p13.1

A:Introns: 41/3

C:Complex: nerve growth factor is composed of two alpha chains, two beta chains, and

C:Keywords: glycoprotein; growth factor; submandibular gland

F:1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>

F:167-286/Product: nerve growth factor beta chain #status predicted <MAP>

F:26,114,159,211/Binding site: carbohydrate (Aan) (covalent) #status predicted

F:181-246,224-274,234-276/Disulfide bonds: #status predicted

Query Match 98.5% Score 648; DB 1; Length 286;  
Best Local Similarity 99.28; Pred. No. 1.9e-61;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PSSSHPIFRNGEFSVCDYSVYVGDRTATDIXGKEVNVLCGVNINSVFNOYFFETKRD 61

DB 167 SSSHPHFRNGEFSVCDYSVYVGDRTATDIXGKEVNVLCGVNINSVFNOYFFETKRD 226

OY 62 PNVDSGCGIDSKHNSCTTTRTFVAKLTMCKQAAMRIRIDTACVLSRKAVRRA 121

DB 227 PNVDSGCGIDSKHNSCTTTRTFVAKLTMCKQAAMRIRIDTACVLSRKAVRRA 286

RESULT 2

I46614

```

Nerve growth factor B - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
Accession: I46614
R:LanDB-Mansals, Y.; Mellink, C.; Verle, M.; Gellin, J.
CytoGenet. Cell Genet. 67, 120-123, 1994
A>Title: A new marker (NGFB) on pig chromosome 4, isolated by using consensus sequence
A:Reference number: I46614; MUID:94313891; PMID:8039422
A:Accession: I46614
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-229 <LH>
A:Cross-references: GB:L31698; NID:g476732; PIDN:AAA21301.1; PID:g533771
A:Gene: NGFB
C:Superfamily: nerve growth factor beta chain

Query Match          97.3% Score 640; DB 2; Length 229;
Best Local Similarity 97.5%; Pred. No. 1.le-60;
Matches 117; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 SSSHHFRGGEFSVCDSDSYWVGDKTTATDIDKGFVNLGEVINNSVFROYFEETKCRD 61
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db       110 SSSHVFRRGESVCDSDSYWVGDKTTATDIDKGFVNVLGEVINNSVFROFFETKCRD 169
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||

QY      62 PNPVDSCRGCIDSKHMNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVLSKRAVRRA 121
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db       170 PNPVDSCRGCIDSKHMNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVLSRKAGRRA 229

RESULT 3
A26312
nerve growth factor beta chain precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999
C:Accession: A26312
R:Meier, R.; Becker-Andres, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A>Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of
A:Reference number: A26312; MUID:86300647; PMID:2427334
A:Accession: A26312
A:Molecule type: mRNA
A:Residues: 1-125 <ME>
A:Cross-references: GB:M26809; NID:g163419; PIDN:AAA30666.1; PID:g163420
C:Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embryot
C:Keywords: growth factor; homodimer; seminal vesicle
F:6-135/Product: nerve growth factor #status predicted <MAT>
F:20-85;63-113;73-115/Dissulfide bonds: #status predicted

Query Match          95.4% Score 628; DB 2; Length 125;
Best Local Similarity 94.2%; Pred. No. 1e-59;
Matches 113; Conservative 5; Mismatches 5; Indels 2; Gaps 0;

QY      2 SSSHPFHRRGESVCDSDSYWVGDKTTATDIDKGFVNLGEVINNSVFROYFEETKCRD 61
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db       6 SSSHVFRRGESVCDSDSYWVGDKTTATDIDKGFVNVLGEVINNSVFROFFETKCRD 65
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||

QY      62 PNPVDSCRGCIDSKHMNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVLSKRAVRRA 121
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db       66 PNPVDSCRGCIDAKHMNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVLSRKRTGORA 125
        |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||

RESULT 4
I36570
beta-nerve growth factor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I36570
R:Whittemore, S. R.; Friedman, P. L.; Larhammar, O. G.; Persson, H.; Gonzalez-Carvajal, M.
J. Neurosci. Res. 20, 403-410, 1988
A>Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippoc
A:Reference number: I36570; MUID:89037223; PMID:3184206

```

A:Accession: I56570  
A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA  
A:Residues: 1-245 <RES>  
A:Cross-references: GB:I56589; NID:g205691; PIDN:AAA1697.1; PTD:g205692

C:Superfamily: nerve growth factor beta chain

Query Match                  91.0%; Score 599; DB 2; Length 245;  
Best Local Similarity        91.6%; Pred. No. 2,7e+56;  
Matches 109; Conservative     4; Mismatches 6; Indels 0; Gaps 0;

OY      2   SSSPIIFRGESVCDSTSYWVGDKTTATDICKGEVAVLSEVINNSVFQFFETFCRD 61  
|||::|||||  
Db     126   STSHVFPMGERSVCDDTSVWGVDKRTTRTDTCKGEVLVEENINNSVFQGYFEEFKRA 185  
|||::|||||

OY      62   PNPDSCGGCGDISKRHMNSTCTTHTFVKALTMDSKOAMRIRITDACVCLSRKAAYR 120  
|||::|||||  
Db     186   PNPVSAGCRGISDRKMNSTCTTHTFVKALTDDKQAAMREIRIDTCACVCLSKAAAR 244  
|||::|||||

RESULT 5

NGMSMG

nerve growth factor beta chain precursor - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 30-Nov-1980 \$sequence\_Revision 19-Feb-1984 \$text\_change 21-Jul-2000  
C:Accession: JI:S6101; A93305; A90366; I49689; I52891; A01400; I49690  
R:Scott, J.; Seibldy, M.; Urdea, M.; Quiroga, M.; Bell, G.T.; Rutter, W.J.  
Nature 302, 538-540, 1983  
A>Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse  
A:Reference number: A93301; MWID:83167518; PMID:6336309  
A:Accession: A93301

A:Molecule type: mRNA  
A:Residues: 1-307 <SCO>  
A:Cross-references: GB:VO0836; NID:g53364; PIDN:CAA24221.1; PID:g53365  
R.Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.  
Nature 303, 821-823, 1983  
A>Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo  
A:Reference number: A93305; MWID:83244969; PMID:6688123  
A:Accession: A93305

A:Molecule type: mRNA  
A:Residues: 1-307 <UTL>  
A:Cross-references: GB:X01759; NID:g200051; PIDN:AAA39820.1; PID:g9378495  
A>Note: These authors believe that Met-67 is probably the amino-terminal residue and  
Biochemistry 12, 100-115, 1973  
R.Angelini, R.H.; Hermodson, M.A.; Bradshaw, R.A.

A>Title: Amino acid sequences of mouse 2,5S nerve growth factor. II. Isolation and ch  
A:Reference number: A90366; MWID:73075048; PMID:456923  
A:Accession: A90366

A:Molecule type: Protein  
A:Residues: 188-216 'N', 218-305 <ANG>  
R.Seidel, M.J.; Edwards, R.; Sharp, F.; Rutter, W.J.  
Mol. Cell. Biol. 7, 3057-3064, 1987

A>Title: Mouse nerve growth factor gene: Structure and expression.  
A:Reference number: I49689; MWID:88038855; PMID:3670305  
A:Accession: I49689

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA  
A:Residues: 1-307 <RES>  
A:Cross-references: GB:M17298; NID:g193493; PIDN:AAA37687.1; PID:g467311  
R.Ollich, A.; Gray, A.; Berman, C.H.; Coussens, L.; Dull, T.J.  
Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983

A>Title: Sequence homology of human and mouse beta-NGF subunit genes.  
A:Reference number: I52891; MWID:84206565; PMID:6327169  
A:Accession: I52891

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA  
A:Residues: 1-307 <RS>  
A:Cross-references: GB:M1805; NID:g200053; PIDN:AAA39821.1; PID:g200054  
C:Comment: The active molecule is a dimer of identical chains associated by noncovalent  
nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels  
C:Genetics:  
A:Gene: NGFB

A:Intron: 21/2: 62/3  
C:Superfamily: nerve growth factor beta chain  
E:1-167/Domain: signal sequence and propeptide *status* predicted <SIG>  
F:118-305/Product: nerve growth factor beta chain *status* experimental <MAT>  
F:135-180/Binding site: carboxylate (Asn) (covalent) *status* predicted  
F:202-267,245-295,255-297/Disulfide bonds: *status* experimental  
F:232/Binding site: carboxylate (Asn) (covalent) *status* absent

Query Match 89.2% Score 587; DB 1; Length 307;  
Best Local Similarity 90.8%; Pred. No. 6.7e-55;  
Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSSHPFRHGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 61  
DB 188 STHHPVFMGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 247  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 120  
DB 248 STHPESGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 306

RESULT 6  
A:65311  
C:Species: Gallus gallus (chicken)  
C:Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 21-Jul-2000  
C:Accession: A26311; A24857; S00127; S12532  
R:Edendal, T.; Larhammar, D.; Persson, H.  
EMBO J. 5, 1483-1487, 1986  
A:Title: Structure and expression of the chicken beta nerve growth factor gene.  
A:Reference number: A26311; MUID:86300646; PMID:3017695  
A:Accession: A26311  
A:Molecule type: mRNA  
A:Cross-references: GB:DD0010; GB:N00010; GB:X04067; MUID:9222840; PIDN:BA00008.1; PID:9  
R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.  
EMBO J. 5, 1489-1493, 1986  
A:Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in  
A:Reference number: A24857; MUID:86300647; PMID:2427334  
A:Accession: A24857  
A:Molecule type: DNA  
A:Residues: 118-243 <MIO>  
A:Cross-references: GB:DD0010; GB:N00010; GB:X04067; MUID:9222840; PIDN:BA00008.1; PID:9  
R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.  
EMBO J. 5, 1489-1493, 1986  
A:Title: Molecular cloning of the avian beta-nerve growth factor gene: delineation of  
A:Reference number: A26312; MUID:86300647; PMID:2427334  
A:Accession: S00127  
A:Status: preliminary: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 121-243 <MET>  
A:Cross-references: GB:M26810; MUID:9212446; PIDN:AAA8984.1; PID:9212447  
R:Danez, C.F.; Hallboeck, F.; Edendal, T.; Persson, H.  
EMBO J. 9, 1477-1483, 1990  
A:Title: Structure-function studies of nerve growth factor: functional importance of his  
A:Reference number: S12532; MUID:90228346; PMID:2328722  
A:Accession: S12532  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 126-243 <TBA>  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: growth factor  
F:1-135/Domain: signal sequence *status* predicted <SIG>  
F:126-243/Product: nerve growth factor beta chain *status* predicted <MAT>

Query Match 88.3% Score 581; DB 2; Length 243;  
Best Local Similarity 88.0%; Pred. No. 2.2e-54;  
Matches 103; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 3 SSSHPFRHGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 62  
DB 126 TAPVLRHGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 185

OY 63 NPVDSGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 119  
DB 186 PNPVDSGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 242

RESULT 7  
A:10097  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 15-Mar-1996  
C:Accession: J10097  
R:Schwartz, M.A.; Fisher, D.; Bradshaw, R.A.; Isackson, P.J.  
J. Neurochem. 52, 1203-1209, 1989  
A:Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the  
A:Reference number: J10097; MUID:89177243; PMID:2926397  
A:Accession: J10097  
A:Molecule type: mRNA  
A:Residues: 1-241 <SCH>  
A:Note: the authors translated the codon GCU for residue 214 as Asp  
C:Genetics:  
A:Gene: Beta-NGF  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: glycoprotein; growth factor; hormone  
F:1-121/Domain: propeptide *status* predicted <PRO>  
F:122-241/Product: nerve growth factor beta chain *status* predicted <MAT>  
F:146-154/Region: receptor binding *status* predicted  
F:69,114/Binding site: carboxylate (Asn) (covalent) *status* predicted

Query Match 88.1% Score 580; DB 2; Length 241;  
Best Local Similarity 87.4%; Pred. No. 2.8e-54;  
Matches 104; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSSHPFRHGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 61  
DB 122 STHHPVFMGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 181  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 120  
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 240

RESULT 8  
A:NCRTBA  
C:Species: Mastomys natalensis  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 18-Jun-1999  
C:Accession: J10343  
R:Fahnestock, M.; Bell, R.A.  
Gene 69, 257-264, 1988  
A:Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from  
A:Reference number: J10343; MUID:89172070; PMID:3234767  
A:Accession: J10343  
A:Molecule type: mRNA  
A:Residues: 1-303 <RAH>  
A:Cross-references: GB:M22748; PIDN:AAA4059.1; PID:9702515  
A:Note: it is uncertain whether Met-1 or Met-63 is the initiator  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: glycoprotein; growth factor; homodimer; submaxillary gland  
F:184-301/Product: nerve growth factor beta chain *status* predicted <MAT>  
F:131,176,228/Binding site: carboxylate (Asn) (covalent) *status* predicted  
F:198-263,241-291,251-293/Disulfide bonds: *status* predicted

Query Match 86.5% Score 569; DB 1; Length 303;  
Best Local Similarity 87.4%; Pred. No. 5.4e-53;  
Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 SSSHPFRHGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 61  
DB 184 STHHPVFMGEFSVCDVSVMVGDKTTATDINGKRENVVLGEVINNSVFRQFEETCRD 243  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFFVKALTMGKQAMRFRIIDTACVLSRAVRR 120

Db 244 RNPVSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLTRKAPRR 302

# RESULT 9

nerve growth factor beta chain precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 16-Jul-1995

C:Accession: S14481

R:Carriero, F.; Campioni, M.; Cardinali, B.; Pierandrei-Amaldi, P.  
submitted to the EMBL Data Library, October 1990

A:Description: Structure and expression of the nerve growth gene in Xenopus oocyte and

A:Reference number: S14481

A:Accession: S14481

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-235 <CAR>

A:Cross-references: EMBL:X55716; NID:964914; PIDN:CAA39249.1; PID:964915

C:Superfamily: nerve growth factor beta chain

Query Match 85.6% Score 563; DB 2; Length 235;  
Best Local Similarity 88.4%; Pred. No. 1,8e-52;  
Matches 99; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 5 HP1FRGSEFVCDVSVMVGDKTATDIDKGEVNLGCVNINSVFQYFEETKCDPNP 64

121 HPVLMHGEYSVCDVSVMVGEKTKATDIDKGEVNLGCVNINSVFQYFEETKCDPNP 180

65 VDSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 116

181 VSSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 232

# RESULT 10

nerve growth factor precursor - many-banded krait

C:Species: Bungarus multicinctus (many-banded krait)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1995

C:Accession: I51193

R:Dane, J.M.; Gardner, J.M.

Growth factors 8, 77-86, 1993

A:Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the

A:Reference number: I51193; MUID:93192074; PMID:7916740

A:Accession: I51193

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-243 <CAN>

A:Cross-references: GB:S56212; NID:9266298; PIDN:AB25729.1; PID:9266299

C:Superfamily: nerve growth factor beta chain

Query Match 74.2% Score 488; DB 2; Length 243;  
Best Local Similarity 73.0%; Pred. No. 1,8e-44;  
Matches 84; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

Db 2 SSSPIRHFGEFVCDVSVMVGDKTATDIDKGEVNLGCVNINSVFQYFEETKCDPNP 61

125 NENPVRNNGEHSVCDVSISWTKTKADIDGNTVTVMVNLNNEVYKQYFEETKCRN 184

62 PNPVDSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 116

185 PNPVDSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 239

# RESULT 11

nerve growth factor beta chain - Russell's viper

C:Species: Vipera russelli (Russell's viper)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S28161

R:Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.

Biochem. Biophys. Acta 1160, 287-292, 1992

A:Title: Purification and amino-acid sequence of a nerve growth factor from the venom of

A:Reference number: S28161; MUID:93120151; PMID:1477101

A:Accession: S28161  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-117 <KQY>  
C:Superfamily: nerve growth factor beta chain

Query Match 73.1% Score 481; DB 2; Length 117;  
Best Local Similarity 73.2%; Pred. No. 4,5e-44;  
Matches 82; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

Db 5 HP1FRGSEFVCDVSVMVGDKTATDIDKGEVNLGCVNINSVFQYFEETKCDPNP 64

1 HPVLMHGEYSVCDVSVMVGEKTKATDIDKGEVNLGCVNINSVFQYFEETKCDPNP 180

65 VDSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 116

181 VSSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 232

61 VPSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 112

# RESULT 12

NGNXXI

nerve growth factor - Indian cobra

C:Species: Naja naja (Indian cobra)

C:Date: 30-Nov-1980 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-2000

C:Accession: S13927; A01401

R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 279, 38-40, 1991

A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.

A:Reference number: S13927; MUID:91138753; PMID:1995338

A:Accession: S13927

A:Molecule type: protein

A:Residues: 1-116 <INO>

A:Experimental source: Venom

A:Note: The source is designated as Naja naja and referred to as Indian cobra, so we

R:Hoque-Angelletti, R.A.; Frazier, W.A.; Jacobs, J.W.; Noll, H.D.; Bradshaw, R.A.

Biochemistry 15, 26-34, 1976

A:Title: Purification, characterization, and partial amino acid sequence of nerve gro

A:Reference number: A01401; MUID:76114772; PMID:1247508

A:Accession: A01401

A:Molecule type: protein

A:Residues: 1-11, 'P', 13-14, 'B', 16, 'TBT', 20-21, 'GV', 23-27, 'N', 29-31, 'AS', 34, 'S', 36-48,

15-116 <HOC>

A:Experimental source: venom

A:Comment: The source is designated as Naja naja and referred to as Indian cobra, so we

C:Complex: homodimer

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; venom

F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match 68.3% Score 449.5; DB 1; Length 116;  
Best Local Similarity 70.5%; Pred. No. 1e-40; 17; Indels 1; Gaps 1;  
Matches 79; Conservative 15; Mismatches 17;

Db 5 HP1FRGSEFVCDVSVMVGDKTATDIDKGEVNLGCVNINSVFQYFEETKCDPNP 64

3 HPVLMHGEYSVCDVSVMVGEKTKATDIDGNTVTVMVNLNNEVYKQYFEETKCRN 61

65 VDSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 116

62 EPSGCGRIGDSKHMNSYCTTHTFVKALITDDROAAMRIRIDTACVCLSRK 113

# RESULT 13

nerve growth factor - Chinese cobra

C:Species: Naja naja atra (Chinese cobra)

C:Date: 16-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997

C:Accession: A58566

R:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.

Biochem. Int. 19, 909-917, 1989

A:Title: Amino acid sequence of nerve growth factor purified from the venom of the Fo

A:Reference number: A58566; MUID:90147847; PMID:2619756

A:Accession: A58566  
 A:Molecule type: protein  
 A:Residues: 1-116 <ODA>  
 A:Experimental source: venom  
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
 C:Complex: homodimer  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: growth factor; homodimer; venom  
 F:14-78,56-106,66-108/Disulfide bonds: status predicted

Query Match 67.7%; Score 445.5; DB 2; Length 116;  
 Best Local Similarity 69.6%; Pred. No. 2,7e-40;  
 Matches 78; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFRGEFVSVDVSVWGDKTATDIDKGEVWVNGEVNINSVRFYFETKCRDPNP 64  
 DB 3 HPVHNLGSHSYCDVSNV-TKTATDIDKNTVTVMENVDKVKYKQFFETCKRNP 61  
 OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRK 116  
 DB 62 EPSGCRGIDSSHNSYCTETDTFIKALTMGNOASMRIRIETACVITRK 113

#### RESULT 14

nerve growth factor beta chain precursor - monocled cobra  
 C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)  
 C:Date: 31-Mar-2000 #sequence, revision 31-Mar-2000 #text\_change 31-Mar-2000  
 C:Accession: A59218; S13965  
 R:Seiby, M.J.; Edwards, R.H.; Rutter, W.J.  
 J:Neurosci. Res. 18, 293-298, 1987  
 A:Title: Cobra nerve growth factor: structure and evolutionary comparison.  
 A:Reference number: A59218; MUID:88090976; PMID:5694712  
 A:Accession: A59218

A:Molecule type: mRNA  
 A:Residues: 1-246 <SEL>  
 R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.  
 FEBS Lett. 279, 38-40, 1991  
 A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.  
 A:Reference number: S13927; MUID:9118755; PMID:1995338  
 A:Accession: S13965  
 A:Molecule type: protein  
 A:Residues: 131-246 <IND>  
 A:Experimental source: venom  
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
 C:Complex: homodimer  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: growth factor; homodimer; venom  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:131-246/Product: nerve growth factor beta chain #status experimental <MAT>  
 F:144-208,186-236,196-238/Disulfide bonds: status predicted

Query Match 67.7%; Score 445.5; DB 2; Length 246;  
 Best Local Similarity 69.6%; Pred. No. 6.3e-40;  
 Matches 78; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFRGEFVSVDVSVWGDKTATDIDKGEVWVNGEVNINSVRFYFETKCRDPNP 64  
 DB 133 HPVHNLGSHSYCDVSNV-TKTATDIDKNTVTVMENVDKVKYKQFFETCKRNP 191  
 OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRK 116  
 DB 192 EPSGCRGIDSSHNSYCTETDTFIKALTMGNOASMRIRIETACVITRK 243

#### RESULT 15

151709  
 nerve growth factor beta chain precursor - southern platyfish  
 C:Species: Xiphophorus maculatus (southern platyfish)  
 C:Date: 13-Sep-1996 #sequence, revision 13-Sep-1996 #text\_change 16-Jul-1999  
 C:Accession: 151709; S28674  
 R:Goetz, R.; Raulf, F.; Scharf, M.  
 J. Neurochem. 59, 432-442, 1992

A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and  
 A:Reference number: 151708; MUID:92333301; PMID:1629719  
 A:Accession: 151709

A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-194 <GOT>  
 A:Cross-references: EMBL:X59941; MUD:965277; PIDN:CAA42566.1; PID:965278  
 C:Genetics:  
 A:Gene: NGF  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor  
 F:1-14/Domain: signal sequence #status predicted <SIG>  
 F:15-79/Domain: propolide #status predicted <PRO>  
 F:80-194/Product: nerve growth factor beta chain #status predicted  
 F:90-155,133-183,143-185/Disulfide bonds: status predicted  
 F:99/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.0%; Score 388; DB 2; Length 194;  
 Best Local Similarity 66.1%; Pred. No. 6.5e-34;  
 Matches 72; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

OY 9 HRGEFVSVDVSVWGDKTATDIDKGEVWVNGEVNINSVRFYFETKCRDPNPVDSG 68  
 DB 83 HRGVSVCSVSVWGNKTKATDIDGKEVTLPYVNNVKKYFETCTHSPSGSR 142  
 OY 69 CRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRK 117  
 DB 143 CLGIDARHNSHCTNSHFEVRLTSSNQVAMRLIRIVACVLSRK 191

Search completed: December 2, 2002, 15:13:58  
 Job time: 10.646 sec



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 4.96483 Seconds  
(without alignments)  
1010.837 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 1 PSSSHPFHRGERSVCDYS.....FIRIDTACVCLSRKAVRA 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	648	98.5	241 1	NGF_HUMAN
2	640	97.3	229 1	NGF_PIG
3	618	93.9	231 1	NGF_BOVIN
4	599	91.0	241 1	NGF_RAT
5	587	89.2	241 1	NGF_MOUSE
6	581	88.3	243 1	NGF_CHICK
7	580	88.1	241 1	NGF_CAVPO
8	569	86.5	241 1	NGF_PANNA
9	563	85.6	231 1	NGF_XENLA
10	488	74.2	243 1	NGF_BUNMU
11	481	73.1	117 1	NGF_DABRR
12	446.5	67.9	116 1	NGF_MAJNA
13	442.5	67.2	116 1	NGF_MAJAT
14	388	59.0	134 1	NGF_XIPMA
15	380.5	57.8	257 1	NGF_CHICK
16	380.5	57.8	257 1	NT3_HUMAN
17	380.5	57.8	258 1	NT3_MOUSE
18	380.5	57.8	258 1	NT3_RAT
19	379.5	57.7	260 1	NT3_XENLA
20	376.5	57.2	257 1	NT3_FELCA
21	370.5	56.3	257 1	NT3_BRARE
22	365.5	55.5	140 1	NT3_CYPCA
23	324.5	49.5	255 1	BDNF_CAVPO
24	324.5	49.3	247 1	BDNF_HUMAN
25	324.5	49.3	247 1	BDNF_PROLO
26	324.5	49.3	247 1	BDNF_URSAR
27	324.5	49.3	247 1	BDNF_URSML
28	324.5	49.3	249 1	BDNF_MOUSE
29	324.5	49.3	249 1	BDNF_RAT
30	324.5	49.3	252 1	BDNF_PIG
31	320.5	48.7	114 1	BDNF_MACMU
32	320.5	48.7	247 1	BDNF_FELCA
33	319.5	48.6	270 1	BDNF_CYPCA

34	318.5	48.4	248 1	BDNF_BOVIN
35	317.5	48.3	246 1	BDNF_CHICK
36	310.5	47.2	269 1	BDNF_XIPMA
37	308.5	46.9	236 1	NT4_XENLA
38	307.5	46.7	210 1	NT5_HUMAN
39	305.5	46.4	209 1	NT5_RAT
40	304.5	46.3	114 1	BDNF_XENLA
41	215	33.7	257 1	NT6B_HUMAN
42	214	33.5	186 1	NT6A_HUMAN
43	212	32.2	257 1	NGF_VIPLE
44	190	28.9	42 1	BDNF_RAVCL
45	129	19.6	43 1	BDNF_RAVCL

ALIGNMENTS

RESULT 1

NGF\_HUMAN

ID NGF\_HUMAN STANDARD: PRT: 241 AA.

AC P01138:

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Beta-nerve growth factor precursor (Beta-NGF).

GN NGFB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid:9606;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-83244969; PubMed-6688123;

RA Ullrich A., Gray A., Berman C., Dull T.J.;

RT "Human beta-nerve growth factor gene sequence highly homologous to

RT that of mouse.";

RL Nature 303:821-825(1983).

RM [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-8420555; PubMed-6327169;

RA Ullrich A., Gray A., Berman C., Cousens L., Dull T.J.;

RT "Sequence homology of human and mouse beta-NGF subunit genes.";

RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).

RM [3]

RP SEQUENCE FROM N.A.

RX TISSUE-Brain;

RX MEDLINE-90326556; PubMed-2374737;

RA Borsani G., Pizzuti A., Ruggeri E.I., Fallini A., Sallani V.,

RT "CDNA sequence of human beta-NGF.";

RL Nucleic Acids Res. 18:4020-4020(1990).

RM [4]

RP SEQUENCE OF 178-219 FROM N.A.

RX TISSUE-Leukocyte;

RX MEDLINE-91222573; PubMed-2025430;

RA Hallboeck F., Ibanez C.F., Persson H.;

RT "Evolutionary studies of the nerve growth factor family reveal a

RT novel member abundantly expressed in xenopus ovary.";

RL Neuron 6:845-858(1991).

CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND

CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT

CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND

CC EMBRYONIC SENSORY NEURONS.

CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY

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[illegible]

Query Match	98.58%	Score 648:	DB 1:	Length 241:
Best Local Similarity	99.23%	Pred. No. 4,46-62:		
Matches 119:	Conservative 1:	Mismatches 0:	Indels 0:	Gaps 0
OY	2	SSSRPIFRHREFVCSVSWYWGDKTTANDIGKRVNVLGEVNNINSVFRQYFETRCRD	61	
DB	122	SSSRPIFRHREFVCSVSWYWGDKTTANDIGKRVNVLGEVNNINSVFRQYFETRCRD	181	
OY	62	PNPVDSCGRGIDSNHNSVCTTTHFVKALITMDGQAAHPRIRIDTACVCLSKAAVRA	122	
DB	182	PNPVDSCGRGIDSNHNSVCTTTHFVKALITMDGQAAHPRIRIDTACVCLSKAAVRA	241	

```

RESULT 2
NGF-PIG          STANDARD:          PRT:          229 AA.
ID NGF-PIG
AC 029074:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxId=9823;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RC MEDLINE=9433891; PubMed=8039422;
RA Lahlid-Mansala Y., Mellink C., Yarle M., Gellin J.;
RL Cytochrome, cell gene. 67:120-125(1984).
RT "A new marker (NGFB) on pig chromosome 4, isolated by using a
   consensus sequence conserved among species.";
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSOR NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPHETIC AND
CC EMBRYONIC SENSOR NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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DR	EMBL: L31898; AAA1301.1; -.
DR	HSPB; P01139; 1BET.
DR	InterPro: IPR002072; NGF.
DR	Pfam: PF00243; NGF_1.
DR	ProDom: PD002052; NGF_1.
DR	SMART: SM00140; NGF_1.
DR	PROSITE: PS00248; NGF_1; 1.
DR	PROSITE: PS50270; NGF_2; 1.
KW	Growth factor; Signal.
FT	NON_TER 1
FT	SIGNAL <1 6
FT	PROPEP 7 109
FT	CHAIN 110 229
FT	DISULFID 124 189
FT	DISULFID 167 217
FT	DISULFID 177 219
FT	CARBOHYD 57 57
FT	CARBOHYD 102 102
FT	CARBOHYD 154 154
SC	SEQUENCE 229 AA; 25275 MW; F889077ICBA3189 CRC64;

	Query Match	97.58;	Score 640;	DB 1;	length 229;
	Best Local Similarity	97.58;	Pred. No. 3e-61		
	Matches 117;	Conservative	2;	Mismatches 1;	Indels 0;
				Gaps	0;
QY	2	SSSHPIFRGFGSCDSVSYWVGDKTTATDINGKEMVLGSEVINNSYFQYFETKCRD	61		
DB	110	SSSHPIFRGFGSCDSVSYWVGDKTTATDINGKEMVLGSEVINNSYFQYFETKCRD	169		
QY	62	PAPVDSGCRGIDSKHNHNSYCTTHTTFFVKALITMDGQAAARFRITDIAVCYLSKAAVRA	221		
DB	170	PAPVDSGCRGIDSKHNHNSYCTTHTTFFVKALITMDGQAAARFRITDIAVCYLSKAAVRA	229		

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RESULT 3
NGF_BOVIN
ID NGF_BOVIN STANDARD; PRT; 231 AA.
AC P13600; 018969;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-JUL-1988 (Rel. 36, last sequence update)
DT 15-JUL-1988 (Rel. 198, last annotation update)
DE Beta-nerve growth factor precursor (beta-NGF) (fragment).
GN NGGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RC MEDLINE=97430845; PubMed=9284944;
RA Eldique C., Laurent P., Hayes H., Rodellier C., Levezuel H.,
RA Zaigosa P.;
RT "Assignment of the beta-nerve growth factor (NGFB) to bovine
RT chromosome 3 band q23 by in situ hybridisation."
RL Cytogenet. Cell Genet. 77:306-307(1997).
RN [2]
RP SEQUENCE OF 107-231 FROM N.A.
RX MEDLINE=86500647; PubMed=2427334;
RA Meier R., Becker Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconerved domains and their
RT relationship to the biological activity and antigenicity of NGF."
RL EMBO J. 5:1489-1493(1986).
-1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS.
CC
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC

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CC CC -1 SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR DR EMBL: Y09566; CAAT0759.1; -.
DR DR EMBL: M28809; AAA30666.1; -.
DR DR PIR: A26312; A26312.
DR DR HSSP: P01139; 1BER.
DR DR InterPro: IPR002072; NCF.
DR DR Pfam: PF00243; NCF_1.
DR DR ProDom: PD002052; NCF_1.
DR DR SMART: SM00140; NCF_1.
DR DR PROSITE: PS00248; NCF_1; 1.
DR DR PROSITE: PS0270; NCF_2; 1.
DR DR Growth factor; Signal.
KW KW FT SIGNAL 1
FT FT NON_TER 1
FT FT PROPEP <1 8 POTENTIAL.
FT FT CHAIN 9 111 BY SIMILARTY.
FT FT DISULFID 112 231 BETA-NERVE GROWTH FACTOR.
FT FT DISULFID 126 191 BY SIMILARTY.
FT FT DISULFID 169 219 BY SIMILARTY.
FT FT DISULFID 179 221 BY SIMILARTY.
FT FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CONFLICT 118 118 L -> F (IN REF. 2).
FT FT CONFLICT 161 161 R -> K (IN REF. 2).
FT FT CONFLICT 230 231 AP -> RA (IN REF. 2).
SQ SQ SEQUENCE 231 AA; 25437 MW; 01605099291A418C CRC64;

Query Match 93.9%; Score 618; DB 1; Length 231;
Best Local Similarity 96.5%; Pred. No. 6.de-59;
Matches 111; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 SSSHPIHRGEFSVCOSVAVGDKTTATDIDKKEVAVLGSEVINNSVSFOYEFEFKCRD 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 112 SSSHPVLHREFSVCDISIVWVGDKTTATDIDKKEVAVLGSEVINNSVSFOYEFEFKCRD 171

Oy 62 PNPDSCCRIDSKHNHSYCCTHTTFVVALTNCKGKAAMRIRIDTRACVCYSRK 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 172 PNPDSCCRIDSKHNHSYCCTHTTFVVALTNCKGKAAMRIRIDTRACVCYSRK 226

RESULT 4
NGF_RAT STANDARD: PRT: 241 AA.
ID_NGF_RAT
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eumetazoa; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; PubMed=3184206;
RA Whittemore S.R., Friedman P.L., Larhammar D.G., Persson H.,
RA Gonzalez-Carvajal M., Holets V.R.;
RT "Rat beta-nerve growth factor sequence and site of synthesis in the
RL adult hippocampus.";
RJ J. Neurosci. Res. 20:403-410(1988).
RN [2]
RP SEQUENCE OF 178-219 FROM N.A.
RX SPRAIN-Sprague-Dawley; Tissue=Liver;
RX MEDLINE=9122373; PubMed=2023430;
RA Haliboeck F., Ibanez C.F., Persson H.,
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RT *Evolutionary studies of the nerve growth factor family reveal a
RT member abundantly expressed in Xenopus ovary.*;
RL Neurin 6:845-858(1991).
CC CC
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSOR NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC
DR EMBL; M36589; AAA41697.1; ALT_INIT.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PFD00243; NGF_1.
DR PRINTS; PR00266; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
KM Growth factor; signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 121 POTENTIAL.
FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
FT DISULFID 136 201 BY SIMILARITY.
FT DISULFID 178 229 BY SIMILARITY.
FT DISULFID 189 231 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 241 AA: 27009 MW: 665F42371563213D CRC64;

Query Match 91.0% Score 599; DB 1; Length 241;
Best Local Similarity 91.6% Pred. No. 7,6e-57;
Matches 109; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SSSHPFRHKESEYCVSVSWYGDGTTTDTDKGKGVAVLGEVAINNSVROTFETKCD 61
DB 122 SSTRPCHMKESEYCVSVSWYGDGTTTDTDKGKGVAVLGEVAINNSVROTFETKCA 181
QY 62 PNPVDSGCRGIDSKHNSYCTTTRTFVAVLMTDGRQAAHFFIIDPACVYSRRAVR 120
DB 182 PNPVDSGCRGIDSKHNSYCTTTRTFVAVLMTDGRQAAHFFIIDPACVYSRRAVR 240

RESULT 5
NGF_MOUSE STANDARD: PRT: 241 AA.
AC P01139; 063864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=83167518; PubMed=6336309;
RA Scott J., Selby M.J., Orde M.S., Quiroga M., Bell G.I., Rutter W.J.;
RT "Isolation and nucleotide sequence of a cDNA encoding the precursor
RT of mouse nerve growth factor.";
RL Nature 302:538-540(1983).
NN [2]

```

RP SEQUENCE FROM N.A.  
 RX MEDLINE-83244969; PubMed-6688123;  
 RA Ullrich A., Gray A., Berman C., Dull T.J.;  
 RT "Human beta-nerve growth factor gene sequence highly homologous to  
 RL that of mouse.";  
 RN Nature 303:821-825(1983).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-84206565; PubMed-6337169;  
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;  
 RT "Sequence homology of human and mouse beta-NGF subunit genes.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-C57BL/6; TISSUE-Submaxillary gland;  
 RA Selby M.J., Edwards R., Sharp F., Rutter M.J.;  
 RT "Mouse nerve growth factor gene: structure and expression.";  
 RL Mol. Cell. Biol. 7:3057-3064(1987).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93264918; PubMed-1284621;  
 RA Yamamoto T., Yamakuni T., Okabe N., Amano T.;  
 RT "Production and secretion of nerve growth factor by clonal striated  
 RL muscle cell line, G8-1.";  
 RN Neurochem. Int. 21:251-258(1992).  
 RP SEQUENCE OF 127-239.  
 RX MEDLINE-73075048; PubMed-4566923;  
 RA Angeletti R.H., Hermodson M.A., Bradshaw R.A.;  
 RT Amino acid sequences of mouse 2.5S nerve growth factor. II.  
 RL Isolation and characterization of the thermolytic and peptic peptides  
 RN and the complete covalent structure.";  
 RP BIOCHEMISTRY 13:1100-115(1973).  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE-93065986; PubMed-1956407;  
 RA McDonald N.O., Lapatto R., Murray-Rust J., Gunning J., Mlodaver A.,  
 RT Blundell T.L.;  
 RL "New protein fold revealed by a 2.3-A resolution crystal structure of  
 RT nerve growth factor.";  
 RN Nature 354:411-414(1991).  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE-94260545; PubMed-8201620;  
 RA Holland D.R., Coussens L.S., Meng W., Matthews B.W.;  
 RT "Nerve growth factor in different crystal forms displays structural  
 RL flexibility and reveals zinc binding sites.";  
 RN J. Mol. Biol. 239:385-400(1994).  
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.  
 RX STRAIN-Swiss Webster; TISSUE-Submaxillary gland;  
 RA MEDLINE-98035451; PubMed-9351801;  
 RT Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;  
 RL "Structure of mouse 7S NGF: a complex of nerve growth factor with  
 RT four binding proteins.";  
 RN Structure 5:1175-1285(1997).  
 RP -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 CC EMBL; M35075; AAA39818.1; ALT\_INIT.

DR EMBL; V00836; CAA24221.1; ALT\_INIT.  
 DR EMBL; K01759; AAA39820.1; ALT\_INIT.  
 DR EMBL; M14805; AAA39821.1; ALT\_INIT.  
 DR EMBL; M17298; AAA37687.1; ALT\_INIT.  
 DR EMBL; M17297; AAA37687.1; JOINED.  
 DR EMBL; M17297; AAA37687.1; JOINED.  
 DR EMBL; S62089; CAB32081.2; ALT\_SEQ.  
 DR PIR; A01400; NGNSMG.  
 DR PDB; 1BET; 31-MAY-94.  
 DR PDB; 1BFG; 08-MAR-96.  
 DR PDB; 1SGF; 27-MAY-98.  
 DR MGD; MGI:97321; NGID.  
 DR InterPro; IPR02072; NGF.  
 DR Pfam; PF00243; NGF; 1.  
 DR PRINTS; PR0268; NGF.  
 DR ProDom; PD02052; NGF; 1.  
 DR SMART; SM00140; NGF; 1.  
 DR PROSITE; PS00248; NGF\_1; 1.  
 DR PROSITE; PS0270; NGF\_2; 1.  
 DR Growth factor; Signal; 3D-structure.  
 KW SIGNAL.  
 FT PROPEP.  
 FT CHAIN.  
 FT DISULFID.  
 FT DISULFID.  
 FT CARBOHYD.  
 FT CARBOHYD.  
 FT CONFLICT.  
 SQ SEQUENCE 241 AA; 27076 MW; 16465ELDC55081 CRC64;  
 Query Match 89.2%; Score 587; DB 1; Length 241;  
 Best Local Similarity 90.8%; Pred. No. 1.5e-55;  
 Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 Oy 2 SSSHPFHRGESEFVCSVWVGDKTTATDIDKGEVNIAGEVINNSVFRQYFEETCRD 61  
 Db 122 SSTRHPFHRGESEFVCSVWVGDKTTATDIDKGEVNIAGEVINNSVFRQYFEETCR 181  
 Oy 62 PNPVDSGCRGIDSKHNSYCTTHTFYVYALTMDSQAAHRRIRIDTCVLSKKAVER 120  
 Db 182 SNPVESGCRGIDSKHNSYCTTHTFYVYALTMDSQAAHRRIRIDTCVLSKKAVER 240  
 RESULT 6  
 NGF\_CHICK STANDARD; PRT; 243 AA.  
 AC P05200;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGFB.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-86300646; PubMed-3017695;  
 RA Ebendahl T., Larhammar D., Persson H.;  
 RT "Structure and expression of the chicken beta nerve growth factor  
 RL gene.";  
 RN EMBL J. 5:1483-1487(1986).  
 RP SEQUENCE OF 118-243 FROM N.A.  
 RX MEDLINE-86248129; PubMed-3720959;  
 RA Wion D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,  
 RT "Molecular cloning of the avian beta-nerve growth factor gene:  
 RT transcription in brain.";  
 RL FEBS Lett. 203:82-86(1986).

```

RN [3]
RP SEQUENCE OF 121-243 FROM N.A.
RX MEDLINE-86300647; PubMed-2427334;
RA Meier R., Becker Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF);
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF.";
RL EMBL J. 5:1489-1493(1986).
RN [4]
RP SEQUENCE OF 181-222 FROM N.A.
RX MEDLINE-91222573; PubMed-2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
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CC -----
DR EMBL: X04003; CAA27633.1; ALT_INIT.
DR EMBL: X04067; CAA27703.1;
DR EMBL: M26810; AAA48984.1;
DR PIR: A24857; A24857.
DR PIR: A26311; A26311.
DR HSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF.1.
DR SMART: SM00140; NGF.1.
DR PROSITE: PS00248; NGF.1;
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 125
FT CHAIN 126 243 BETA-NERVE GROWTH FACTOR.
FT DISULFID 139 204 BY SIMILARITY.
FT DISULFID 182 232 BY SIMILARITY.
FT DISULFID 192 234 BY SIMILARITY.
SQ SEQUENCE 243 AA; 27138 MM; 74C306CB2079DA07 CRC64;

Query Match 88.38; Score 581; DB 1; Length 243;
Best Local Similarity 88.08; Pred. No. 6.4e-55;
Matches 103; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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GN NGF.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OC NCBI_TaxID:10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89177243; PubMed-2926397;
RA Schwartz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;
RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
RT from the guinea pig prostate gland.";
RL J. Neurochem. 52:1203-1209(1989).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
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CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
DR PIR: J10097; J10097.
DR HSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF.1.
DR SMART: SM00140; NGF.1.
DR PROSITE: PS00248; NGF.1;
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 121
FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
FT DISULFID 136 201 BY SIMILARITY.
FT DISULFID 179 229 BY SIMILARITY.
FT DISULFID 189 231 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 241 AA; 26821 MM; 2F4E26B197804BF4 CRC64;

Query Match 88.18; Score 580; DB 1; Length 241;
Best Local Similarity 87.48; Pred. No. 8.1e-55;
Matches 104; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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RESULT 7
NGF_CAVPO STANDARD: PRT; 241 AA.
ID NGF_CAVPO
AC P19093;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).

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RESULT 8
NGF_PRANA STANDARD: PRT; 241 AA.
ID NGF_PRANA
AC P20675;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OC NCBI_TaxID:10112;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89172070; PubMed-3234767;
RA Fahnestock M., Bell R.A.;
RT "Molecular cloning of a cDNA encoding the nerve growth factor
RT precursor from Mastomys natalensis.";
Gene 69:257-264(1988).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M22748; AAA40599.1; ALT_INIT.
CC PIR: J70343; NGRTBA.
CC HSSP: P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF_1.
CC PRINTS: PR00268; NGF.
CC PRODOM: PD002052; NGF_1.
CC SMART: SM00140; NGF_1.
CC DR PROSITE: PS00248; NGF_1;
CC DR PROSITE: PS50270; NGF_2; 1.
CC Growth factor; Signal.
CC KW SIGNAL.
CC FT PROPEP 1 18 POTENTIAL.
CC FT CHAIN 19 121 BETA-NERVE GROWTH FACTOR.
CC FT DISULFID 132 241 BY SIMILARITY.
CC FT DISULFID 136 201 BY SIMILARITY.
CC FT DISULFID 179 229 BY SIMILARITY.
CC FT CARBOHYD 189 231 BY SIMILARITY.
CC FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 241 AA; 27035 MW; 88FB8207A1FEB2E7 CRC64;

Query Match 86.5%; Score 569; DB 1; Length 241;
Best Local Similarity 87.4%; Pred. No. 1.2e-53;
Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 SSHPHFRGEFVSVCDSVSVWVGDKTTATDINGKEVNLGGEVNIINSVFRQYFEETKCRD 61
DB 122 SSTHPVPMGEFVSVCDSVSVWVGDKTTATDINGKEVNLGGEVNIINSVFRQYFEETKCR 181
OY 62 PNPVDSGRCIDSKHNSYCTTHTFEVKALTMDSKQAMRFIRIDTACVCLSKAVRR 120
DB 182 RNPVSSGCRIDSKHNSYCTTHTFEVKALTMDSKQAMRFIRIDTACVCLSKAVRR 240

RESULT 9
NGF_XENLA STANDARD: PRT; 231 AA.
ID NGF_XENLA
AC P31617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African Clawed Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8155;
RN [1]
RP MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campioni M., Cardinale B., Pierandrea-Amaldi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [2]
RC SEQUENCE OF 170-211 FROM N.A.
TISSUE=Liver:

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RX MEDLINE=91222573; PubMed=2025430;
RA Hallboeck F., Ihanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL: X55716; CAA39249.1; ALT_INIT.
CC PIR: S14481; S14481.
CC HSSP: P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF_1.
CC PRINTS: PR00268; NGF.
CC PRODOM: PD002052; NGF_1.
CC SMART: SM00140; NGF_1.
CC DR PROSITE: PS00248; NGF_1;
CC DR PROSITE: PS50270; NGF_2; 1.
CC Growth factor; Signal.
CC KW SIGNAL.
CC FT PROPEP 1 18 POTENTIAL.
CC FT CHAIN 19 114 NERVE GROWTH FACTOR.
CC FT DISULFID 115 231 BY SIMILARITY.
CC FT DISULFID 128 193 BY SIMILARITY.
CC FT DISULFID 171 221 BY SIMILARITY.
CC FT CARBOHYD 181 223 BY SIMILARITY.
CC FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;

Query Match 85.6%; Score 563; DB 1; Length 231;
Best Local Similarity 88.4%; Pred. No. 5.1e-53;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 5 HPFHRGEFVSVCDSVSVWVGDKTTATDINGKEVNLGGEVNIINSVFRQYFEETKCRDNP 64
DB 117 HPVLHKGESVSCDSVSVWVGDKTTATDINGKEVNLGGEVNIINSVFRQYFEETKCRDNP 176
OY 65 VDSGCRGIDSKHNSYCTTHTFEVKALTMDSKQAMRFIRIDTACVCLSKR 116
DB 177 VSSGCRGIDSKHNSYCTTHTFEVKALTMDSKQAMRFIRIDTACVCLSKR 228

RESULT 10
NGF_BUNMU STANDARD: PRT; 243 AA.
ID NGF_BUNMU
AC P34128;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Bungarus multicinctus (Many-banded Krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea.
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Venom gland;
RC MEDLINE=93192074; PubMed=7916740;
RA Danse J.M., Garnier J.M.;

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RT      "Molecular cloning of a cDNA encoding a nerve growth factor precursor
RL      from the krait, Bungarus multicinctus."
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC      or send an email to license@1sb.ch)
CC      -----
DR      EMBL: S56213; AAB25729.1; -
DR      HSSP: P01139; 1BET.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      PRINTS: PR00268; NGF.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS50270; NGF_2; 1.
DR      PROSITE: PS50270; NGF_2; 1.
KM      Growth factor, Signal.
FT      SIGNAL 1 18
FT      PROPEP 19 125
FT      CHAIN 126 243
FT      DISULFID 139 204
FT      DISULFID 182 232
FT      DISULFID 192 234
FT      DISULFID 192 234
SQ      SEQUENCE 243 AA; 27514 MW; E33F6B142179A08 CRC64;

Query Match 74.2%; Score 488; DB 1; Length 243;
Best Local Similarity 73.0%; Pred. No. 5.5e-45;
Matches 84; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY      2 SSSPIRFRGEFSVCDVSVWVGDKTATDIDKREVMVLGEVINNSVPROYFETKCRDNP 61
DB      125 NENPVPNNGEHSVCDVSVWVGDKTATDIDKREVMVLGEVINNSVPROYFETKCRN 184
OY      62 PNPVDSGCRGIDSKHNSYCTTTHTFVKALYMDGKQAMRFRIIDPACVCLSRK 116
DB      185 PNPVDSGCRGIDSKHNSYCTTTHTFVKALYMDGKQAMRFRIIDPACVCLSRK 239

RESULT 11
NGF_DABRR
ID      NGF_DABRR STANDARD; PRT; 117 AA.
AC      P30894;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      Nerve growth factor (NGF).
OS      Dabola russelli russelli (Russell's viper) (Vipera russelli russelli).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Viperidae; Viperinae; Dabola.
OX      NCBI_TaxID=31159;
RN      [1]
RP      SEQUENCE.
RC      TISSUE-Venom;
RL      MEDLINE=91120151; PubMed=1477101;
RA      Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT      "Purification and amino acid sequence of a nerve growth factor from
RT      the venom of Vipera russelli russelli."
RL      Biochem. Biophys. Acta 1160:287-292(1992).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT

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CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      PIR: S28161; S28161.
DR      HSSP: P01139; 1BET.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      PRINTS: PR00268; NGF.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS50270; NGF_2; 1.
KM      Glycoprotein; Growth factor.
FT      DISULFID 12 77
FT      DISULFID 55 105
FT      DISULFID 65 107
FT      CARBOHYD 21 21
FT      CARBOHYD 21 21
SQ      SEQUENCE 117 AA; 13283 MW; A64559C5FEC11P66 CRC64;

Query Match 73.1%; Score 481; DB 1; Length 117;
Best Local Similarity 73.2%; Pred. No. 1.4e-44;
Matches 82; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

OY      5 HPFRFRGEFSVCDVSVWVGDKTATDIDKREVMVLGEVINNSVPROYFETKCRDNP 64
DB      1 HPFRFRGEFSVCDVSVWVGDKTATDIDKREVMVLGEVINNSVPROYFETKCRDNP 60
OY      65 VDSGCRGIDSKHNSYCTTTHTFVKALYMDGKQAMRFRIIDPACVCLSRK 116
DB      61 VDSGCRGIDSKHNSYCTTTHTFVKALYMDGKQAMRFRIIDPACVCLSRK 112

RESULT 12
NGF_NAJNA
ID      NGF_NAJNA STANDARD; PRT; 116 AA.
AC      P01140;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      01-JUL-1993 (Rel. 26, Last annotation update)
DE      Nerve growth factor (NGF).
OS      Naja naja (Indian cobra).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC      Elapidae; Elapinae; Naja.
OX      NCBI_TaxID=35670;
RN      [1]
RP      SEQUENCE.
RC      TISSUE-Venom;
RL      MEDLINE=91138755; PubMed=1995338;
RA      Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT      "Amino acid sequences of nerve growth factors derived from cobra
RT      venoms."
RL      FEBS Lett. 279:38-40(1991).
RN      [2]
RP      PRELIMINARY SEQUENCE.
RC      TISSUE-Venom;
RL      MEDLINE=76114772; PubMed=1247508;
RA      Hogue-Angelotti R.A., Frazier W.A., Jacobs J.W., Mall H.D.,
RA      Bradshaw R.A.;
RT      "Purification, characterization, and partial amino acid sequence of
RT      nerve growth factor from cobra venom."
RL      Biochemistry 15:26-34(1976).
CC      -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC      MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC      STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC      EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC      NEURONS IN THE BRAIN.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      PIR: A01401; NGNXXI.
DR      PIR: S13927; S13927.

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DR  HSP: P01139; 1BET.
DR  InterPro: IPR002400; GF_CYSKNOT.
DR  Pfam: PFO0243; NGF_1.
DR  PRINTS: PR00243; NGF_1.
DR  PRINTS: PR00438; GFCYSKNOT.
DR  PRODOM: P0002052; NGF_1.
DR  SMART: SM00140; NGF_1.
DR  PROSITE: PS00248; NGF_1; 1.
DR  PROSITE: PS50270; NGF_2; 1.
DR  PROSITE: PS50270; NGF_2; 1.
DR  Growth factor.
DR  DISULFID 14 78 BY SIMILARITY.
DR  DISULFID 56 106 BY SIMILARITY.
DR  DISULFID 66 108 BY SIMILARITY.
DR  SEQUENCE 116 AA: 13022 MW: DAB346B1093E7E06 CRC64;

Query Match 67.9%; Score 446.5; DB 1; Length 116;
Best Local Similarity 69.6%; Pred. No. 6,6e-41;
Matches 78; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFHGEFSCDSVSVWGDKTATDICKKEVNVLCGEVNIINSVFOYFEETKCRDNP 64
DB 3 HPVNLGEHSVCDSVSNW-TKTATDICKNTVTMEVNLNDKVKYKEFEETKCRKPNP 61

OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVLSRK 116
DB 62 EPSGCRGIDSHNSYCTETDIFIKALTMDSKQAMRFIRIDTACVLSRK 113

RESULT 13
NGF_NAJAT
ID NGF_NAJAT STANDARD; PRT: 116 AA.
AC P21377;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Nerve growth factor (NGF).
OS Naja atra (Chinese cobra), and
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosteus; Squamata; Sclerozoa; Serpentes; Colubridae;
OC Elapidae; Elapine; Naja.
OX NCBI_Taxid=8656, 8649;
RN 11;
RP SEQUENCE.
RC SPECIES-N.a.atra: TISSUE-Venom;
RA MEDLINE-90147847; PubMed-2619756;
RA Oda T., Ohta M., Inoue S., Ikeda K., Furukawa S., Hayashi K.;
RT "Amino acid sequence of nerve growth factor purified from the venom
of the Formosan cobra Naja atra.";
RL Biochem. Int. 19:909-917(1989).
RN 12;
RP SEQUENCE.
RC SPECIES-N.a.kaouthia: TISSUE-Venom;
RA MEDLINE-9113875; PubMed-1995338;
RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT "Amino acid sequences of nerve growth factors derived from cobra
venoms.";
RL FEBS Lett. 279:38-40(1991).
RN 13;
RP MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR HSP: P01139; 1BET.
DR InterPro: IPR002400; GF_CYSKNOT.
DR InterPro: IPR002072; NGF.
DR Pfam: PFO0243; NGF_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00268; NGF.

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DR  PRODOM: P0002052; NGF_1.
DR  SMART: SM00140; NGF_1.
DR  PROSITE: PS00248; NGF_1; 1.
DR  PROSITE: PS50270; NGF_2; 1.
DR  PROSITE: PS50270; NGF_2; 1.
DR  Growth factor.
DR  DISULFID 14 78 BY SIMILARITY.
DR  DISULFID 56 106 BY SIMILARITY.
DR  DISULFID 66 108 BY SIMILARITY.
DR  SEQUENCE 116 AA: 13064 MW: DAB3421093E7E06 CRC64;

Query Match 67.2%; Score 442.5; DB 1; Length 116;
Best Local Similarity 68.8%; Pred. No. 1,8e-40;
Matches 77; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

OY 5 HPFHGEFSCDSVSVWGDKTATDICKKEVNVLCGEVNIINSVFOYFEETKCRDNP 64
DB 3 HPVNLGEHSVCDSVSNW-TKTATDICKNTVTMEVNLNDKVKYKEFEETKCRKPNP 61

OY 65 VDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVLSRK 116
DB 62 EPSGCRGIDSHNSYCTETDIFIKALTMDSKQAMRFIRIDTACVLSRK 113

RESULT 14
NGF_XIPMA
ID NGF_XIPMA STANDARD; PRT: 194 AA.
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_Taxid=8083;
RN 11;
RP SEQUENCE FROM N.A.
RA MEDLINE-9233301; PubMed-1629719;
RA Gotz R., Raulf F., Schmitt M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
structure and function than nerve growth factor during vertebrate
evolution.";
RL J. Neurochem. 59:432-442(1992).
RN 12;
RP MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: X59941; CAA42566.1; -.
DR HSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PFO0243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODOM: P0002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; FALSE_NEG.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
DR SIGNAL 1 30 POTENTIAL.
DR PROPER 31 79

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FT CHAIN 80 194 NERVE GROWTH FACTOR.  
 FT DISULFID 90 155 BY SIMILARITY.  
 FT DISULFID 133 183 BY SIMILARITY.  
 FT DISULFID 143 183 BY SIMILARITY.  
 SQ SEQUENCE 194 AA: 21596 MW: 0369E0F4A51147AE CRC64:

Query Match 59.0%; Score 388; DB 1; Length 194;  
 Best Local Similarity 66.1%; Pred. No. 2, 1e-34;  
 Matches 72; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

OY 9 HRGEFVCDVSVMVGDKTATDITDKGKEMVLGEVNNINSVFROYFETKCRDPNPVDSG 68  
 DB 83 HNGVSVCESSVWVGMKTATDITSGKEVTLVPMNNVKKKQYFETTCSPSGGR 142  
 OY 69 CRGIDSKHNSYCTTHTFVATLMDCKQAMRFIRIDTACVCLSRKA 117  
 DB 143 CIGIDARHNSGCHNSHTFVATLTSSENOVAMRLIRINVCVCLSRKS 191

## RESULT 15

NT3\_CHICK

ID NT3\_CHICK

STANDARD: PRT: 257 AA.

AC P25433:

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)

DE (Nerve growth factor 2) (NGF-2).

GN NT3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-93091238; PubMed-1457809;

RA Maisongrande P., Belluscio L., Conover J.C., Yancopoulos G.D.;

RT "Gene sequences of chicken BDNF and NT-3.";

RL DNA Seq. 3:49-54(1992).

RN [2]

RP SEQUENCE OF 194-236 FROM N.A.

RX MEDLINE-9122573; PubMed-2025430;

RA Hallboeck F., Ibanez C.F., Persson H.;

RT "Evolutionary studies of the nerve growth factor family reveal a

RT novel member abundantly expressed in Xenopus ovary.";

RL Neuron 6:845-858(1991).

CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND

CC PROPRIOCEPTIVE SENSORY NEURONS.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

CC -----

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CC -----

CC EMBL: M83378; AAA68880.1; -.

DR HSSP: P20783; 188K.

DR InterPro: IPR002400; GF\_cysknot.

DR Pfam: PF00243; NGF\_1.

DR PRINTS: PR00438; GFCSKNOT.

DR PRODOM: PD002052; NGF\_1.

DR SMART: SM00140; NGF\_1.

DR PROSITE: PS00248; NGF\_1; 1.

DR PROSITE: PS00270; NGF\_2; 1.

KW Growth factor; Signal.

FT SIGNAL 1 16

FT POTENTIAL.

FT

FT

FT

FT PROPEP 17 138  
 FT CHAIN 139 257 NEUROTROPHIN-3.  
 FT DISULFID 132 217 BY SIMILARITY.  
 FT DISULFID 195 246 BY SIMILARITY.  
 FT DISULFID 205 248 BY SIMILARITY.  
 FT CARBOHYD 131 131 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 257 AA: 29701 MW: E043BA2A005C1E7 CRC64:

Query Match 57.8%; Score 380.5; DB 1; Length 257;  
 Best Local Similarity 59.8%; Pred. No. 1, 8e-33;  
 Matches 67; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

OY 9 HRGEFVCDVSVMVGDKTATDITDKGKEMVLGEVNNINSVFROYFETKCRDPNPVDSG 68  
 DB 145 HRGEYVCDSESLMTWDRSSAIDIRGHQVTVLGEIKTGNSPVROGYFETKCRDPNPVDSG 204  
 OY 69 CRGIDSKHNSYCTTHTFVATLMDCKQAMRFIRIDTACVCLSRKA 119  
 DB 205 CRGIDSKHNSYCTTHTFVATLMDCKQAMRFIRIDTACVCLSRKA 256

Search completed: December 2, 2002, 15:12:42  
 Job time : 4.96483 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:42 : Search time 18.7245 Seconds  
(without alignments)  
1331.501 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 658

Sequence: 1 PSSHPHFHRCFEVSCDSVS.....FIRIDPACVCLSKAVRRA 121

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MNC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_PROTOCT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	98.5	241	4 O9P208	O9P208 homo sapien
2	648	98.5	241	4 O9UKT8	O9UKT8 homo sapien
3	648	98.5	241	6 O9N2T1	O9N2T1 pan troglod
4	648	98.5	241	6 O9N2F0	O9N2F0 gorilla gor
5	648	98.5	241	6 O9N2E9	O9N2E9 pongo pygma
6	648	97.3	241	4 O9P6P0	O9P6P0 homo sapien
7	578	87.8	217	6 O9N183	O9N183 macaca fusc
8	529	80.4	294	11 O91XB4	O91XB4 mus musculu
9	499	75.8	241	13 O9OWJ8	O9OWJ8 bothrops ja
10	492	74.8	241	13 O9PDE9	O9PDE9 crocatus du
11	459	69.8	87	6 O9RTC3	O9RTC3 cervus elap
12	458	69.6	87	4 O9P2Z4	O9P2Z4 homo sapien
13	348	52.9	286	13 O91988	O91988 xiphophorus
14	338.5	51.4	241	6 O9N182	O9N182 macaca fusc
15	324.5	49.3	153	11 O9CYL3	O9CYL3 mus musculu
16	324.5	49.3	247	6 O97759	O97759 allurus ful

17	324.5	49.3	249	11 O9VHK4	O9VHK4 mus musculu
18	318.5	48.4	246	13 O8OG76	O8OG76 japedura sp
19	317.5	48.3	177	13 O918L2	O918L2 poephila sp
20	314.5	47.8	270	13 O9YH42	O9YH42 brachydantio
21	312.5	47.5	246	13 O8OG75	O8OG75 phrynocephala
22	304.5	46.3	246	13 O8OG74	O8OG74 cyclophorus
23	296.5	45.1	247	13 O8OG77	O8OG77 cyclophorus
24	291.5	44.3	101	6 O9PRT2	O9PRT2 macaca fusc
25	283	43.0	324	13 O9XK95	O9XK95 lampetra fl
26	271.5	41.3	186	12 O9J5D9	O9J5D9 fowlpox vlr
27	224	34.0	42	6 O02802	O02802 trichosaurus
28	223	33.9	85	6 O02790	O02790 macropus fu
29	217	33.0	85	6 O13114	O13114 isodon mac
30	217	33.0	85	6 O13122	O13122 tarapaea ro
31	217	33.0	85	6 O02795	O02795 ornithorhyn
32	217	33.0	85	6 O02798	O02798 petarus br
33	217	33.0	85	6 O13104	O13104 cercartacus
34	217	33.0	85	6 O02792	O02792 notoryctes
35	217	33.0	85	6 O13105	O13105 dasyuroides
36	217	33.0	85	6 O02801	O02801 lachylosus
37	216	32.8	85	6 O02803	O02803 trichosurus
38	211	32.1	42	6 O02794	O02794 ornithorhyn
39	209	31.8	42	6 O02800	O02800 tachylosus
40	166	25.2	42	13 O13118	O13118 protoplerus
41	156	23.7	185	11 O99NV9	O99NV9 pedetes cap
42	156	23.7	186	6 O9BFL0	O9BFL0 chetophrac
43	155	23.6	184	6 O9BFL5	O9BFL5 lupala mmo
44	155	23.6	185	6 O9BFL6	O9BFL6 talpa alai
45	155	23.6	185	6 O9BFL5	O9BFL5 condylura c

## ALIGNMENTS

## RESULT 1

ID O9P208 PRELIMINARY; PRT: 241 AA.

AC O9P208: 01-OCT-2000 (T-EMBLrel. 15, Created)

DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DE Beta-nerve growth factor (Fragment).

GN BETA-NGF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kitano T., Kobayakawa H., Saitou N.;

RT "Silver Project".

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL: AB037517; BAA90437.1; --

DR HSSP; P01139; 1BET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

FT NON\_TER 241

SQ SEQUENCE 241 AA: 26998 MW: D5531ED82596C14 CRC64:

Query Match 98.5% Score 648; DB 4; Length 241;

Best Local Similarity 99.2% Pred No. 2,4e-65;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPHFHRCFEVSCDSVSVMGDKTATDIDGKEVMVLGEVNIINSVFRQYFEETRCRD 61  
DB 122 SSSHPHFHRCFEVSCDSVSVMGDKTATDIDGKEVMVLGEVNIINSVFRQYFEETRCRD 101  
OY 62 PNVPDSCRGIDSKHNNVSCCTTHTFVKALITMDGKQAMRFRIIDTACVCLSKAVRRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 241

## RESULT 2

ID 090KL8 PRELIMINARY: PRT: 241 AA.

AC 090KL8: 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Nerve growth factor B.

GN NGF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99256269; PubMed=10322959;

RA Tong Y., Wang H., Chen W.;

RT Cloning and sequencing of the gene for premature beta nerve growth

RT factor.

RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Tong Y., Wang H.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF150960; AAD55975.1;

DR HSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

SO SEQUENCE 241 AA; 26959 MW; 619DFC65E3B0671 CRC64;

Query Match

Best Local Similarity 99.5%; Score 648; DB 4; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFHNGEFSVCDVSVMVGDKTTATDIDKREVMVLGEVINNSVFRQYFEETKCRD 61

DB 122 SSSHPIFHNGEFSVCDVSVMVGDKTTATDIDKREVMVLGEVINNSVFRQYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 241

RESULT 3

O9N2F1

ID 09N2F1 PRELIMINARY: PRT: 241 AA.

AC 09N2F1:

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Beta-nerve growth factor (Fragment).

GN BETA-NGF.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

OX NCBI\_TaxID=9599;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CHIMP-220;

RA Kikano T., Kobayakawa H., Saitou N.;

RT "Silver Project";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB037518; BAA90438.1;

DR HSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

FT NON\_TER 241

SO SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match

Best Local Similarity 99.5%; Score 648; DB 6; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFHNGEFSVCDVSVMVGDKTTATDIDKREVMVLGEVINNSVFRQYFEETKCRD 61

DB 122 SSSHPIFHNGEFSVCDVSVMVGDKTTATDIDKREVMVLGEVINNSVFRQYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 241

RESULT 4

O9N2FO

ID 09N2FO PRELIMINARY: PRT: 241 AA.

AC 09N2FO:

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Beta-nerve growth factor (Fragment).

GN BETA-NGF.

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.

OX NCBI\_TaxID=9593;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GORILLA-UI;

RA Kikano T., Kobayakawa H., Saitou N.;

RT "Silver Project";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB037519; BAA90439.1;

DR HSP: P01139; 18ET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF.1; 1.

DR PROSITE: PS50270; NGF.2; 1.

FT NON\_TER 241

SO SEQUENCE 241 AA; 26915 MW; 6F54D163C384B834 CRC64;

Query Match

Best Local Similarity 99.5%; Score 648; DB 6; Length 241;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFHNGEFSVCDVSVMVGDKTTATDIDKREVMVLGEVINNSVFRQYFEETKCRD 61

DB 122 SSSHPIFHNGEFSVCDVSVMVGDKTTATDIDKREVMVLGEVINNSVFRQYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCGKAAMRFIRIDTACVLSRKAARRA 241

RESULT 5

O9N2E9

ID 09N2E9 PRELIMINARY: PRT: 241 AA.

AC 09N2E9:

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

```
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta-nerve growth factor (Fragment).
CN Beta-NGF.
CN Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORAN-UI;
RA Kitano T., Kobayakawa H., Saitou N.;
RT Silver Project.
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037520; BA90440.1; -.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF_1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF_1.
DR SMART; SM00140; NGF_1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
FT NON_TER 241
FT 241
SO SEQUENCE 241 AA; 26876 MW; DFC168E7E4E01F15 CRC64;

Query Match 98.5%; Score 648; DB 6; Length 241;
Best Local Similarity 99.2%; Pred. No. 2,4e-65;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVSVDVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 61
DB 122 SSSHPFHRGFEFVSVDVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 181
OY 62 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRIDACVLSRAAVRA 121
DB 182 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRIDACVLSRAAVRA 241

RESULT 6
OY 096P60 PRELIMINARY; PRT; 241 AA.
AC 096P60;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Nerve growth factor beta.
GN NGF8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411526; AAL05874.1; -.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF_1.
DR PRODOM; PD002052; NGF_1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
FT NON_TER 241
FT 241
SO SEQUENCE 241 AA; 26866 MW; 745216485C21E558 CRC64;

Query Match 97.3%; Score 640; DB 4; Length 241;
Best Local Similarity 97.5%; Pred. No. 2e-64;
Matches 117; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVSVDVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 61
DB 122 SSSHPFHRGFEFVSVDVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 181
OY 62 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRIDACVLSRAAVRA 121
DB 182 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRIDACVLSRAAVRA 241

DB 182 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRIDACVLSRAAVRA 241

RESULT 7
OY 09N183 PRELIMINARY; PRT; 217 AA.
AC 09N183;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta nerve growth factor (fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE-99270338; PubMed-10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys.
RL J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222682; AAF33790.1; -.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF_1.
DR PRINTS; PR00268; NGF_1.
DR PRODOM; PD002052; NGF_1.
DR SMART; SM00140; NGF_1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
FT NON_TER 217
FT 217
SO SEQUENCE 217 AA; 24240 MW; 36A5A2D1DFCD8D5C CRC64;

Query Match 87.8%; Score 578; DB 6; Length 217;
Best Local Similarity 99.1%; Pred. No. 1.8e-57;
Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFHRGFEFVSVDVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 61
DB 112 SSSHPFHRGFEFVSVDVSWVGDKTATADIKGEVNVGLGVNINSVFRQYFFETKCRD 171
OY 62 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRID 107
DB 172 PNPVDSGCGIDSKHNSYCTTHTTFVKALTMGKQAAAFRIRID 217

RESULT 8
OY 091XB4 PRELIMINARY; PRT; 294 AA.
AC 091XB4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Similar to nerve growth factor, beta.
GN NGF8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Salivary Gland;
RA Strausberg R.;
```





FT NON\_TER 1 1  
 FT NON\_TER 241 241  
 SO SEQUENCE 241 AA: 27803 MW: AB95E457C7B07113 CRC64:

Query Match 51.44: Score 338.5: DB 6: Length 241:  
 Best Local Similarity 59.08: Pred. No. 2.8e-30:  
 Matches 59: Conservative 18: Mismatches 22: Indels 1: Gaps 1:

OY 9 HNGEFSVCDSDSVWVGDTATDIDKKEVNVLCSEVNNINSFROFFETKCRDPNPDVG 68  
 DB 142 HNGEFSVCDSDSLMTYDSSAIDIRGHQVTVLCEIKGNSPVKQYFETKCRKAPVKNG 201

OY 69 GCRGIDSKHNSCYCTTHTEFVKALTMDSG-KOANRFIRIDT 107  
 DB 202 GCRGIDSKHNSCYCTTHTEFVKALTMDSG-KOANRFIRIDT 241

RESULT 15

OYCYL3 PRELIMINARY: PRT: 153 AA.  
 AC 09CYL3:  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE Brain derived neurotrophic factor.  
 GN BDNF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Frieschmann W., Gaasterland T., Giasi C., King B., Kochiya H.,  
 Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,  
 Schirml L.M., Staudt F., Suzuki R., Tomita K., Wagner L., Washio T.,  
 Sakai K., Oikio T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 Wyshaw-Borja A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK017559; BAB30805.1; -  
 DR HSP: P23560; 188M.  
 DR MGD: MGI:88145; Bdnf.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF; 1; 1.  
 DR PROSITE: PS50270; NGF; 2; 1.  
 SO SEQUENCE 153 AA: 17519 MW: CA8EB8944CE5B37 CRC64:

OY 68 GCRGIDSKHNSCYCTTHTEFVKALTMDSG-KOANRFIRIDTACVYLSKRAVR 119  
 DB 101 GCRGIDSKHNSCYCTTHTEFVKALTMDSG-KOANRFIRIDTACVYLSKRAVR 153

Search completed: December 2, 2002, 15:12:01  
 Job time: 19.7245 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 8.36928 Seconds  
(without alignments)  
425.386 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 1 PSSMPTFRGEFVSVDVS.....FIRIDTACVLSRAKAVRRA 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*\n2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*\n3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*\n4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*\n5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*\n6: /cgn2\_6/ptodata/1/1aa/Dackfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	121	4	US-09-675-503-2
2	651	98.9	120	3	US-08-970-865-2
3	648	98.9	120	4	US-09-363-573-2
4	648	98.5	120	1	US-08-440-040-3
5	648	98.5	120	2	US-08-441-513A-3
6	648	98.5	120	3	US-08-581-662-31
7	648	98.5	120	4	US-08-845-541B-1
8	648	98.5	120	4	US-09-066-065A-1
9	648	98.5	120	4	US-09-447-356-1
10	648	98.5	120	4	US-09-664-295-31
11	648	98.5	120	5	PCT-US95-06918-3
12	648	98.5	241	1	US-08-266-0808-4
13	648	98.5	241	1	US-08-451-947-5
14	648	98.5	241	2	US-08-424-826A-5
15	648	98.5	241	2	US-08-595-043A-75
16	648	98.5	241	3	US-08-970-865-1
17	648	98.5	241	3	US-08-928-694-5
18	648	98.5	241	4	US-09-363-573-1
19	648	98.5	241	4	US-09-447-356-3
20	648	98.5	241	5	PCT-US91-06950-5
21	648	98.5	241	5	PCT-US95-05423-4
22	648	98.5	242	4	US-09-575-503-1
23	639	97.1	119	3	US-08-753-642-2
24	639	97.1	153	4	US-09-675-922-2
25	639	97.1	157	4	US-09-675-922-4
26	639	97.1	163	4	US-09-675-922-6
27	639	97.1	167	4	US-09-675-922-8

28	634	96.4	120	4	US-08-845-541B-3	Sequence 3, Appl1
29	634	96.4	120	4	US-09-066-065A-3	Sequence 3, Appl1
30	631	95.9	120	4	US-08-845-541B-4	Sequence 4, Appl1
31	631	95.9	120	4	US-09-066-065A-4	Sequence 4, Appl1
32	626	95.1	120	4	US-08-845-541B-12	Sequence 12, Appl1
33	626	95.1	120	4	US-09-066-065A-12	Sequence 12, Appl1
34	625	95.0	120	4	US-08-845-541B-17	Sequence 17, Appl1
35	625	95.0	120	4	US-08-845-541B-20	Sequence 20, Appl1
36	625	95.0	120	4	US-09-066-065A-17	Sequence 17, Appl1
37	625	95.0	120	4	US-09-066-065A-20	Sequence 20, Appl1
38	623	94.7	120	4	US-08-845-541B-18	Sequence 18, Appl1
39	623	94.7	120	4	US-08-845-541B-21	Sequence 21, Appl1
40	623	94.7	120	4	US-09-066-065A-18	Sequence 18, Appl1
41	623	94.7	120	4	US-09-066-065A-21	Sequence 21, Appl1
42	620	94.2	120	4	US-08-845-541B-13	Sequence 13, Appl1
43	620	94.2	120	4	US-08-845-541B-19	Sequence 19, Appl1
44	620	94.2	120	4	US-09-066-065A-13	Sequence 13, Appl1
45	620	94.2	120	4	US-09-066-065A-19	Sequence 19, Appl1

## ALIGNMENTS

```

RESULT 1
US-09-675-503-2
; Sequence 2, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; TITLE OF INVENTION: ISOLATION OF NEUROTROPINS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPIN VARIANTS
; FILE REFERENCE: GENE 037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-675-503-2

Query Match          100.0%  Score 658  DB 4  Length 121:
Best Local Similarity 100.0%  Pred. No. 4, 1e-75:
Matches 121: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSSMPTFRGEFVSVDVSVMWDKTTATDTRKKEVWVIGEVNINSVPROFEFTKCR 60
    |||||||
Db 1 PSSMPTFRGEFVSVDVSVMWDKTTATDTRKKEVWVIGEVNINSVPROFEFTKCR 60
    |||||||
OY 61 DPNPVDSGCGIDSKHMSYCTTHTFEKALTDGKQAMRFTRIDTACVLSRAKAVR 120
    |||||||
Db 61 DPNPVDSGCGIDSKHMSYCTTHTFEKALTDGKQAMRFTRIDTACVLSRAKAVR 120
    |||||||
OY 121 A 121
Db 121 A 121

RESULT 2
US-08-970-865-2
; Sequence 2, Application US/08970865

```



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Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-May-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-970-865-2

Query Match 98.9% Score 651: DB 3: Length 120:
Best Local Similarity 100.0% Pred. No. 3.1e-74:
Matches 120: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 2 SSSHPHFHREFEVSVCDSVSWVGDKTATADIKGKEVNLGEVNIINNSVFRQYFEETKCRD 61
Db 1 SSSHPHFHREFEVSVCDSVSWVGDKTATADIKGKEVNLGEVNIINNSVFRQYFEETKCRD 60
Qy 62 PNPVDSRCRIGIDSKHNNSTCTTHFFVRLTMDGQAAHREIRIDTACVCLSKAVRA 121
Db 61 PNPVDSRCRIGIDSKHNNSTCTTHFFVRLTMDGQAAHREIRIDTACVCLSKAVRA 120

RESULT 3
US-09-363-573-2
Sequence 2, Application US/09363573
Patent No. 6184360
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-May-1997
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-363-573-2

Query Match 98.9% Score 651: DB 4: Length 120:
Best Local Similarity 100.0% Pred. No. 3.1e-74:
Matches 120: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 2 SSSHPHFHREFEVSVCDSVSWVGDKTATADIKGKEVNLGEVNIINNSVFRQYFEETKCRD 61
Db 1 SSSHPHFHREFEVSVCDSVSWVGDKTATADIKGKEVNLGEVNIINNSVFRQYFEETKCRD 60
Qy 62 PNPVDSRCRIGIDSKHNNSTCTTHFFVRLTMDGQAAHREIRIDTACVCLSKAVRA 121
Db 61 PNPVDSRCRIGIDSKHNNSTCTTHFFVRLTMDGQAAHREIRIDTACVCLSKAVRA 120

RESULT 4
US-08-440-049-3
Sequence 3, Application US/08440049
Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Ulfert, Roman
APPLICANT: Presta, Leonard G.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANROTROPIC NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino acid  
TOPOLOGY: Linear  
US-08-440-049-3

Query Match 98.5%: Score 648; DB 1; Length 120;  
Best Local Similarity 99.2%: Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 61  
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 60  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 5  
US-08-441-513A-3  
Sequence 3, Application US/08441513A  
Patent No. 5981480

GENERAL INFORMATION:  
APPLICANT: Ufer, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John W.  
TITLE OF INVENTION: Pantropic Neurotrophic Factors  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,513A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-441-513A-3

Query Match 98.5%: Score 648; DB 2; Length 120;  
Best Local Similarity 99.2%: Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 61  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 60  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 6  
US-08-581-662-31  
Sequence 31, Application US/08581662  
Patent No. 6121235

GENERAL INFORMATION:  
APPLICANT: Gao, Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments  
FILE REFERENCE: P0981  
CURRENT APPLICATION NUMBER: US/08/581,662  
CURRENT FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 36  
SEQ ID NO 31  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-581-662-31

Query Match 98.5%: Score 648; DB 3; Length 120;  
Best Local Similarity 99.2%: Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 61  
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 60  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 7  
US-08-845-541B-1  
Sequence 1, Application US/08845541B  
Patent No. 6333310

GENERAL INFORMATION:  
APPLICANT: Presta, Leonard  
APPLICANT: Ufer, Roman  
APPLICANT: Winslow, John  
TITLE OF INVENTION: NGF VARIANTS  
FILE REFERENCE: GENENT. 039A  
CURRENT APPLICATION NUMBER: US/08/845,541B  
CURRENT FILING DATE: 1995-04-25  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows version 4.0  
SEQ ID NO 1  
LENGTH: 120  
TYPE: PRT  
ORGANISM: homo sapien  
US-08-845-541B-1

Query Match 98.5%: Score 648; DB 4; Length 120;  
Best Local Similarity 99.2%: Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 61  
DB 1 SSSHPIFRHGEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFRQYFFETKCD 60  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDCQAAAFRIRIDTACVCLSRKAVRRA 120

RESULT 8  
US-09-066-065A-1  
Sequence 1, Application US/09066065A

Patent No. 6365373  
GENERAL INFORMATION:  
APPLICANT: Leonard G. Presta, Roman Urfer, John W. Winslow  
TITLE OF INVENTION: NGF Variants  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/066,065A  
FILING DATE: 24-Apr-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/044918  
FILING DATE: 25-Apr-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1098R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-066-065A-1

Query Match 98.5% Score 648; DB 4; Length 120;  
Best Local Similarity 99.2% Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKGEVNLGEVININSVFROYFEETKCRD 61  
DB 1 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKGEVNLGEVININSVFROYFEETKCRD 60

QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSKRAVRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSKRAVRA 120

RESULT 9  
US-09-447-356-1  
Sequence 1, Application US/09447356  
Patent No. 6395513  
GENERAL INFORMATION:  
APPLICANT: FOSTER, KEITH ALAN  
APPLICANT: DUGGAN, MICHAEL JOHN  
APPLICANT: SHONE, CLIFFORD CHARLES  
TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL  
TITLE OF INVENTION: SENSORY AFFERENT FUNCTIONS  
FILE REFERENCE: 023223/0104  
CURRENT APPLICATION NUMBER: US/09/447,356  
CURRENT FILING DATE: 1999-11-22  
PRIOR APPLICATION NUMBER: 08/945,037  
PRIOR FILING DATE: 1998-01-12  
PRIOR APPLICATION NUMBER: GB 9508204.6  
PRIOR FILING DATE: 1995-04-21  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 120  
TYPE: PRT

ORGANISM: Mouse sp.  
US-09-447-356-1

Query Match 98.5% Score 648; DB 4; Length 120;  
Best Local Similarity 99.2% Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKGEVNLGEVININSVFROYFEETKCRD 61  
DB 1 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKGEVNLGEVININSVFROYFEETKCRD 60

QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSKRAVRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSKRAVRA 120

RESULT 10  
US-09-664-295-31  
Sequence 31, Application US/09664295  
Patent No. 6429196  
GENERAL INFORMATION:  
APPLICANT: Gao, Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments  
FILE REFERENCE: GENENT. 051C1  
CURRENT APPLICATION NUMBER: US/09/664,295  
CURRENT FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 08/581,662  
PRIOR FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 37  
SEQ ID NO 31  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-664-295-31

Query Match 98.5% Score 648; DB 4; Length 120;  
Best Local Similarity 99.2% Pred. No. 7.4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKGEVNLGEVININSVFROYFEETKCRD 61  
DB 1 SSSHPFHRGFEFVCDVSVMVGDKTTATDIDKGEVNLGEVININSVFROYFEETKCRD 60

QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSKRAVRA 121  
DB 61 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSKRAVRA 120

RESULT 11  
PCT-US95-06918-3  
Sequence 3, Application PC/TU9506918  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: PANITROPIC NEUROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06918  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 905PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US95-06918-3

Query Match 98.58; Score 648; DB 5; Length 120;  
Best Local Similarity 99.28; Pred. No. 7,4e-74;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEFVCDVSVMVGDKTTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 61  
DB 1 SSSHPFHRGEFVCDVSVMVGDKTTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 60  
QY 62 PNPVDSGCGIDSKHNSYCTTHTTFVKAALTMDSKQAARFIRIDACVCVLSRAVRA 121  
DB 61 PNPVDSGCGIDSKHNSYCTTHTTFVKAALTMDSKQAARFIRIDACVCVLSRAVRA 120

RESULT 12  
US-08-266-080B-4  
Sequence 4, Application US/08266080B  
Patent No. 5606031

## GENERAL INFORMATION:

APPLICANT: Jack Lile  
APPLICANT: Tadshiko Kohno  
APPLICANT: Duane Bonam  
TITLE OF INVENTION: Production of Biologically Active  
TITLE OF INVENTION: Recombinant Neurotrophic Protein  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: wordperfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,080B  
FILING DATE: 27-JUNE-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,122  
FILING DATE: 09-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/087,912  
FILING DATE: 06-JULY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/680,681  
FILING DATE: 04-APRIL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/594,126  
FILING DATE: 09-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/547,750  
FILING DATE: 02-JULY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/505,441

ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: SYNE200C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Inferred amino acid sequence of human NGF  
US-08-266-080B-4

Query Match 98.58; Score 648; DB 1; Length 241;  
Best Local Similarity 99.28; Pred. No. 1.9e-73;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEFVCDVSVMVGDKTTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 61  
DB 122 SSSHPFHRGEFVCDVSVMVGDKTTATDINGKEVWVLEGVNINNSVFRQYFFETKCRD 181  
QY 62 PNPVDSGCGIDSKHNSYCTTHTTFVKAALTMDSKQAARFIRIDACVCVLSRAVRA 121  
DB 182 PNPVDSGCGIDSKHNSYCTTHTTFVKAALTMDSKQAARFIRIDACVCVLSRAVRA 241

RESULT 13  
US-08-451-947-5  
Sequence 5, Application US/08451947  
Patent No. 5702906

## GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Pafin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,947  
FILING DATE:

## CLASSIFICATION:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-947-5

Query Match 98.5%; Score 648; DB 1; Length 241;  
Best Local Similarity 99.2%; Pred. No. 1.9e-73;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEEFVCDVSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCRD 61  
DB 122 SSSHPFHRGEEFVCDVSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCRD 181  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRRA 121  
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRRA 241

RESULT 14  
US-08-424-826A-5  
Sequence 5, Application US/08424826A  
Patent No. 5830858  
GENERAL INFORMATION:  
APPLICANT: Rosenthal, Arnon  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,826A  
FILING DATE: 19-Apr-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240387  
FILING DATE: 10-May-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/548482  
FILING DATE: 31-Jan-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0666P1C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-424-826A-5

Query Match 98.5%; Score 648; DB 2; Length 241;  
Best Local Similarity 99.2%; Pred. No. 1.9e-73;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEEFVCDVSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCRD 61  
DB 122 SSSHPFHRGEEFVCDVSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCRD 181  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRRA 121  
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRRA 241

RESULT 15  
US-08-595-043A-75  
Sequence 75, Application US/08595043A  
Patent No. 5935824  
GENERAL INFORMATION:  
APPLICANT: SCARLATO, GREGORY D.  
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/595,043A  
FILING DATE: 31-Jan-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: SGAR-00371  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-595-043A-75

Query Match 98.5%; Score 648; DB 2; Length 241;  
Best Local Similarity 99.2%; Pred. No. 1.9e-73;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPFHRGEEFVCDVSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCRD 61  
DB 122 SSSHPFHRGEEFVCDVSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCRD 181  
QY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRRA 121  
DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAAMRFIRIDTACVCLSRKAVRRA 241

Search completed: December 2, 2002, 15:09:42  
Job time : 8.36928 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OK protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 : Search time 4.25557 seconds  
(without alignments)  
452.778 Million cell updates/sec

Title: US-10-072-681-2

Perfect score: 1 PSSSHPIFRGSEYVCDYSVS.....FIRIDTACVLSRAVRA 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US05\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	658	100.0	121	12	US-10-072-681-2
2	648	98.5	241	8	US-08-450-842-5
3	648	98.5	241	10	US-09-822-263-16
4	648	98.5	242	12	US-10-072-681-1
5	639	97.1	153	10	US-09-798-338-2
6	639	97.1	157	10	US-09-798-338-4
7	639	97.1	163	10	US-09-798-338-6
8	639	97.1	167	10	US-09-798-338-8
9	625	95.0	121	9	US-09-813-398-9
10	594	90.3	121	12	US-10-072-681-3
11	455	69.1	142	8	US-08-450-842-52
12	387	58.8	119	10	US-09-848-664-21
13	385.5	58.6	119	10	US-09-745-032-6
14	385.5	58.6	119	10	US-09-742-600-6
15	385.5	58.6	119	10	US-09-872-090-6
16	385.5	58.6	120	10	US-09-745-032-3
17	385.5	58.6	120	10	US-09-742-600-3
18	385.5	58.6	120	10	US-09-872-090-3
19	384.5	58.4	117	10	US-09-745-032-7

20	384.5	58.4	117	10	US-09-742-600-7	Sequence 7, Appl1
21	384.5	58.4	117	10	US-09-872-090-7	Sequence 7, Appl1
22	384.5	58.4	118	10	US-09-745-032-5	Sequence 5, Appl1
23	384.5	58.4	118	10	US-09-742-600-5	Sequence 5, Appl1
24	384.5	58.4	118	10	US-09-872-090-5	Sequence 5, Appl1
25	380.5	57.8	120	10	US-09-745-032-1	Sequence 1, Appl1
26	380.5	57.8	120	10	US-09-742-600-1	Sequence 1, Appl1
27	380.5	57.8	120	10	US-09-872-090-1	Sequence 1, Appl1
28	380.5	57.8	125	8	US-08-450-842-4	Sequence 4, Appl1
29	374	56.8	120	9	US-09-813-398-11	Sequence 11, Appl1
30	371	56.4	120	12	US-10-072-681-5	Sequence 5, Appl1
31	334.5	50.8	120	10	US-09-745-032-10	Sequence 10, Appl1
32	334.5	50.8	120	10	US-09-742-600-10	Sequence 10, Appl1
33	330.5	50.2	120	10	US-09-745-032-9	Sequence 9, Appl1
34	330.5	50.2	120	10	US-09-742-600-9	Sequence 9, Appl1
35	326.5	49.6	130	8	US-08-450-842-47	Sequence 47, Appl1
36	324.5	49.3	120	10	US-09-745-032-8	Sequence 8, Appl1
37	324.5	49.3	120	10	US-09-742-600-8	Sequence 8, Appl1
38	324.5	49.3	120	8	US-08-450-842-3	Sequence 3, Appl1
39	313	47.6	132	8	US-08-450-842-51	Sequence 51, Appl1
40	309.5	46.9	130	8	US-08-450-842-23	Sequence 23, Appl1
41	308.5	46.9	119	12	US-10-072-681-4	Sequence 4, Appl1
42	307.5	46.7	130	8	US-08-450-842-22	Sequence 22, Appl1
43	307.5	46.7	131	9	US-09-813-398-12	Sequence 12, Appl1
44	307.5	46.7	168	8	US-08-450-842-6	Sequence 6, Appl1
45	307.5	46.7	210	8	US-08-450-842-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-072-681-2  
Sequence 2, Application US/10072681  
Patent No. US20020137833A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmeizer, Charles H.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: PURIFICATION OF NGF  
FILE REFERENCE: GENENT 031C3  
CURRENT APPLICATION NUMBER: US/10/072,681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675,503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapien

Query Match 100.0%; Score 658; DB 12; Length 121;  
Best Local Similarity 100.0%; Pred. No. 5.2e-69;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSSSHPIFRGSEYVCDYSVS...GKTTATDTDKGKENVVGLGVNINSVROTFETKCR 60  
DB 1 PSSSHPIFRGSEYVCDYSVS...GKTTATDTDKGKENVVGLGVNINSVROTFETKCR 60  
OY 61 DPNPVDSCGKIGDLSKHMNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVRA 120  
DB 61 DPNPVDSCGKIGDLSKHMNSYCTTHTFVKALTMDCQKAAHFRIDTACVLSRAVRA 120

OY 121 A 121  
DB 121 A 121

## RESULT 2

US-08-450-842-5  
Sequence 5, Application US/08450842  
Patent No. US20020045576A1

## GENERAL INFORMATION:

APPLICANT: GENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PacIn (Gentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842

FILING DATE:  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 666P2CID3

TELEPHONE: 415/425-8674

TELEFAX: 415/952-9881

SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-842-5

Query Match 98.5%: Score 648; DB 8; Length 241;

Best Local Similarity 99.2%: Pred. No. 1,7e-67;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFRRGEFVSVDVWVGDKTATDINGKENVVLGEVNIINSVFROYFEETKCRD 61

DB 122 SSSHPFRRGEFVSVDVWVGDKTATDINGKENVVLGEVNIINSVFROYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALITDGRQAAARFIRIDTACVCLSKRAVRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALITDGRQAAARFIRIDTACVCLSKRAVRA 241

RESULT 3

US-09-822-263-16

Sequence 16, Application US/09822263

Patent No. US20020036598A1

GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas

APPLICANT: Verneet, Corine

APPLICANT: Shimkels, Richard A

APPLICANT: Burgess, Catherine

APPLICANT: Szytek, Kimberly

APPLICANT: Tchiernev, Velizar T

TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded

FILE REFERENCE: 15966-572 CIP1

CURRENT APPLICATION NUMBER: US/09/822,263

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 09/672,665

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/156,745

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/158,942

PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: 60/159,248

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/169,344

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/215,048

PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 241

TYPE: PRT

ORGANISM: Homo sapiens

US-09-822-263-16

Query Match 98.5%: Score 648; DB 10; Length 241;

Best Local Similarity 99.2%: Pred. No. 1,7e-67;

Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPFRRGEFVSVDVWVGDKTATDINGKENVVLGEVNIINSVFROYFEETKCRD 61

DB 122 SSSHPFRRGEFVSVDVWVGDKTATDINGKENVVLGEVNIINSVFROYFEETKCRD 181

OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALITDGRQAAARFIRIDTACVCLSKRAVRA 121

DB 182 PNPVDSGCRGIDSKHNSYCTTHTFVKALITDGRQAAARFIRIDTACVCLSKRAVRA 241

RESULT 4

US-10-072-681-1

Sequence 1, Application US/10072681

Patent No. US20020137893A1

GENERAL INFORMATION:

APPLICANT: Burton, Louis E.

APPLICANT: Schmelzer, Charles H.

TITLE OF INVENTION: PURIFICATION OF NGF

FILE REFERENCE: GENT 037C3

CURRENT APPLICATION NUMBER: US/10/072,681

CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: 60/030838

PRIOR FILING DATE: 1996-11-15

PRIOR APPLICATION NUMBER: 60/047855

PRIOR FILING DATE: 1997-05-29

PRIOR APPLICATION NUMBER: 08/970865

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: 09/363573

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/675,503

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 242

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-681-1

Query Match 98.5%: Score 648; DB 12; Length 242;  
Best Local Similarity 99.2%: Pred. No. 1,7e-67;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 61  
DB 123 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 182  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 121  
DB 183 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 242

RESULT 5

US-09-798-338-2  
Sequence 2, Application US/09798338  
Patent No. US20010020086A1

GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schense, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798,338  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141,153  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 153  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence:Artificial  
OTHER INFORMATION: Protein Sequence  
US-09-798-338-2

Query Match 97.1%: Score 639; DB 10; Length 153;  
Best Local Similarity 99.2%: Pred. No. 1,1e-66;  
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 61  
DB 35 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 94  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 119  
DB 95 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 152

RESULT 6

US-09-798-338-4  
Sequence 4, Application US/09798338  
Patent No. US20010020086A1

GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schense, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798,338  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141,153  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 157

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence:Artificial  
OTHER INFORMATION: Protein Sequence  
US-09-798-338-4

Query Match 97.1%: Score 639; DB 10; Length 157;  
Best Local Similarity 99.2%: Pred. No. 1,1e-66;  
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 61  
DB 39 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 98  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 119  
DB 99 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 156

RESULT 7

US-09-798-338-6  
Sequence 6, Application US/09798338  
Patent No. US20010020086A1

GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schense, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798,338  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141,153  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 163  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence:Artificial  
OTHER INFORMATION: Protein Sequence  
US-09-798-338-6

Query Match 97.1%: Score 639; DB 10; Length 163;  
Best Local Similarity 99.2%: Pred. No. 1,2e-66;  
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 61  
DB 45 SSSHPIFRGFEFVSVDVSVWVGDKTTATDINKGEVWVLGEVINNSVFRQYFFETKCRD 104  
OY 62 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 119  
DB 105 PNPVDSGCRGIDSKHNSYCTTHTFVKALTNQKQAAAFRIIDTACVLSRAAVR 162

RESULT 8

US-09-798-338-8  
Sequence 8, Application US/09798338  
Patent No. US20010020086A1

GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schense, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798,338  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141,153



PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 167  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Artificial  
US-09-798-338-8

Query Match 97.1% Score 639; DB 10; Length 167;  
Best Local Similarity 99.2% Pred. No. 1.2e-66;  
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSHPHFHGRGFSVCDVSVVWGDGKTATDIDKGEVAVLGEVNNINSVROFFETKCRD 61  
DB 49 SSSHPHFHGRGFSVCDVSVVWGDGKTATDIDKGEVAVLGEVNNINSVROFFETKCRD 108  
QY 62 PNPVDSGCGIDSKHMNSYCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 119  
DB 109 PNPVDSGCGIDSKHMNSYCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 166

RESULT 9  
US-09-813-398-9  
Sequence 9, Application US/09813398  
Patent No. US20020169292A1

GENERAL INFORMATION:  
APPLICANT: Bruce D. Weintraub  
APPLICANT: Mariusz W. Szekulinski  
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: US/09/813.398  
CURRENT APPLICATION NUMBER: US/09/813.398  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US98/19772  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 121  
TYPE: PRF  
ORGANISM: HOMO SAPIEN  
US-09-813-398-9

Query Match 95.0% Score 625; DB 9; Length 121;  
Best Local Similarity 95.0% Pred. No. 3.3e-65;  
Matches 115; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PSSSHPIFRHGRGFSVCDVSVVWGDGKTATDIDKGEVAVLGEVNNINSVROFFETKCR 60  
DB 1 PSSSHPIFRHGRGFSVCDVSVVWGDGKTATDIDKGEVAVLGEVNNINSVROFFETKCR 60  
QY 61 DPNPVDGCGIDSKHMNSYCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120  
DB 61 DPNPVDGCGIDSKHMNSYCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120

QY 121 A 121  
DB 121 A 121

RESULT 10  
US-10-072-681-3  
Sequence 3, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schweizer, Charles H.

APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: PURIFICATION OF NGF  
FILE REFERENCE: GENENT.037C3  
CURRENT APPLICATION NUMBER: US/10/072.681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675,503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 121  
TYPE: PRF  
ORGANISM: mouse  
US-10-072-681-3

Query Match 90.3% Score 594; DB 12; Length 121;  
Best Local Similarity 90.8% Pred. No. 1.3e-61;  
Matches 109; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 PSSSHPIFRHGRGFSVCDVSVVWGDGKTATDIDKGEVAVLGEVNNINSVROFFETKCR 60  
DB 1 PSSSHPIFRHGRGFSVCDVSVVWGDGKTATDIDKGEVAVLGEVNNINSVROFFETKCR 60  
QY 61 DPNPVDGCGIDSKHMNSYCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120  
DB 61 ASNPVDSGCGIDSKHMNSYCTTHTFVKALTMDSKQAMRFIRIDPACVLSRKA VR 120

RESULT 11  
US-08-450-842-52

Sequence 52, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 142 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-52

Query Match 69.1%; Score 455; DB 8; Length 142;  
Best Local Similarity 64.8%; Pred. No. 1.7e-45;  
Matches 92; Conservative 11; Mismatches 17; Indels 22; Gaps 4;

OY 2 SSSPIRHRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSV----- 49  
DB 1 SSSPIRHRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVVLGEVPAAGSP 60  
OY 50 FROYFETKCRDNPVD-----SSCGIDSKHNSYCTTHFEVKALTMDCR-QAAMR 101  
DB 61 LRGYFETKCRDNPVD-----SSCGIDSKHNSYCTTHFEVKALTMDCR-QAAMR 120  
OY 102 FRIIDTA--CVCVLSRAVRA 121  
DB 121 WIRIDTACVCLSRRAVRA 142

RESULT 12  
US-09-848-664-21  
Sequence 21, Application US/09848664  
Patent No. US20020146414A1  
GENERAL INFORMATION:  
APPLICANT: Sakiyama-Elbert, Shelly E.  
APPLICANT: Hubbard, Jeffrey A.  
TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth  
FILE REFERENCE: ETH 108  
CURRENT APPLICATION NUMBER: US/09/848,664  
PRIOR FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/298,084  
PRIOR FILING DATE: 1999-04-22  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 21  
LENGTH: 72  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-848-664-21

Query Match 58.8%; Score 387; DB 10; Length 72;  
Best Local Similarity 98.6%; Pred. No. 5.1e-38;  
Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSSPIRHRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVFRGYFETKCRD 61  
DB 1 SSSPIRHRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVFRGYFETKCRD 60  
OY 62 PNPVDSGCGCID 73  
DB 61 PNPVDSGCGCID 72

RESULT 13  
US-09-745-032-6  
Sequence 6, Application US/09745032  
Patent No. US20010027179A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.

APPLICANT: Cheung, Ellen N.  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411A US Revised 073100  
CURRENT APPLICATION NUMBER: US/09/745,032  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 09/214,214  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 6  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Human  
US-09-745-032-6

Query Match 58.6%; Score 385.5; DB 10; Length 119;  
Best Local Similarity 60.7%; Pred. No. 1.4e-37;  
Matches 68; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

OY 9 HRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVFRGYFETKCRDNPVDSG 68  
DB 7 HRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVFRGYFETKCRDNPVDSG 66  
OY 69 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDTACVLSRAVR 119  
DB 67 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDTACVLSRAVR 118

RESULT 14  
US-09-742-600-6  
Sequence 6, Application US/09742600  
Patent No. US20020010135A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen N.  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411A US Revised 073100  
CURRENT APPLICATION NUMBER: US/09/742,600  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 09/214,214  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 6  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Human  
US-09-742-600-6

Query Match 58.6%; Score 385.5; DB 10; Length 119;  
Best Local Similarity 60.7%; Pred. No. 1.4e-37;  
Matches 68; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

OY 9 HRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVFRGYFETKCRDNPVDSG 68  
DB 7 HRGEFVSVDVWVGDKTATDIDGKEVNLGEVNNINSVFRGYFETKCRDNPVDSG 66  
OY 69 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDTACVLSRAVR 119  
DB 67 CRGIDSKHNSYCTTHFEVKALTMDCR-QAAMRFRIDTACVLSRAVR 118

RESULT 15  
US-09-872-090-6  
Sequence 6, Application US/09872090

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; Patent No. US20020052488A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngai Yln
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: Analogs of NT-3 (As Amended)
; FILE REFERENCE: A-4118
; CURRENT APPLICATION NUMBER: US/09/872,090
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/255,953
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 119
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; US-09-872-090-6

Query Match      58.6%; Score 385.5; DB 10; Length 119;
Best Local Similarity 60.7%; Pred. No. 1,4e-37;
Matches 68; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

OY 9 HREGSYVCDSSVWYGDITATDINKKEVYVLEVINNSVFRQYFFETKCRDNPVDSG 68
   |||:||||| |:| |||: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 7 HREGSYVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETKCEAPVDNG 66
   |||:||||| |:| |||: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
OY 69 CRGIDSKHNSYCTTHTFVKALTM-D-GKQAMRFIRIDTACVYLRSKAVR 119
   ||||| ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 67 CRGIDSKHNSCKTSQTYVRLTSENKLVGMIRIDTSCVCLSRKIGR 118
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 Job time : 5.25557 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:37 : Search time 24.1149 seconds  
(without alignments)  
668.605 Million cell updates/sec

Title: US-10-072-681-3

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/genesep-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	646	98.9	307	5	AAW48887
3	646	98.9	307	5	AAW48887
4	646	98.9	307	5	AAW48887
5	643	98.5	120	13	AAW48887
6	643	98.5	120	13	AAW48887
7	640	98.0	23	23	AAW48887
8	639	97.9	118	13	AAW48887
9	635	97.2	118	13	AAW48887
10	633	96.9	120	13	AAW48887

11	631	96.6	120	13	AAW48887	Chimeric neurotrop
12	624	95.6	120	13	AAW48887	Chimeric neurotrop
13	622	95.3	120	13	AAW48887	Chimeric neurotrop
14	618	94.6	120	15	AAW48887	Nerve growth facto
15	611.5	93.6	121	15	AAW48887	Chimeric neurotrop
16	610	93.4	122	13	AAW48887	Chimeric neurotrop
17	608	93.1	118	13	AAW48887	Chimeric neurotrop
18	607	93.0	120	13	AAW48887	Chimeric neurotrop
19	603	92.3	120	13	AAW48887	Chimeric neurotrop
20	595	91.1	120	13	AAW48887	Chimeric neurotrop
21	591	90.5	119	10	AAW48887	Human nerve growth
22	585	89.6	307	14	AAW48887	Human NCF. Homo s
23	584	89.4	120	21	AAW48887	Nerve growth facto
24	584	89.4	120	21	AAW48887	N-terminal of neut
25	584	89.4	120	22	AAW48887	Nerve growth facto
26	584	89.4	120	22	AAW48887	NCF-beta amino aci
27	584	89.4	124	13	AAW48887	Chimeric neurotrop
28	584	89.4	241	12	AAW48887	Human NCF Smat-Apa
29	584	89.4	241	12	AAW48887	Human nerve growth
30	584	89.4	241	12	AAW48887	Human nerve growth
31	584	89.4	241	12	AAW48887	Human nerve growth
32	584	89.4	241	16	AAW48887	NCF with pro-regio
33	584	89.4	241	16	AAW48887	Human nerve growth
34	584	89.4	241	18	AAW48887	Human nerve growth
35	584	89.4	241	19	AAW48887	Human prepro-nerve
36	584	89.4	241	20	AAW48887	Human nerve growth
37	584	89.4	241	22	AAW48887	Amino acid sequenc
38	584	89.4	241	22	AAW48887	Human NCF. Homo s
39	584	89.4	241	23	AAW48887	Human beta nerve g
40	584	89.4	241	23	AAW48887	Human beta nerve g
41	584	89.4	245	5	AAW48887	Sequence encoded b
42	584	89.4	307	14	AAW48887	Human pre-pro nerv
43	584	89.4	307	19	AAW48887	Human beta-nerve g
44	579	88.7	118	10	AAW48887	Human nerve growth
45	579	88.7	119	5	AAW48887	Sequence encoded b

#### ALIGNMENTS

RESULT 1	AAW48887	standard; Protein: 120 AA.
ID	AAW48887	
AC	AAW48887	
DT	12-OCT-1998	(first entry)
XX		
DE	Mouse nerve growth factor.	
XX		
KW	Neurotrophin; nerve growth factor; NGF; mouse; purification;	
KW	hydrophobic interaction chromatography.	
OS	Mus sp.	
XX		
FT	Key	Location/Qualifiers
FT	Region	58..68
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
FT	Region	108..110
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
XX		
PN	W09821234-A2.	
XX		
PD	22-MAY-1998.	
XX		
PF	14-NOV-1997;	97MO-US21068.
XX		
PR	29-MAY-1997;	97US-0047855.
PR	15-NOV-1996;	96US-0030838.
XX		
PA	(GETH) GENENTECH INC.	

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XX Beck JT, Burton LE, Schmelzer CH:
XX WPI: 1998-322333/28.
XX
XX Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated
XX variant(s) - using hydrophobic interaction chromatography.
XX optional in combination with high performance cation exchange
XX chromatography
XX
XX Disclosure: Page 36; 59pp; English.
XX
XX This polypeptide comprises mouse nerve growth factor (NGF) mature
XX polypeptide. Methods are provided for large-scale purification of
XX neurotrophins, including mature NGF, suitable for clinical use. A
XX claimed method comprises: (1) separating the neurotrophin from the
XX other proteins using a hydrophobic interaction chromatography resin
XX (HICR); and optionally (2) separating the neurotrophin from a
XX chemical variant by high performance cation exchange chromatography
XX (HPEC). The processes can also be used for purification of e.g.
XX human NGF (see AAM48886), brain-derived neurotrophic factor (see
XX AAM48888), neurotrophin-4/5 (see AAM48890) and neurotrophin-3 (see
XX AAM48889). The processes allow separation of neurotrophins from
XX various undesirable misprocessed, misfolded, size, glycosylated or
XX charge forms. They allow selective separation from variants and
XX other molecules, and from other polypeptides with high pI. The
XX processes are applicable to starting materials from various
XX sources, including fermentation broths or lysed bacterial or
XX mammalian cells.
XX
XX Sequence 120 AA:
XX
XX Query Match 98.9%; Score 646; DB 19; Length 120;
XX Best Local Similarity 100.0%; Pred. No. 1e-66;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 SSTRHPFHMGESVCSVSWGDKTTATDIDKGEVTVLAENVNNSVFRQFFETGCA 61
XX |
XX DB 1 SSTRHPFHMGESVCSVSWGDKTTATDIDKGEVTVLAENVNNSVFRQFFETGCA 60
XX
XX QY 62 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 121
XX |
XX DB 61 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 120
XX
XX RESULT 2
XX AAP40036 standard; Protein: 307 AA.
XX ID AAP40036;
XX AC AAP40036;
XX
XX XX 25-JAN-1992 (first entry)
XX
XX DE Sequence encoded by the human beta-nerve growth factor (NGF) gene
XX DE and flanking regions on phage lambda h-beta-N8.
XX
XX KW Nerve damage: therapy.
XX
XX OS Homo sapiens.
XX
XX PI EPI21338-A.
XX
XX PD 10-OCT-1984.
XX
XX PF 02-MAR-1984; 84EP-0301377.
XX
XX PR 03-MAR-1983; 83US-0471962.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Gray AM, Ullrich A;
XX
XX WPI: 1984-251909/41.
XX

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DR N-PSDB; AAN40031.
XX
XX Human beta-nerve growth factor free from other proteins - obtd.
XX PT by recombinant DNA techniques for treating nerve damage
XX
XX Example: Fig 2; 42pp; English.
XX
XX PS The inventors claim human beta-nerve growth factor (NGF) free from
XX CC other proteins of human origin. Also claimed are the DNA sequence
XX CC encoding human beta-NGF operably linked with a DNA sequence capable
XX CC of effecting its expression in a recombinant host cell; a replicable
XX CC expression vector contg. the DNA; and host cells transformed with
XX CC the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using
XX CC the plasmid, larger amounts of pure beta-NGF are obtainable than by
XX CC extn. of natural materials, see e.g. EP-2139.
XX
XX SQ Sequence 307 AA:
XX
XX Query Match 98.9%; Score 646; DB 5; Length 307;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-66;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 SSTRHPFHMGESVCSVSWGDKTTATDIDKGEVTVLAENVNNSVFRQFFETGCA 61
XX |
XX DB 188 SSTRHPFHMGESVCSVSWGDKTTATDIDKGEVTVLAENVNNSVFRQFFETGCA 247
XX
XX QY 62 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 121
XX |
XX DB 248 SNPEVSCRCIDSKHWNSTCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRATRG 307
XX
XX RESULT 3
XX AAP40039 standard; Protein: 307 AA.
XX ID AAP40039;
XX AC AAP40039;
XX
XX XX 25-JAN-1992 (first entry)
XX
XX DE Sequence encoded by human prepro-beta-nerve growth factor
XX DE (NGF) gene.
XX
XX KW Nerve damage: therapy.
XX
XX OS Homo sapiens.
XX
XX PI Key Location/Qualifiers
XX PI Peptide 1..187
XX PI Protein 188..307
XX
XX PN EPI21338-A.
XX
XX PD 10-OCT-1984.
XX
XX PF 02-MAR-1984; 84EP-0301377.
XX
XX PR 03-MAR-1983; 83US-0471962.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Gray AM, Ullrich A;
XX
XX WPI: 1984-251909/41.
XX
XX DR N-PSDB; AAN40034.
XX
XX PT Human beta-nerve growth factor free from other proteins - obtd.
XX PT by recombinant DNA techniques for treating nerve damage
XX
XX PS Example: Fig 6; 42pp; English.
XX
XX CC The inventors claim human beta-nerve growth factor (NGF) free from
XX CC other proteins of human origin. Also claimed are the DNA sequence

```

CC encoding human beta-NGF operably linked with a DNA sequence capable  
 CC of effecting its expression in a recombinant host cell; a replicable  
 CC expression vector contg. the DNA; and host cells transformed with  
 CC the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using  
 CC the plasmid, larger amounts of pure beta-NGF are obtainable than by  
 CC extrn. of natural materials, see e.g. EP-2139.

XX Sequence 307 AA;

Query Match 98.9%; Score 646; DB 5; Length 307;

Best Local Similarity 100.0%; Pred. No. 3,5e-66; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 61  
 DB 188 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 247  
 Oy 62 SNPVESGCGIDSKHMNSCTTHTFVKALTTDEKQAMRFIRIDPACVLSRKATRRG 121  
 DB 248 SNPVESGCGIDSKHMNSCTTHTFVKALTTDEKQAMRFIRIDPACVLSRKATRRG 307

RESULT 4

AAR45240 standard; Protein: 307 AA.

AAR45240;

20-JUN-1994 (first entry)

Cloned mouse pre-pro nerve growth factor.

Mouse human: beta-nerve growth factor; mouse; pre-pro portion;  
 expression: NGF; hNGF; treatment: Alzheimer's disease; murine.

Mus musculus.

Key Location/Qualifiers

Peptide 1..187

Peptide /note="signal peptide"

Peptide 188..307

Peptide /note="mature peptide"

US5272063-A.

21-DEC-1993.

20-JUN-1989; 89US-0383118.

22-NOV-1988; 88US-0274878.

20-JUL-1989; 89US-0383118.

(SYNT ) SYNTAX USA INC.

Baecker PA, Barnett JW, Bursztyr-Petregrew H, Chan HW, Nguyen BT;

Ward C;

WPI; 1993-413401/51.

N-PSDB; AA054282.

Prodn. of active mature human beta-nerve growth factor in insect  
 cells - using baculovirus expression system, and potential use of  
 recombinant hNGF in treatment of Alzheimer's disease

PS Disclosure: Fig 1; 23pp; English.

CC The sequence is that of mouse pre-pro nerve growth factor  
 CC which was used in a method of producing biologically active  
 CC mature human beta-nerve growth factor in insect cells.

XX Sequence 307 AA;

Query Match 98.9%; Score 646; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 3,5e-66; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 61

DB 188 SSTRHVFHMGESVCDSSVWVGDKTTATDCKGEVTLAEVINNSVROFFETKCA 247

Oy 62 SNPVESGCGIDSKHMNSCTTHTFVKALTTDEKQAMRFIRIDPACVLSRKATRRG 121

DB 248 SNPVESGCGIDSKHMNSCTTHTFVKALTTDEKQAMRFIRIDPACVLSRKATRRG 307

RESULT 5

AAR21868 standard; Protein: 120 AA.

AAR21868;

10-JUN-1992 (first entry)

Chimeric neurotrophic factor S6.

Human BDNF; brain derived neurotrophic factor; NGF;

neurotrophic growth factor; Alzheimer's disease; ageing;

peripheral neuropathies; Parkinson's disease; Huntington's chorea;

amyotrophic lateral sclerosis; nervous system disorders.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..50

Peptide /note="mouse NGF residues 1-50"

Peptide /note="human BDNF residues 51-58"

Peptide /note="mouse NGF residues 59-120"

WO9202620-A.

20-FEB-1992.

07-AUG-1991; 91WO-US05610.

08-AUG-1990; 90US-0564929.

(REGG-) REGENERON PHARM INC.

Shooter EM, Suter U, Ip N, Squinto SP, Furch ME, Lindsay RM;

Yancopoulos GD;

WPI; 1992-080074/10.

New chimeric neurotrophic factors - useful in treating nervous

conditions caused by trauma, surgery, ischemia, infection,

metabolic diseases, nutritional deficiency, etc.

Claim 29; Fig 10; 114pp; English.

XX The sequence is that of a chimeric neurotrophic factor (NF) S6 which

XX comprises the mouse neurotrophic growth factor (NGF) residues 1-50.

XX human brain derived growth factor (hBNF) residues 51-58 and mouse NGF

XX residues 59-120. It may provide the activity of 2 NFs in a single mol.

XX or may serve as a superagonist of an endogenous NF thereby enabling an

XX increased biological response at lower doses. It may also be useful in

XX targeting an active cpd. to cells responsive to NF. The design of

XX chimeric NFs, such as S6, which retain specific biological activity

XX but which are directed to a subset of factor-responsive cells may

XX enable treatment of neurological disorders but avoid the complications

XX of more widespread activity of parent mols. It may be used in the

XX treatment to eliminate diseased cells, e.g. virus infected cells or

XX tumours of nervous system origin. It may also be used to treat patients

XX whose nervous system has been damaged by trauma, surgery, ischemia,

XX infection (e.g. polio or AIDS), metabolic disease, nutritional

deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's disease, ageing, peripheral neuropathies, Parkinson's disease, Huntington's chorea or amyotrophic lateral sclerosis. S6 or antibodies to it can also be used in the diagnosis and study of nervous system disorders. See also AAR21851-R21874 and AAQ22080-Q22131.

Sequence 120 AA:

Query Match 98.5%; Score 643; DB 13; Length 120;  
Best Local Similarity 99.2%; Pred. No. 2,3e-66;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRHVFHMGFEFVCDVSVMWGDKTTATDIDKGEVTLAEVNIINSVPROFEETKRA 61  
DB 1 SSTRHVFHMGFEFVCDVSVMWGDKTTATDIDKGEVTLAEVNIINSVPROFEETKRA 60  
OY 62 SNPEVSGCRGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 121  
DB 61 SNPEVSGCRGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 120

RESULT 6  
AAR21873  
ID AAR21873 standard; Protein: 120 AA.

XX AAR21873;  
XX  
XX 10-JUN-1992 (first entry)

XX Chimeric neurotrophic factor S11.

XX Human BDNF; brain derived neurotrophic factor; NGF;  
XX neurotrophic growth factor; Alzheimer's disease; ageing;  
XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
XX amyotrophic lateral sclerosis; nervous system disorders.

XX Homo sapiens.

XX Key location/Qualifiers  
XX Peptide 1..101 /note= "mouse NGF residues 1-101"  
XX Peptide 102..110 /note= "human BDNF residues 103-111"  
XX Peptide 111..120 /note= "mouse NGF residues 111-120"

XX MO9202620-A.

XX 20-FEB-1992.

XX 07-AUG-1991; 91WO-US05610.

XX 08-AUG-1990; 90US-0564929.

XX (REGC-) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinco SP, Furch ME, Lindsay RM;  
XX Yancopoulos CD;

XX WPI: 1992-080074/10.

XX New chimeric neurotrophic factors - useful in treating nervous  
XX conditions caused by trauma, surgery, ischemia, infection,  
XX metabolic diseases, nutritional deficiency, etc.

XX Claim 34; Fig 10; 11app; English.

XX The sequence is that of a chimeric neurotrophic factor (NF) S11 which  
XX comprises the mouse neurotrophic growth factor (NGF) residues 1-101,  
XX human brain derived growth factor (hBDNF) residues 103-111 and mouse  
XX residues 111-120. It may provide the activity of 2 NFs in a single mol.  
XX or may serve as a superagonist of an endogenous NF thereby enabling an  
XX increased biological response at lower doses. It may also be useful in

CC targeting an active cpd. to cells responsive to NF. The design of  
CC chimeric NFs, such as S11, which retain specific biological activity  
CC but which are directed to a subset of factor-responsive cells may  
CC enable treatment of neurological disorders but avoid the complications  
CC of more widespread activity of parent mole. It may be used in the  
CC treatment to eliminate diseased cells, e.g. virus infected cells or  
CC tumours of nervous system origin. It may also be used to treat patients  
CC whose nervous system has been damaged by trauma, surgery, ischemia,  
CC infection (e.g. Polio or AIDS), metabolic disease, nutritional  
CC deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's  
CC disease, ageing, peripheral neuropathies, Parkinson's disease,  
CC Huntington's chorea or amyotrophic lateral sclerosis. S11 or antibodies  
CC to it can also be used in the diagnosis and study of nervous system  
CC disorders. See also AAR21851-R21874 and AAQ22080-Q22131.

Sequence 120 AA:

Query Match 98.5%; Score 643; DB 13; Length 120;  
Best Local Similarity 99.2%; Pred. No. 2,3e-66;  
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRHVFHMGFEFVCDVSVMWGDKTTATDIDKGEVTLAEVNIINSVPROFEETKRA 61  
DB 1 SSTRHVFHMGFEFVCDVSVMWGDKTTATDIDKGEVTLAEVNIINSVPROFEETKRA 60  
OY 62 SNPEVSGCRGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 121  
DB 61 SNPEVSGCRGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRKATRRG 120

RESULT 7

AAAM50845  
ID AAAM50845 standard; Protein: 240 AA.

XX AAAM50845;

XX 01-MAY-2002 (first entry)

XX Mouse nerve growth factor.

XX Beta-nerve growth factor; NGF; mouse; neurotrophic factor; NTF;  
XX Huntington's disease; Parkinson's disease; Alzheimer's disease;  
XX neurotrophic lateral sclerosis; neurodegenerative disease; cancer;  
XX cyostatic; therapy.

XX Mus musculus.

XX Key location/Qualifiers  
XX Peptide 1..18 /label= Signal\_peptide  
XX Peptide 19..121 /label= Propeptide  
XX Protein 122..240 /label= Mature\_protein  
XX Disulfide-bond 136..201  
XX Disulfide-bond 179..229  
XX Disulfide-bond 189..231

XX Modified-site 69 /note= "N-glycosylated"  
XX Modified-site 114 /note= "N-glycosylated"

XX Misc-difference 233..240 /note= "conflict, replaced by CSACRLOEPA"

XX MO200203071-A2.

XX 10-JAN-2002.

XX 05-JUL-2001; 2001WO-US21472.

XX 05-JUL-2000; 2000US-215778P.

XX

PA (PANG-) PANGENE CORP.  
 PI Bates AT:  
 XX  
 XX  
 DR WP1: 2002-179638/23.  
 XX  
 PT Screening for a neurotrophic factor mimetic, useful for treating, e.g.,  
 PT cancer and Alzheimer's, comprises combining a candidate mimetic with a  
 PT fragment of a tyrosine kinase protein  
 XX  
 PS Disclosure: Fig 5; 107pp: English.  
 XX  
 CC The present sequence is that of murine beta-nerve growth factor  
 CC (NGF), a neurotrophic factor (NTF) that binds to TrkA receptor  
 CC tyrosine kinase. The invention concerns Trks and their ligands  
 CC that modulate cell growth, differentiation and survival. Trk  
 CC proteins are known to mediate the activities of neurotrophins and  
 CC are also known proto-oncogenes. Methods are claimed for screening  
 CC for small molecule NTF mimetics, such as the cyclic peptide given  
 CC in AA050844, capable of binding to a Trk protein or of modulating  
 CC the binding of a neurotrophin to a Trk protein. Also claimed are  
 CC medicaments comprising a small molecule NTF mimetic and their use  
 CC in claimed methods for treatment of cancer or a neurodegenerative  
 CC disease selected from Huntington's disease, Parkinson's disease,  
 CC Alzheimer's disease and amyotrophic lateral sclerosis.  
 XX  
 SQ Sequence 240 AA:  
 Query Match 98.0%; Score 640; DB 23; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-65;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 SSTRPFFHMGESVCDVSVMGDKTTATDTRKGEVTLAEVINNSVROFFETKCA 61  
 DB 132 SSTRPFFHMGESVCDVSVMGDKTTATDTRKGEVTLAEVINNSVROFFETKCA 161  
 OY 63 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDRACVLSRKATRR 120  
 DB 182 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDRACVLSRKATRR 240  
 RESULT 8  
 ID AAR21862 standard; Protein; 132 AA.  
 XX  
 AC AAR21862;  
 XX  
 DT 10-JUN-1992 (first entry)  
 XX  
 DE Chimeric neurotrophic factor NM1.  
 XX  
 KW Human BDNF: brain derived neurotrophic factor; NGF;  
 KW neurotrophic growth factor; Alzheimer's disease; ageing;  
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; nervous system disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..4  
 FT Peptide /note= "mouse NGF preprosequence"  
 FT 5..122  
 FT Peptide /note= "mouse NGF residues 1-118"  
 FT 123..132  
 FT Peptide /note= "10 amino acid antigenic peptide fragment  
 of human myc protein"  
 XX  
 MO9202620-A.  
 XX  
 PD 20-FEB-1992.  
 XX  
 PF 07-AUG-1991; 91WO-US05610.  
 XX

PR 08-AUG-1990; 90US-0564929.  
 PA (RECE-) REGENERON PHARM INC.  
 XX  
 XX  
 PI Shooter EM, Suter U, Ip N, Squinto SP, Furch ME, Lindsay RM;  
 PI Yancopoulos GD;  
 XX  
 DR WP1: 1992-080074/10.  
 XX  
 PT New chimeric neurotrophic factors - useful in treating nervous  
 PT conditions caused by trauma, surgery, ischemia, infection,  
 PT metabolic diseases, nutritional deficiency, etc.  
 XX  
 PS Claim 46; Fig 5; 114pp: English.  
 XX  
 CC The sequence is that of a chimeric neurotrophic factor (NF) NM1 which  
 CC comprises the preprosequence of mouse neurotrophic growth factor (NGF),  
 CC residues 1-118 of mouse NGF and a 10 amino acid antigenic peptide  
 CC fragment of human myc protein. It may provide the activity of 2 NFs  
 CC in a single mol. or may serve as a superagonist of an endogenous NF  
 CC thereby enabling an increased biological response at lower doses. It  
 CC may also be useful in targeting an active cpd. to cells responsive to  
 CC NF. The design of chimeric NFs, such as NM1, which retain specific  
 CC biological activity but which are directed to a subset of factor-  
 CC responsive cells may enable treatment of neurological disorders but  
 CC avoid the complications of more widespread activity of parent mol's.  
 CC It may be used in the treatment to eliminate diseased cells, e.g.  
 CC virus infected cells or tumours of nervous system origin. It may also  
 CC be used to treat patients whose nervous system has been damaged by  
 CC trauma, surgery, ischemia, infection (e.g. polio or AIDS), metabolic  
 CC disease, nutritional deficiency, malignancy or toxic agents. Also to  
 CC treat e.g. Alzheimer's disease, ageing, peripheral neuropathies,  
 CC Parkinson's disease, Huntington's chorea or amyotrophic lateral  
 CC sclerosis. NM1 or antibodies to it can also be used in the diagnosis  
 CC and study of nervous system disorders. See also AAR21851-R21874 and  
 CC AA022080-Q22131.  
 XX  
 SQ Sequence 132 AA:  
 Query Match 97.9%; Score 639; DB 13; Length 132;  
 Best Local Similarity 99.2%; Pred. No. 7.5e-66;  
 Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 SSTRPFFHMGESVCDVSVMGDKTTATDTRKGEVTLAEVINNSVROFFETKCA 61  
 DB 5 SSTRPFFHMGESVCDVSVMGDKTTATDTRKGEVTLAEVINNSVROFFETKCA 64  
 OY 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDRACVLSRKATRR 121  
 DB 65 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDRACVLSRKATRR 124  
 RESULT 9  
 ID AAR29493 standard; Protein; 118 AA.  
 XX  
 AC AAR29493;  
 XX  
 DT 22-APR-1993 (first entry)  
 XX  
 DE NGF, mouse.  
 XX  
 KW Neurotrophin; NT; nerve growth factor; NGF;  
 KW brain-derived neurotrophic factor; BDNF.  
 XX  
 OS Mus musculus.  
 XX  
 MO9220365-A.  
 XX  
 PD 26-NOV-1992.  
 XX  
 PF 20-MAY-1992; 92MO-US04266.  
 XX



PR 21-MAY-1991; 91US-0703450.  
 PR 12-JUL-1991; 91US-0729253.  
 PR 23-JUL-1991; 91US-0734422.  
 PR 28-AUG-1991; 91US-0751356.  
 PR 20-SEP-1991; 91US-0762674.  
 PR 14-NOV-1991; 91US-0781924.  
 (REG-) REGENERON PHARM INC.  
 PA Hallbook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD.  
 PI WPI: 1992-415468/50.  
 XX  
 DR Use of neurotrophin-4 for promoting growth and survival of nerve  
 PT cells - useful in treating neurological, fertility and  
 PT immunological disorders and in diagnosis  
 XX  
 PS Disclosure: Page 105-106 + Fig 4B; 180pp; English.  
 CC  
 CC A comparison of the mature NT-4 protein (xenopus) to the mature  
 CC NGF, BDNF, and NT-3 proteins from mouse revealed 51%, 60% and 58%  
 CC amino acid identity respectively. See sequences AAR29491 and  
 CC AAR39493-95.  
 CC  
 SQ Sequence 118 AA:  
 Query Match 97.2%; Score 635; DB 13; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-65;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 SSTRPVFMHGEFSCDSVSWVGDKTTATDIDKKEVTVLAENVINNSVFRQYFFETCRRA 61  
 DB 1 SSTRPVFMHGEFSCDSVSWVGDKTTATDIDKKEVTVLAENVINNSVFRQYFFETCRRA 60  
 OY 62 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 119  
 DB 61 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 118  
 RESULT 10  
 AAR21864  
 ID AAR21864 standard; Protein: 120 AA.  
 XX  
 AC AAR21864;  
 XX  
 DT 10-JUN-1992 (first entry)  
 XX  
 DE Chimeric neurotrophic factor S2.  
 XX  
 KW Human BDNF; brain derived neurotrophic factor; NGF;  
 KW neurotrophic growth factor; Alzheimer's disease; ageing;  
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; nervous system disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..9  
 FT /note= "mouse NGF residues 1-9"  
 FT Peptide 10..22  
 FT /note= "human BDNF residues 8-20"  
 FT Peptide 23..120  
 FT /note= "mouse NGF residues 23-120"  
 XX  
 OS W09202620-A.  
 FM  
 FH  
 XX 20-FEB-1992.  
 PD  
 XX 07-AUG-1991; 91MO-US05610.  
 PF  
 XX 08-AUG-1990; 90US-0564929.  
 PR  
 FT  
 XX (REG-) REGENERON PHARM INC.

XX  
 PI Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsey RM;  
 PI Yancopoulos GD;  
 XX  
 DR WPI: 1992-080074/10.  
 XX  
 PT New chimeric neurotrophic factors - useful in treating nervous  
 PT conditions caused by trauma, surgery, ischemia, infection,  
 PT metabolic diseases, nutritional deficiency, etc.  
 XX  
 PS Claim 25; Fig 10; 114pp; English.  
 CC  
 CC The sequence is that of a chimeric neurotrophic factor (NF) S2 which  
 CC comprises the mouse neurotrophic growth factor (NGF) residues 1-9,  
 CC human brain derived growth factor (hBDNF) residues 8-20 and mouse NGF  
 CC residues 23-120. It may provide the activity of 2 NFs in a single mol-  
 CC or may serve as a superagonist of an endogenous NF thereby enabling an  
 CC increased biological response at lower doses. It may also be useful in  
 CC targeting an active cpd. to cells responsive to NF. The design of  
 CC chimeric NFs, such as S2, which retain specific biological activity  
 CC but which are directed to a subset of factor-responsive cells may  
 CC enable treatment of neurological disorders but avoid the complications  
 CC of more widespread activity of parent mols. It may be used in the  
 CC treatment to eliminate diseased cells, e.g. virus infected cells or  
 CC tumours of nervous system origin. It may also be used to treat patients  
 CC whose nervous system has been damaged by trauma, surgery, ischemia,  
 CC infection (e.g. polio or AIDS), metabolic disease, nutritional  
 CC deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's  
 CC disease, ageing, peripheral neuropathies, Parkinson's disease,  
 CC Huntington's chorea or amyotrophic lateral sclerosis. S2 or antbodies  
 CC to it can also be used in the diagnosis and study of nervous system  
 CC disorders. See also AAR21851-R21874 and AAQ22080-022131.  
 CC  
 SQ Sequence 120 AA:  
 Query Match 96.9%; Score 633; DB 13; Length 120;  
 Best Local Similarity 97.5%; Pred. No. 3.3e-65;  
 Matches 117; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 SSTRPVFMHGEFSCDSVSWVGDKTTATDIDKKEVTVLAENVINNSVFRQYFFETCRRA 61  
 DB 1 SSTRPVFMHGEFSCDSISSEMGDKTTATDIDKKEVTVLAENVINNSVFRQYFFETCRRA 60  
 OY 62 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 121  
 DB 61 SNPVESGCRGIDSKHNNSTCTTHTFVKALTTDEKQAMRFRIIDTACVLSRKATR 120  
 RESULT 11  
 AAR21870  
 ID AAR21870 standard; Protein: 120 AA.  
 XX  
 AC AAR21870;  
 XX  
 DT 10-JUN-1992 (first entry)  
 XX  
 DE Chimeric neurotrophic factor S8.  
 XX  
 KW Human BDNF; brain derived neurotrophic factor; NGF;  
 KW neurotrophic growth factor; Alzheimer's disease; ageing;  
 KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; nervous system disorders.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..68  
 FT /note= "mouse NGF residues 1-68"  
 FT Peptide 69..80  
 FT /note= "human BDNF residues 69-80"  
 FT Peptide 81..120  
 FT /note= "mouse NGF residues 81-120"  
 XX

PN M09202620-A.  
 XX 20-FEB-1992.  
 XX 07-AUG-1991: 91MO-US05610.  
 XX 08-AUG-1990: 90US-0564929.  
 XX (REG-) REGENERON PHARM INC.  
 XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsey RM,  
 XX Yancopoulos GD;  
 XX WPI: 1992-080074/10.  
 XX New chimeric neurotrophic factors - useful in treating nervous  
 XX conditions caused by trauma, surgery, ischemia, infection,  
 XX metabolic diseases, nutritional deficiency, etc.  
 XX Claim 31: Fig 10; 114pp: English.  
 XX The sequence is that of a chimeric neurotrophic factor (NF) S8 which  
 XX comprises the mouse neurotrophic growth factor (NGF) residues 1-68,  
 XX human brain derived growth factor (hBDNF) residues 69-80 and mouse NGF  
 XX residues 81-120. It may provide the activity of 2 NFs in a single mol.  
 XX or may serve as a superagonist of an endogenous NF thereby enabling an  
 XX increased biological response at lower doses. It may also be useful in  
 XX targeting an active cpd. to cells responsive to NF. The design of  
 XX chimeric NFs, such as S8, which retain specific biological activity  
 XX but which are directed to a subset of factor-responsive cells may  
 XX enable treatment of neurological disorders but avoid the complications  
 XX of more widespread activity of parent moles. It may be used in the  
 XX treatment to eliminate diseased cells, e.g. virus infected cells or  
 XX tumours of nervous system origin. It may also be used to treat patients  
 XX whose nervous system has been damaged by trauma, surgery, ischemia,  
 XX infection (e.g. polio or AIDS), metabolic disease, nutritional  
 XX deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's  
 XX disease, ageing, peripheral neuropathies, Parkinson's disease,  
 XX Huntington's chorea or amyotrophic lateral sclerosis. S8 or antibodies  
 XX to it can also be used in the diagnosis and study of nervous system  
 XX disorders. See also AAR21851-R21874 and AAQ22080-Q22131.  
 XX Sequence 120 AA;  
 XX  
 XX Query Match 96.6%; Score 631; DB 13; Length 120;  
 XX Best Local Similarity 97.5%; Pred. No. 5.6e-65;  
 XX Matches 117; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 SSTRPVFHMGEFSVCDSSVWVGDKTTATDINGKKEVTVLAEVNINNSVPROFFETKCA 61  
 DB 1 SSTRPVFHMGEFSVCDSSVWVGDKTTATDINGKKEVTVLAEVNINNSVPROFFETKCA 60  
 OY 62 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKOAAMRFIRIDPACVLSRKATRRG 121  
 DB 61 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKOAAMRFIRIDPACVLSRKATRRG 120  
 RESULT 12  
 AAR21866  
 ID AAR21866 standard; Protein: 120 AA.  
 AC AAR21866;  
 XX 10-JUN-1992 (first entry)  
 XX Chimeric neurotrophic factor S4.  
 XX Human BDNF: brain derived neurotrophic factor; NGF:  
 XX neurotrophic growth factor; Alzheimer's disease; ageing;  
 XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
 XX amyotrophic lateral sclerosis; nervous system disorders.  
 XX Homo sapiens.  
 XX

XX Key Location/Qualifiers  
 XX Peptide 1..33  
 XX Peptide /note- "mouse NGF residues 1-33"  
 XX Peptide 34..42  
 XX Peptide /note- "human BDNF residues 34-42"  
 XX Peptide 43..120  
 XX /note- "mouse NGF residues 43-120"  
 XX  
 XX M09202620-A.  
 XX 20-FEB-1992.  
 XX 07-AUG-1991: 91MO-US05610.  
 XX 08-AUG-1990: 90US-0564929.  
 XX (REG-) REGENERON PHARM INC.  
 XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsey RM,  
 XX Yancopoulos GD;  
 XX WPI: 1992-080074/10.  
 XX New chimeric neurotrophic factors - useful in treating nervous  
 XX conditions caused by trauma, surgery, ischemia, infection,  
 XX metabolic diseases, nutritional deficiency, etc.  
 XX Claim 27: Fig 10; 114pp: English.  
 XX The sequence is that of a chimeric neurotrophic factor (NF) S4 which  
 XX comprises the mouse neurotrophic growth factor (NGF) residues 1-33,  
 XX human brain derived growth factor (hBDNF) residues 34-42 and mouse NGF  
 XX residues 43-120. It may provide the activity of 2 NFs in a single mol.  
 XX or may serve as a superagonist of an endogenous NF thereby enabling an  
 XX increased biological response at lower doses. It may also be useful in  
 XX targeting an active cpd. to cells responsive to NF. The design of  
 XX chimeric NFs, such as S4, which retain specific biological activity  
 XX but which are directed to a subset of factor-responsive cells may  
 XX enable treatment of neurological disorders but avoid the complications  
 XX of more widespread activity of parent moles. It may be used in the  
 XX treatment to eliminate diseased cells, e.g. virus infected cells or  
 XX tumours of nervous system origin. It may also be used to treat patients  
 XX whose nervous system has been damaged by trauma, surgery, ischemia,  
 XX infection (e.g. polio or AIDS), metabolic disease, nutritional  
 XX deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's  
 XX disease, ageing, peripheral neuropathies, Parkinson's disease,  
 XX Huntington's chorea or amyotrophic lateral sclerosis. S4 or antibodies  
 XX to it can also be used in the diagnosis and study of nervous system  
 XX disorders. See also AAR21851-R21874 and AAQ22080-Q22131.  
 XX Sequence 120 AA;  
 XX  
 XX Query Match 95.6%; Score 624; DB 13; Length 120;  
 XX Best Local Similarity 96.7%; Pred. No. 3.6e-44;  
 XX Matches 116; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 SSTRPVFHMGEFSVCDSSVWVGDKTTATDINGKKEVTVLAEVNINNSVPROFFETKCA 61  
 DB 1 SSTRPVFHMGEFSVCDSSVWVGDKTTATDINGKKEVTVLAEVNINNSVPROFFETKCA 60  
 OY 62 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKOAAMRFIRIDPACVLSRKATRRG 121  
 DB 61 SNPEVSGCRGIDSKHMNSYCTTHTFVKALTTDEKOAAMRFIRIDPACVLSRKATRRG 120  
 RESULT 13  
 AAR21871  
 ID AAR21871 standard; Protein: 120 AA.  
 AC AAR21871;  
 XX 10-JUN-1992 (first entry)  
 XX

XX Chimeric neurotrophic factor S9.

XX Human BDNF: brain derived neurotrophic factor; NGF;  
XX neurotrophic growth factor; Alzheimer's disease; aging;  
XX peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
XX amyotrophic lateral sclerosis; nervous system disorders.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..80 /note= "mouse NGF residues 1-80"

FT Peptide 81..91 /note= "human BDNF residues 81-91"

FT Peptide 92..120 /note= "mouse NGF residues 92-120"

XX MO9202620-A.

XX 20-FEB-1992.

XX 07-AUG-1991; 91WO-US05610.

XX 08-AUG-1990; 90US-0564929.

XX (REG- ) REGENERON PHARM INC.

XX Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsay RM;  
XX rancopoulous GD;

XX WPI: 1992-080074/10.

XX New chimeric neurotrophic factors - useful in treating nervous  
XX conditions caused by trauma, surgery, ischemia, infection,  
XX metabolic diseases, nutritional deficiency, etc.

XX Claim 32: Fig 10; 114pp: English.

XX The sequence is that of a chimeric neurotrophic factor (NF) S9 which  
XX comprises the mouse neurotrophic growth factor (NGF) residues 1-80,  
XX human brain derived growth factor (hBNDF) residues 81-91 and mouse NGF  
XX residues 92-120. It may provide the activity of 2 NFs in a single mol.  
XX or may serve as a superagonist of an endogenous NF thereby enabling an  
XX increased biological response at lower doses. It may also be useful in  
XX targeting an active cpd. to cells responsive to NF. The design of  
XX chimeric NFs, such as S9, which retain specific biological activity  
XX but which are directed to a subset of factor-responsive cells may  
XX enable treatment of neurological disorders but avoid the complications  
XX of more widespread activity of parent moIs. It may be used in the  
XX treatment to eliminate diseased cells, e.g. virus infected cells or  
XX tumours of nervous system origin. It may also be used to treat patients  
XX whose nervous system has been damaged by trauma, surgery, ischemia,  
XX infection (e.g. polio or AIDS), metabolic disease, nutritional  
XX deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's  
XX disease, aging, peripheral neuropathies, Parkinson's disease,  
XX Huntington's chorea or amyotrophic lateral sclerosis. S9 or antibodies  
XX to it can also be used in the diagnosis and study of nervous system  
XX disorders. See also AAR21851-R21874 and AAQ22080-Q22131.

XX Sequence 120 AA:

Query Match 95.3%; Score 622; DB 13; Length 120;  
Best Local Similarity 95.8%; Pred. No. 6, 1e-64;  
Matches 115; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKREVTYLAENVINNSVFRQYFEETKRA 61  
DB 1 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKREVTYLAENVINNSVFRQYFEETKRA 60  
OY 62 SNPEVSGCRGIDSKHMSNCTTTHTFVKALTTDEKQAAARRIRIDTACVCLSKKATRRG 121  
DB 61 SNPEVSGCRGIDSKHMSNCTTTHTFVKALTTDEKQAAARRIRIDTACVCLSKKATRRG 120

RESULT 14

ID AAR54084 standard; protein; 120 AA.

XX AAR54084;

XX 10-NOV-1994 (first entry)

XX Nerve growth factor.

XX Nerve growth factor; NGF; chimeric neurotrophin; neurotrophic factor;  
XX brain-derived neurotrophic factor; BDNF; neurotrophin-3; NF-3;  
XX TrkA; TrkB; TrC; receptor; neurological disorder;  
XX Parkinson disease; Alzheimer disease.

XX Rattus sp.

XX MO9412539-A.

XX 09-JUN-1994.

XX 19-NOV-1993; 93WO-US11292.

XX 20-NOV-1992; 92US-0979630.

XX (MCIN/) MCINTYRE K R.

XX Idanez CFM, Persson HB;

XX WPI: 1994-200202/24.

XX New chimeric neurotrophic factors and DNA - used to develop  
XX prodcs. for use in the treatment and diagnosis of neurological  
XX disorders

XX Disclosure: Page 48-49; 79pp; English.

XX Sequences are provided for rat nerve growth factor (AAR54084), rat  
XX brain-derived neurotrophic factor (AAR54085) and rat neurotrophin-3  
XX (AAR54086). Chimeric neurotrophins capable of binding TrkA, TrkB and  
XX TrC are obtained by substituting amino acids 3-9, 28-37, 40-49,  
XX 61-66, 81-88, 94-98 or 95-97 of a neurotrophin with corresponding  
XX amino acids from NGF, BDNF or NT-3. Recombinant chimeric  
XX neurotrophins are used to treat e.g. Alzheimer disease and  
XX Parkinson disease.

XX Sequence 120 AA:

Query Match 94.6%; Score 618; DB 15; Length 120;  
Best Local Similarity 94.2%; Pred. No. 1, 8e-63;  
Matches 113; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKREVTYLAENVINNSVFRQYFEETKRA 61  
DB 1 SSTRPVFHNKEFSVCDVSVMWGDKTTATDINGKREVTYLAENVINNSVFRQYFEETKRA 60  
OY 62 SNPEVSGCRGIDSKHMSNCTTTHTFVKALTTDEKQAAARRIRIDTACVCLSKKATRRG 121  
DB 61 SNPEVSGCRGIDSKHMSNCTTTHTFVKALTTDEKQAAARRIRIDTACVCLSKKATRRG 120

RESULT 15

ID AAR21872 standard; protein; 121 AA.

XX AAR21872;

XX 10-JUN-1992 (first entry)

XX Chimeric neurotrophic factor S10.

DB 121 G 121  
Search completed: December 2, 2002, 15:08:38  
Job time : 25.1149 secs

KW Human BDNF; brain derived neurotrophic factor; NGF;  
KW neurotrophic growth factor; Alzheimer's disease; ageing;  
KW peripheral neuropathies; Parkinson's disease; Huntington's chorea;  
KW amyotrophic lateral sclerosis; nervous system disorders.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
FT Peptide 1..91  
FT /note="mouse NGF residues 1-91"  
FT Peptide 92..102  
FT /note="human BDNF residues 92-102"  
FT Peptide 103..121  
FT /note="mouse NGF residues 102-120"

MO9202620-A.

20-FEB-1992.

07-AUG-1991: 91WO-US05610.

08-AUG-1990: 90US-0564929.

(REGG-) REGENERON PHARM INC.

Shooter EM, Suter U, Ip N, Squinto SP, Furth ME, Lindsay RM;  
Yancopoulos GD;

WPI: 1992-080074/10.

New chimeric neurotrophic factors - useful in treating nervous  
PT conditions caused by trauma, surgery, ischemia, infection,  
PT metabolic diseases, nutritional deficiency, etc.

PS Claim 33: Flg 10: 114pp: English.

XX  
CC The sequence is that of a chimeric neurotrophic factor (NF) S10 which  
CC comprises the mouse neurotrophic growth factor (NGF) residues 1-91,  
CC human brain derived growth factor (hBNDF) residues 92-102 and mouse NGF  
CC residues 102-120. It may provide the activity of 2 NFs in a single mol.  
CC or may serve as a superagonist of an endogenous NF thereby enabling an  
CC increased biological response at lower doses. It may also be useful in  
CC targeting an active cpd. to cells responsive to NF. The design of  
CC chimeric NFs, such as S10, which retain specific biological activity  
CC but which are directed to a subset of factor-responsive cells may  
CC enable treatment of neurological disorders but avoid the complications  
CC of more widespread activity of parent moIs. It may be used in the  
CC treatment to eliminate diseased cells, e.g. virus infected cells or  
CC tumours of nervous system origin. It may also be used to treat patients  
CC whose nervous system has been damaged by trauma, surgery, ischemia,  
CC infection (e.g. polio or AIDS), metabolic disease, nutritional  
CC deficiency, malignancy or toxic agents. Also to treat e.g. Alzheimer's  
CC disease, ageing, peripheral neuropathies, Parkinson's disease,  
CC Huntington's chorea or amyotrophic lateral sclerosis. S10 or antibodies  
CC to it can also be used in the diagnosis and study of nervous system  
CC disorders. See also AAR21851-R21874 and AAQ22080-Q22131.

SQ Sequence 121 AA:

Query Match 93.6%: Score 611.5; DB 13: Length 121;

Best Local Similarity 95.0%: Pred. No. 1e-62; Matches 115; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

OY 2 SSTRPVFHMGEFVCDVSVWVGDKTTATDIDKREVTYLAENVINNSVFRQYFFETCRGA 61  
DB 1 SSTRPVFHMGEFVCDVSVWVGDKTTATDIDKREVTYLAENVINNSVFRQYFFETCRGA 60

OY 62 SNFVSGCGIDSKHNSCTTHTEFKALTFD-EKQAAAFIRIDRACVCVLSRKATRR 120  
DB 61 SNFVSGCGIDSKHNSCTTHTEFKALTFDQSKRIGMRFIRIDRACVCVLSRKATRR 120  
OY 121 G 121

GenCore version 5.1.3  
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OM protein - protein search, using BW model

Run on: December 2, 2002, 15:05:43 : Search time 9.64596 Seconds  
(Without alignments)  
1205.921 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653  
Sequence: 1 PSSHPVFMGCEFSVCDVS.....FIRIDTACVCLSRKATRRG 121

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5.

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	98.9	307	1	NGMSMG
2	636	95.9	245	2	beta-nerve growth
3	606	92.8	303	1	NGRTSA
4	593	90.8	241	2	neurotrophin-3 pre
5	584	89.4	286	1	NGHUBM
6	583	89.3	229	2	neurotrophin-3 pre
7	571	87.4	125	2	A26312
8	546	83.6	243	2	A26311
9	532	81.5	235	2	S14481
10	475	77.7	117	2	S28151
11	471	77.1	117	2	S15133
12	436.3	68.8	116	1	NGNMXI
13	432.5	66.2	116	1	A58566
14	432.5	66.2	246	2	A59218
15	390	59.7	194	2	I51709
16	378.5	58.0	257	2	C40304
17	378.5	58.0	257	2	I50400
18	378.5	58.0	258	2	S09155
19	378.5	58.0	282	2	A53781
20	347.5	53.2	286	2	S50855
21	325.5	49.8	247	2	A40304
22	325.5	49.8	249	2	S12555
23	325.5	49.8	249	2	B40304
24	325.5	49.8	252	2	A30361
25	320.5	49.1	114	2	I84765
26	319.5	48.9	248	2	JC6183
27	313.5	48.0	114	2	I50605
28	312.5	47.9	210	2	A42687
29	311.5	47.7	269	2	I51708

30	310.5	47.5	236	2	JH0400	neurotrophin-4 pre
31	307.5	47.1	209	2	B42687	neurotrophin-4 pre
32	304.5	46.6	114	2	I51599	brain-derived neur
33	81	12.4	229	2	C69806	hypothetical prote
34	79.5	12.2	475	2	T23355	hypothetical prote
35	76	11.6	478	2	D96603	hypothetical prote
36	74.5	11.4	116	2	S50449	phosphoglycerate k
37	74.5	11.4	425	2	S26623	phosphoglycerate k
38	73.5	11.3	459	2	S33637	protein kinase clk
39	73.5	11.3	693	2	T26415	hypothetical prote
40	72	11.0	399	2	S71368	phosphoglycerate k
41	71.5	10.9	835	2	C97322	probable alpha-ara
42	71	10.9	166	2	S55496	fibrillar protein p
43	71	10.9	331	1	A54932	zeta-crystallin /
44	70.5	10.8	290	2	S19426	hypothetical prote
45	69	10.6	3083	2	AK2493	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

NGMSMG nerve growth factor beta chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Nov-1980 #sequence\_revision 19-Feb-1984 #text\_change 21-Jul-2000  
C:Accession: A93301; A93305; A90366; I49689; I52891; A01400; I49690  
R:Scott, J.; Selby, M.; Urdew, M.; Quiroga, M.; Bell, G.I.; Rutter, W.J.  
Nature 302, 538-540, 1983  
A>Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse  
A:Reference number: A93301; MOID:83167518; PMID:6336309  
A:Accession: A93301  
A:Molecule type: mRNA  
A:Residues: 1-307 <SCD>  
A:Cross-references: GB:V00836; MID:953364; PIDN:CA24221.1; PID:953365  
R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.  
Nature 303, 821-825, 1983  
A>Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo  
A:Reference number: A93305; MOID:83244969; PMID:6688123  
A:Accession: A93305  
A:Molecule type: mRNA  
A:Residues: 1-307 <ULD>  
A:Cross-references: GB:K01759; MID:9200051; PIDN:AAA39820.1; PID:9387495  
A:Note: These authors believe that Met-67 is probably the amino-terminal residue and  
R:Angelletti, R.H.; Herndon, M.A.; Bradshaw, R.A.  
Biochemistry 12, 100-115, 1973  
A>Title: Amino acid sequences of mouse 2.5S nerve growth factor. II. Isolation and ch  
A:Reference number: A90366; MOID:73075048; PMID:4566923  
A:Accession: A90366  
A:Molecule type: protein  
A:Residues: 188-216, 'N', 218-305 <ANG>  
R:Selby, M.J.; Edwards, R.; Sharp, F.; Rutter, W.J.  
Mol. Cell. Biol. 7, 3057-3064, 1987  
A>Title: Mouse nerve growth factor gene: Structure and expression.  
A:Reference number: I49689; MOID:88038855; PMID:3670305  
A:Accession: I49689  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-307 <RES>  
A:Cross-references: GB:M17298; MID:9193493; PIDN:AAA37687.1; PID:9467311  
R:Ullrich, A.; Gray, A.; Berman, C.H.; Coussens, L.; Dull, T.J.  
Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983  
A>Title: Sequence homology of human and mouse beta-NGF subunit genes.  
A:Reference number: I52891; MOID:84406565; PMID:6327169  
A:Accession: I52891  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-307 <RB3>  
A:Cross-references: GB:M14805; MID:9200053; PIDN:AAA39821.1; PID:9200054  
C:Comment: The active molecule is a dimer of identical chains associated by noncovalent  
C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and  
C:Comment: nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels  
C:Genetics:

A:Gene: NGF  
 A:Introns: 21/2: 62/3  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor; homodimer  
 E:1-187/Domain: signal sequence and propeptide status predicted <SIG>  
 F:188-305/Product: nerve growth factor beta chain status experimental <MAT>  
 F:135-180/Binding site: carbohydrate (Asn) (covalent) status predicted  
 F:202-267,245-295,255-297/Disulfide bonds: status experimental  
 F:233/Binding site: carbohydrate (Asn) (covalent) status absent

Query Match 98.9%; Score 646; DB 1; Length 307;  
 Best Local Similarity 100.0%; Pred. No. 1,8e-59;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 61  
 DB 188 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 247  
 OY 62 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 121  
 DB 248 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 307

RESULT 2  
 156570  
 beta-nerve growth factor - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: 156570  
 R:Whittemore, S.R.; Friedman, P.L.; Larhammar, D.G.; Persson, H.; Gonzalez-Carvajal, M.; J. Neurosci. Res. 20, 403-410, 1988  
 A:Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippo  
 A:Reference number: 156570; MUID:89037223; PMID:3184206  
 A:Accession: 156570  
 A:Structure: preliminary; translated from 68/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-245 <RES>  
 A:Cross-references: GR:M36589; NID:9205691; PIDN:AAA1697.1; PID:9205692  
 C:Superfamily: nerve growth factor beta chain

Query Match 95.9%; Score 626; DB 2; Length 245;  
 Best Local Similarity 95.8%; Pred. No. 1.7e-57;  
 Matches 115; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 61  
 DB 126 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 185  
 OY 62 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 121  
 DB 186 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 245

RESULT 3  
 NGRTBA  
 nerve growth factor beta chain precursor - multimammate rat (Mastomys natalensis)  
 C:Species: Mastomys natalensis  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 18-Jun-1999  
 C:Accession: J0343  
 R:Fahnestock, M.; Bell, R.A.  
 Gene 69, 257-264, 1988  
 A:Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from Ma  
 A:Reference number: J0343; MUID:89172070; PMID:3224767  
 A:Accession: J0343  
 A:Molecule type: mRNA  
 A:Residues: 1-303 <PAM>  
 A:Cross-references: GB:M22748; NID:9202514; PIDN:AAA0599.1; PID:9202515  
 A:Note: It is uncertain whether Met-1 or Met-63 is the initiator  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor; homodimer; submaxillary gland  
 F:184-301/Product: nerve growth factor beta chain status predicted <MAT>  
 F:131,176,228/Binding site: carbohydrate (Asn) (covalent) status predicted  
 F:198-263,241-291,251-293/Disulfide bonds: status predicted

Query Match 92.8%; Score 606; DB 1; Length 303;  
 Best Local Similarity 92.5%; Pred. No. 2.5e-55;  
 Matches 111; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 61  
 DB 184 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 243  
 OY 62 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 121  
 DB 244 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 303

RESULT 4  
 J0097  
 nerve growth factor beta chain precursor - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 15-Mar-1996  
 C:Accession: J0097  
 R:Schwarz, M.A.; Fisher, D.; Bradshaw, R.A.; Jackson, P.J.  
 J. Neurochem. 52, 1203-1209, 1989  
 A:Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the  
 A:Reference number: J0097; MUID:89177243; PMID:2926397  
 A:Accession: J0097  
 A:Molecule type: mRNA  
 A:Residues: 1-241 <SCH>  
 A:Note: The authors translated the codon GCU for residue 214 as Asp  
 C:Genetics:  
 A:Gene: Beta-NGF  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor; hormone  
 F:1-121/Domain: propeptide status predicted <PRO>  
 F:122-241/Product: nerve growth factor beta chain status predicted <MAT>  
 F:166-154/Region: receptor binding status predicted  
 F:69,114/Binding site: carbohydrate (Asn) (covalent) status predicted

Query Match 90.8%; Score 593; DB 2; Length 241;  
 Best Local Similarity 90.0%; Pred. No. 4.4e-54;  
 Matches 108; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 2 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 61  
 DB 122 SSTRPVPFHMGESVCDSDSVWVGDKTTATDIDKGEVTLAEVNNINSVPROFFETKCA 181  
 OY 62 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 121  
 DB 182 SNPEVSGCGIDSKHNNISCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 241

RESULT 5  
 NGHUBM  
 nerve growth factor beta chain precursor - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 18-Jun-1999  
 C:Accession: A01399; S10253  
 R:Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.  
 Nature 303, 821-825, 1983  
 A:Title: Human beta-nerve growth factor gene sequence, highly homologous to that of mo  
 A:Reference number: A93305; MUID:83244569; PMID:6688123  
 A:Accession: A01399  
 A:Molecule type: DNA  
 A:Residues: 1-286 <ULL>  
 R:Boersant, G.; Pizutti, A.; Rugerli, E.L.; Fallini, A.; Silani, V.; Sidoli, A.; Scarla  
 Nucleic Acids Res. 18, 4020, 1990  
 A:Title: cDNA sequence of human beta-NGF.  
 A:Reference number: S10253; MUID:90326556; PMID:2374737  
 A:Accession: S10253  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 46-286 <BOB>  
 A:Cross-references: EMBL:X52599; NID:929476; PIDN:CAA36837.1; PID:929477  
 C:Comment: Nerve growth factor is found in submaxillary gland in large quantities and



DB 186 RPVSSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDTACVCVLSRSGR 242

## RESULT 9

S14481

nerve growth factor beta chain precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 16-Jul-1999

C:Accession: S14481

R:Carriero, F.; Campion, M.; Cardinalli, B.; Pierandrei-Amaldi, P.

Submitted to the EMBL Data Library, October 1990

A:Description: Structure and expression of the nerve growth gene in Xenopus oocyte and

A:Reference number: S14481

A:Accession: S14481

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-235 &lt;CAR&gt;

A:Cross-references: EMBL:X55716; NID:664914; PIDD:CAA39249.1; PID:664915

C:Superfamily: nerve growth factor beta chain

Query Match 81.5%: Score 532; DB 2; Length 235;

Best Local Similarity 84.2%: Pred. No. 9.2e-48;

Matches 96; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 3 STHPVFMHGEFVSVDVSVWGDGTTATDIDKKEVTLAEVINNSVFRQFFETKCRAS 62

DB 119 TVHPLHKGESVCDVSVWVGEKTKATDIDKKEVTLAEVINNSVFRQFFETKCRDP 178

OY 63 NPVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDTACVCVLSRK 116

DB 179 KPVSSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDTACVCVLSRK 232

## RESULT 10

S28161

nerve growth factor beta chain - Russell's viper

C:Species: Vipera russelli (Russell's viper)

C&gt;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S28161

R:Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.

Biochem. Biophys. Acta 1160, 287-292, 1992

A:Title: Purification and amino-acid sequence of a nerve growth factor from the venom of

A:Reference number: S28161; MUID:93120151; PMID:1477101

A:Accession: S28161

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-117 &lt;ROY&gt;

C:Superfamily: nerve growth factor beta chain

Query Match 72.7%: Score 475; DB 2; Length 117;

Best Local Similarity 73.2%: Pred. No. 3.6e-42;

Matches 82; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

OY 5 HPVFMHGEFVSVDVSVWGDGTTATDIDKKEVTLAEVINNSVFRQFFETKCRASNP 64

DB 1 HPHVNMHGEFVSVDVSVWVANKTATDIDKKEVTLAEVINNSVFRQFFETKCRKNRP 60

OY 65 VESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDTACVCVLSRK 116

DB 61 VPSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDTACVCVLSRK 112

## RESULT 11

S15193

nerve growth factor precursor - many-banded krait

C:Species: Bungarus multicinctus (many-banded krait)

C&gt;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C:Accession: S15193

R:Danse, J.M.; Garnier, J.M.

Growth Factors 8, 77-86, 1993

A:Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the

A:Reference number: S15193; MUID:93192074; PMID:7916740

A:Accession: S15193

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-243 &lt;DAN&gt;

A:Cross-references: GB:S56212; NID:9266298; PIDD:AA835729.1; PID:9266299

C:Superfamily: nerve growth factor beta chain

Query Match 72.1%: Score 471; DB 2; Length 243;

Best Local Similarity 72.2%: Pred. No. 2.1e-41;

Matches 83; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

OY 2 STHPVFMHGEFVSVDVSVWGDGTTATDIDKKEVTLAEVINNSVFRQFFETKCR 61

DB 125 NHPVNMHGEFVSVDVSVWVANKTATDIDKKEVTLAEVINNSVFRQFFETKCRN 184

OY 62 NPVSGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDTACVCVLSRK 116

DB 185 RPVSSGCGIDAKHNSYCTTHTFVKALTMESGQAAMRFIRIDTACVCVLSRK 239

## RESULT 12

MGNDXI

nerve growth factor - Indian cobra

C:Species: Naja naja (Indian cobra)

C&gt;Date: 30-Nov-1980 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-2000

C:Accession: S13927; A01401

R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 219, 38-40, 1981

A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.

A:Reference number: S13927; MUID:9118755; PMID:199538

A:Accession: S13927

A:Molecule type: protein

A:Residues: 1-116 &lt;INO&gt;

A:Experimental source: venom

A:Note: the source is designated as Naja naja and referred to as Indian cobra, so ve

R:Hoque-Angeletti, R.A.; Frazier, W.A.; Jacobs, J.M.; Nall, R.D.; Bradshaw, R.A.

Biochemistry 15, 26-34, 1976

A:Title: Purification, characterization, and partial amino acid sequence of nerve gro

A:Reference number: A01401; MUID:76114772; PMID:1247508

A:Accession: A01401

A:Molecule type: protein

A:Residues: 1-11, 'P', '13-14', 'B', '16', 'TBR', '20-21', 'GV', '23-27', 'N', '29-31', 'AS', '34', 'S', '36-48,

15-116 &lt;NO&gt;

A:Experimental source: venom

A:Note: the source is designated as Naja naja and referred to as Indian cobra, so ve

C:Comment: Nerve growth factor is necessary for the development of embryonic symphat

C:Complex: homodimer

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; venom

F:14-78,56-106,66-108/Distal folds: #status predicted

Query Match 66.8%: Score 436.5; DB 1; Length 116;

Best Local Similarity 69.6%: Pred. No. 3.6e-38;

Matches 78; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

OY 5 HPVFMHGEFVSVDVSVWGDGTTATDIDKKEVTLAEVINNSVFRQFFETKCRASNP 64

DB 3 HPHVNMHGEFVSVDVSVWVANKTATDIDKKEVTLAEVINNSVFRQFFETKCRKNRP 61

OY 65 VESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDTACVCVLSRK 116

DB 62 EPSGCGIDSHNSYCTETDIFKALTMESGQAAMRFIRIDTACVCVITKK 113

## RESULT 13

A58566

nerve growth factor - Chinese cobra

C:Species: Naja naja atra (Chinese cobra)

C&gt;Date: 16-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997

C:Accession: A58566

R:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.

Biochem. Int. 19, 909-917, 1989

A:Title: Amino acid sequence of nerve growth factor purified from the venom of the Fo

A:Reference number: A58566; MUID:90147847; PMID:2619756



A:Accession: A58566  
 A:Molecule type: protein  
 A:Residues: 1-116 <ODA>  
 A:Experimental source: Venom  
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
 C:Complex: homodimer  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: growth factor; homodimer; venom  
 F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match 66.2% Score 432.5; DB 2; Length 116;  
 Best Local Similarity 68.8%; Pred. No. 9,2e-38;  
 Matches 77; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 5 HPVHMGESVCDVSVWVGDKTATDIDKGEVYLAEVNINNSVFRQYFETKCRASNP 64  
 DB 3 HPVHNLGESHVCDVSVWVGDKTATDIDKGNVTYVENVNLDNKYKQYFETKCKNPNP 61

OY 65 VESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 116  
 DB 62 EPSCGRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 113

#### RESULT 14

A:Accession: A59218  
 A:Molecule type: protein  
 C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 31-Mar-2000  
 A:Accession: A59218; S13965

R:Selby, M.J.; Edwards, R.H.; Rutter, W.J.  
 J. Neurosci. Res. 18, 293-298, 1987  
 A:Title: Cobra nerve growth factor: structure and evolutionary comparison.  
 A:Reference number: A59218; MUID:88090976; PMID:3694712

A:Accession: A59218  
 A:Molecule type: mRNA  
 A:Residues: 1-246 <SEL>  
 R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.  
 FEBS Lett. 279, 38-40, 1991

A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.  
 A:Reference number: S13927; MUID:91138755; PMID:1995338  
 A:Accession: S13965  
 A:Molecule type: protein  
 A:Residues: 131-246 <IMO>  
 A:Experimental source: Venom  
 C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
 C:Complex: homodimer  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: growth factor; homodimer; venom  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:131-246/Product: nerve growth factor beta chain #status experimental <MAT>  
 F:144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match 66.2% Score 432.5; DB 2; Length 246;  
 Best Local Similarity 68.8%; Pred. No. 2,1e-37;  
 Matches 77; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 5 HPVHMGESVCDVSVWVGDKTATDIDKGEVYLAEVNINNSVFRQYFETKCRASNP 64  
 DB 133 HPVHNLGESHVCDVSVWVGDKTATDIDKGNVTYVENVNLDNKYKQYFETKCKNPNP 191

OY 65 VESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 116  
 DB 192 EPSCGRGIDSKHNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 243

RESULT 15  
 151709  
 nerve growth factor beta chain precursor - southern platyfish

C:Species: xiphophorus maculatus (southern platyfish)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
 C:Accession: 151709; S26674  
 R:Gotz, R.; Raulf, F.; Scharf, M.  
 J. Neurochem. 59, 432-442, 1992

A:Title: Brain-derived neurotrophic factor is more highly conserved in structure and  
 A:Reference number: 151708; MUID:92333301; PMID:1629719

A:Accession: 151709  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A:Residues: 1-194 <GOR>  
 A:Cross-references: EMBL:X59941; NID:965277; PID:CAA42566.1; PID:965278  
 C:Genetics: NGF

C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein; growth factor  
 F:1-14/Domain: signal sequence #status predicted <SIG>  
 F:15-79/Domain: propeptide #status predicted <PRO>  
 F:80-194/Product: nerve growth factor beta chain #status predicted <MAT>  
 F:90-155,133-183,143-185/Disulfide bonds: #status predicted  
 F:99/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 59.7% Score 390; DB 2; Length 194;  
 Best Local Similarity 66.1%; Pred. No. 4,2e-33;  
 Matches 72; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

OY 9 HMGESVCDVSVWVGDKTATDIDKGEVYLAEVNINNSVFRQYFETKCRASNPVPSG 68  
 DB 83 HRGVSVCDVSVWVGDKTATDIDKGEVYLAEVNINNSVFRQYFETKCRASNPVPSGSR 142

OY 69 CNGISKIMNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSRK 117  
 DB 143 CIGIDARHNSHCTNSHTFVRLTSSENGVAMRLIRINACVCLSRK 191

Search completed: December 2, 2002, 15:13:58  
 Job time: 9.64596 secs

GenCore version 5.1.3  
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OH protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 : Search time 4.96483 seconds  
(without alignments)  
1010.837 Million cell updates/sec

Title: US-10-072-681-3

Sequence: 1 PSSHPHFVHMGFSVCDSVS.....FIRIDACVCLSRKATRRG 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	666	98.9	241 1	NGF_MOUSE
2	626	95.9	241 1	NGF_RAT
3	606	92.8	241 1	NGF_PRAWA
4	593	90.8	241 1	NGF_CAVPO
5	584	89.4	241 1	NGF_HUMAN
6	583	89.3	229 1	NGF_HUMAN
7	564	86.4	231 1	NGF_PIG
8	566	83.6	231 1	NGF_BOVIN
9	532	81.5	231 1	NGF_CHICK
10	475	72.1	117 1	NGF_XENLA
11	471	72.1	243 1	NGF_DABRR
12	433.5	66.4	116 1	NGF_NAJNA
13	429.5	65.8	116 1	NGF_NAJNA
14	390	59.7	194 1	NGF_XIPMA
15	379.5	58.1	140 1	NGF_CYPCA
16	378.5	58.0	257 1	NGF_CHICK
17	378.5	58.0	257 1	NGF_CHICK
18	378.5	58.0	258 1	NGF_XENLA
19	378.5	58.0	258 1	NGF_XENLA
20	377.5	57.8	260 1	NT3_XENLA
21	374.5	57.4	233 1	NT3_XENLA
22	374.5	57.4	255 1	NT3_XENLA
23	374.5	57.4	255 1	NT3_XENLA
24	374.5	57.4	255 1	NT3_XENLA
25	374.5	57.4	255 1	NT3_XENLA
26	374.5	57.4	255 1	NT3_XENLA
27	374.5	57.4	255 1	NT3_XENLA
28	374.5	57.4	255 1	NT3_XENLA
29	374.5	57.4	255 1	NT3_XENLA
30	374.5	57.4	255 1	NT3_XENLA
31	374.5	57.4	255 1	NT3_XENLA
32	374.5	57.4	255 1	NT3_XENLA
33	374.5	57.4	255 1	NT3_XENLA

34	319.5	48.9	270 1	BDNF_CYPCA	090322 cyprinus ca
35	318.5	48.8	246 1	BDNF_CHICK	P25429 gallus gall
36	312.5	47.9	210 1	NT5_HUMAN	P34130 homo sapien
37	311.5	47.7	269 1	BDNF_XIPMA	002193 xiphophorus
38	310.5	47.5	236 1	NT4_XENLA	P24127 xenopus lae
39	307.5	47.1	209 1	NT5_XENLA	P34131 retius norv
40	304.5	46.6	114 1	BDNF_XENLA	P25432 xenopus lae
41	229	35.1	257 1	NT6B_HUMAN	P34133 homo sapien
42	224	34.3	186 1	NT6G_HUMAN	P34134 homo sapien
43	222	34.0	257 1	NT6A_HUMAN	P34132 homo sapien
44	165	25.3	42 1	NGF_VIPLE	P25426 vipera lebe
45	130	19.9	43 1	NT3_RAVCL	P25434 reja clavat

## ALIGNMENTS

RESULT 1	NGF_MOUSE	STANDARD:	PRT:	241 AA.
AC	P01139: 063864:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Beta-nerve growth factor precursor (Beta-NGF).			
GN	NGFB.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-83167518: PubMed-6336309;			
RA	Scott J., Selby M.J., Urdan M.S., Quiroga M., Bell G.I., Rutter W.J.;			
RT	* Isolation and nucleotide sequence of a cDNA encoding the precursor			
RL	of mouse nerve growth factor.*;			
RN	Nature 302:538-540(1983).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-83244969: PubMed-6688123;			
RA	Ullrich A., Gray A., Berman C., Dull T.J.;			
RT	* Human beta-nerve growth factor gene sequence highly homologous to			
RL	that of mouse.*;			
RN	Nature 303:821-825(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-84206565: PubMed-6337169;			
RA	Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;			
RT	* Sequence homology of human and mouse beta-NGF subunit genes.*;			
RL	Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CS7BL/6; TISSUE-Submaxillary gland;			
RA	MEDLINE-88038855: PubMed-3670305;			
RT	Selby M.J., Edwards R., Sharp F., Rutter W.J.;			
RL	* Mouse nerve growth factor gene: structure and expression.*;			
RN	Mol. Cell. Biol. 7:3057-3064(1987).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-93264918: PubMed-1284621;			
RA	Yamamoto T., Yamakuni T., Okabe N., Amano T.;			
RT	* Production and secretion of nerve growth factor by clonal striated			
RL	muscle cell line, G8-1.*;			
RN	Neurochem. Int. 21:251-258(1992).			
RN	[6]			
RP	SEQUENCE OF 122-239.			
RX	MEDLINE-73075048: PubMed-4566923;			
RA	Angelini R.H., Hermodson M.A., Bradshaw R.A.;			
RT	* Amino acid sequences of mouse 2.5S nerve growth factor. II.			
RL	Isolation and characterization of the thermolytic and peptic peptides			
RN	and the complete covalent structure.*;			
RN	Biochemistry 12:100-115(1973).			
RN	[7]			

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=92065986; PubMed=1956407;  
 RA McDonald N.O., Lapatto R., Murrey-Rust J., Gunning J., Nlodawer A.,  
 BLundell T.L.;  
 RT "New protein fold revealed by a 2.3-A resolution crystal structure of  
 RT nerve growth factor.";  
 RL Nature 354:411-414(1991).  
 RM [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=94260545; PubMed=8201620;  
 RA Holland D.R., Cousens L.S., Meng W., Matthews B.W.;  
 RT "Nerve growth factor in different crystal forms displays structural  
 RT flexibility and reveals zinc binding sites.";  
 RL J. Mol. Biol. 239:385-400(1994).  
 RM [9]  
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.  
 RC STRAIN-SVARS Webster; TISSUE-SUBMAXILLARY gland;  
 RX MEDLINE=98035451; PubMed=9351801;  
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;  
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with  
 RT four binding proteins.";  
 RL Structure 5:1275-1285(1997).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSOR NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: M35075; AAA39818.1; ALT\_INIT.  
 DR EMBL: V00836; CAA24221.1; ALT\_INIT.  
 DR EMBL: K01759; AAA39820.1; ALT\_INIT.  
 DR EMBL: M14805; AAA39821.1; ALT\_INIT.  
 DR EMBL: M17298; AAA37687.1; ALT\_INIT.  
 DR EMBL: M17296; AAA37687.1; JOINED.  
 DR EMBL: M17297; AAA37687.1; JOINED.  
 DR EMBL: S62089; CAB32081.2; ALT\_SEQ.  
 DR PIR: A01400; NCMSMG.  
 DR PDB: 1BET; 31-MAY-94.  
 DR PDB: 1BTG; 08-MAR-96.  
 DR PDB: 1SGF; 27-MAY-98.  
 DR MGD: MGI:97321; NGFb.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF; 1; 1.  
 DR PROSITE: PS50270; NGF; 2; 1.  
 KM Growth factor; Signal; 3D-structure.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 121  
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.  
 FT DISULFID 136 201  
 FT DISULFID 179 229  
 FT DISULFID 189 231  
 FT CARBOHYD 69 69  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 233 241 LSKATIRRG->CSAGRIQEEA (IN REF. 5).  
 SQ SEQUENCE 241 AA; 27076 MW; 164465EDC550081 CRC64;

QY 2 SSTRPVFMGEESVCDSSVWVGDKTATADIKREVTVAEVLNINSVROFFETKRA 61  
 DB 122 SSTHPFHHGEESVCDSSVWVGDKTATADIKREVTVAEVLNINSVROFFETKRA 181  
 QY 62 SNPVESGCGIDSKHNSYCTTTFVVALTTDEKQAAHFITIDACVCVLSRRATRG 121  
 DB 182 SNPVESGCGIDSKHNSYCTTTFVVALTTDEKQAAHFITIDACVCVLSRRATRG 241  
 RESULT 2  
 NGF RAT  
 ID NGF RAT STANDARD: PRT: 241 AA.  
 AC P25427;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGFB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8903723; PubMed=3184206;  
 RA Whittemore S.R., Friedman P.L., Larhammar D.G., Persson H.,  
 RA Gonzalez-Carvajal M., Holets V.R.;  
 RT "Rat beta-nerve growth factor sequence and site of synthesis in the  
 RT adult hippocampus.";  
 RL J. Neurosci. Res. 20:403-410(1988).  
 RM [2]  
 RP SEQUENCE OF 178-219 FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;  
 RX MEDLINE=9122573; PubMed=2025430;  
 RA Hallboeek F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary.";  
 RL Neuron 6:845-858(1991).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSOR NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: M3589; AAA41697.1; ALT\_INIT.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00258; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF; 1; 1.  
 DR PROSITE: PS50270; NGF; 2; 1.  
 KM Growth factor; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 121  
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.  
 FT DISULFID 136 201  
 FT DISULFID 179 229  
 FT DISULFID 189 231 BY SIMILARITY.  
 FT CARBOHYD 69 69  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 241 AA; 27009 MW; 665F42371553213D CRC64;

Query Match 98.9%; Score 646; DB 1; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-62;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 95.9%; Score 626; DB 1; Length 241;

Best Local Similarity 95.8%; Pred. No. 2, 1e-60;

Matches 111; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 2 STHPVFMGEFVSVCDSVWVGDKTTATDIDKREVTYLAEVNINNSVROFFETKRA 61  
 |||||  
 Db 122 STHPVFMGEFVSVCDSVWVGDKTTATDIDKREVTYLAEVNINNSVROFFETKRA 181  
 |||||  
 Oy 62 SNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDACVCLSRATRRG 121  
 |||||  
 Db 182 PNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDACVCLSRATRRG 241

# RESULT 3

NGF\_PRANA STANDARD: PRT: 241 AA.  
 AC P20675;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGF.  
 OS *Proxymys natalensis* (African soft-furred rat) (*Mastomys natalensis*).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 OC *Mastomys*.  
 NCBI\_TaxID=10112;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=89172070; PubMed=3234767;  
 RA Fainstock M., Bell R.A.;  
 RT "Molecular cloning of a cDNA encoding the nerve growth factor precursor from *Mastomys natalensis*."  
 RL Gene 69:257-264(1988).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: M22748; AAA40599.1; ALT\_INIT.  
 DR PIR: J70343; NCRTBA.  
 DR HSSP: P01139; 1BTG.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRINTS: PRO0268; NGF.1.  
 DR PRODOM: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF.1; 1.  
 DR PROSITE: PS50270; NGF.2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 121  
 FT CHAIN 122 241  
 FT DISULFID 136 201  
 FT DISULFID 179 229  
 FT DISULFID 189 231  
 FT CARBOHYD 69 69  
 FT CARBOHYD 114 114  
 FT CARBOHYD 166 166  
 SQ SEQUENCE 241 AA: 27035 MW: 85BBS207ALFEB2EF CCK64;

Query Match 92.8%; Score 606; DB 1; Length 241;

Best Local Similarity 92.5%; Pred. No. 3e-58;

Matches 111; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 2 STHPVFMGEFVSVCDSVWVGDKTTATDIDKREVTYLAEVNINNSVROFFETKRA 61  
 |||||  
 Db 122 STHPVFMGEFVSVCDSVWVGDKTTATDIDKREVTYLAEVNINNSVROFFETKRA 181  
 |||||  
 Oy 62 SNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDACVCLSRATRRG 121  
 |||||  
 Db 182 PNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDACVCLSRATRRG 241

# RESULT 4

NGF\_CAVPO STANDARD: PRT: 241 AA.  
 AC P19093;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGF.  
 OS *Cavia porcellus* (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=prostate;  
 RA MEDLINE=89177243; PubMed=2926397;  
 RA Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;  
 RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig prostate gland."  
 RL J. Neurochem. 52:1203-1209(1989).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC PIR: J10097; J10097.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRINTS: PRO0268; NGF.1.  
 DR PRODOM: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF.1; 1.  
 DR PROSITE: PS50270; NGF.2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 121  
 FT CHAIN 122 241  
 FT DISULFID 136 201  
 FT DISULFID 179 229  
 FT DISULFID 189 231  
 FT CARBOHYD 69 69  
 FT CARBOHYD 114 114  
 SQ SEQUENCE 241 AA: 26821 MW: 2F4E26B197804BF4 CCK64;

Query Match 90.8%; Score 593; DB 1; Length 241;

Best Local Similarity 90.0%; Pred. No. 7.7e-57;

Matches 108; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Oy 2 STHPVFMGEFVSVCDSVWVGDKTTATDIDKREVTYLAEVNINNSVROFFETKRA 61  
 |||||  
 Db 122 STHPVFMGEFVSVCDSVWVGDKTTATDIDKREVTYLAEVNINNSVROFFETKRA 181  
 |||||  
 Oy 62 SNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDACVCLSRATRRG 121  
 |||||  
 Db 182 PNPVSGCGRGIDSKHNSYCTTHTFVKALTTDEKQAAAFRIRIDACVCLSRATRRG 241

# RESULT 5

NGF\_HUMAN STANDARD: PRT: 241 AA.  
 ID NGF\_HUMAN  
 AC P01136;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN NGF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83244969; PubMed-6688123;  
 RA Ullrich A., Gray A., Berman C., Dull T.J.;  
 RT "Human beta-nerve growth factor gene sequence highly homologous to  
 RT that of mouse.";  
 RL Nature 303:821-825(1983).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-84205655; PubMed-6327169;  
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;  
 RT "Sequence homology of human and mouse beta-NGF subunit genes.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-90326556; PubMed-2374737;  
 RA Boran G., Pizzuti A., Rugarli E.I., Falini A., Sillani V.,  
 RT "cDNA sequence of human beta-NGF.";  
 RL Nucleic Acids Res. 18:4020-4020(1990).  
 RN [4]  
 RP SEQUENCE OF 178-219 FROM N.A.  
 RC TISSUE-Leukocyte;  
 RX MEDLINE-9122573; PubMed-2025430;  
 RA Hallboeck F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary.";  
 RL Neuron 6:845-858(1991).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC  
 CC EMBL: V01511; CAA24755.1;  
 DR EMBL: M21062; AA05931.1;  
 DR EMBL: X52599; CAA36832.1;  
 DR PIR: A01399; NC000001.  
 DR PIR: S10253; S10253.  
 DR HSSP: P01139; 1BET.  
 DR Genew: HGNC:7808; NGFB.  
 DR MIM: 162030;  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF.1;  
 DR PROSITE: PS0270; NGF.2; 1.  
 KW Growth factor; Signal; 1.  
 FT SIGNAL 1 18  
 FT  
 FT POTENTIAL.

PROPEP 19 121  
 CHAIN 122 241  
 DISULFID 136 201  
 DISULFID 179 229  
 DISULFID 189 231  
 CARBOHYD 69 69  
 CARBOHYD 114 114  
 SEQUENCE 241 AA; 26987 MW; CFIDB4DC6B735B0F CRC64;  
 Query Match 89.48; Score 584; DB 1; Length 241;  
 Best Local Similarity 89.98; Pred. No. 7, 2e-56;  
 Matches 107; Conserved 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 SSTRPVFMHGEFVSCDSVSWGCKTATTDIKGEVTLAEVINNSVRFQFFETKCA 61  
 DB 122 SSSHPFHRGFEVSCDSVSWGCKTATTDIKGEVTLAEVINNSVRFQFFETKCD 181  
 QY 62 SNVFECCGICGSKHNSVCTTTFVVALTDKQANRIRIDTACVLSRKATR 120  
 DB 182 PNPVDSGCRGIDSKHNSVCTTTFVVALTDKQANRIRIDTACVLSRKAVR 240  
 RESULT 6  
 NGF\_PIG STANDARD: PRT: 229 AA.  
 ID NGF\_PIG  
 AC 029074;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).  
 GN NGFB.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Large white; TISSUE-Blood;  
 RX MEDLINE-94313891; PubMed-8039422;  
 RA Lahlilb-Mansais Y., Mellink C., Yerle M., Gellin J.;  
 RT "A new marker (NGFB) on pig chromosome 4, isolated by using a  
 RT consensus sequence conserved among species.";  
 RL Cytogenet. Cell Genet. 67:120-125(1994).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC  
 CC EMBL: L31898; AAA21301.1;  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRODOM: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF.1;  
 DR PROSITE: PS0270; NGF.2; 1.  
 KW Growth factor; Signal; 1.  
 KW NON\_TER 1 1  
 FT SIGNAL <1 6  
 FT PROPEP 7 109  
 FT CHAIN 110 229  
 FT DISULFID 124 189  
 FT DISULFID 167 217  
 FT  
 FT POTENTIAL.  
 FT BY SIMILARITY.  
 FT BETA-NERVE GROWTH FACTOR.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.

FT DISULFID 177 219 BY SIMILARITY.  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 229 AA; 25275 MW; F8890771CBA189 CRC64.

Query Match 89.3%; Score 583; DB 1; Length 229;  
 Best Local Similarity 90.8%; Pred. No. 8.7e-56;  
 Matches 108; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKRA 61  
 DB 110 SSSHPVLRHGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKCD 169  
 OY 62 SNPVSGCGRIGDSKRNNSCTTHTFVKALTDERKQAAFRIRIDPACVLSRKATR 120  
 DB 170 PNPVDSGCGRIGDSKRNNSCTTHTFVKALTDGKQAAFRIRIDPACVLSRKAGR 228

RESULT 7  
 NGF\_BOVIN STANDARD; PRT: 231 AA.  
 AC P13600: 018969;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).  
 GN NGF.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid=9913;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-Blood.  
 RX MEDLINE=97430845; PubMed=9284944;  
 RA Elounga C., Laurent P., Hayes H., Rodellar C., Levezuel H.,  
 RA Zaragoza P.;  
 RT "Assignment of the beta-nerve growth factor (NGF) to bovine  
 RT chromosome 3 band q23 by in situ hybridization.";  
 RL Cytogenet. Cell Genet. 77:306-307(1997).  
 [2]  
 RN SEQUENCE OF 107-231 FROM N.A.  
 RP MEDLINE=86300647; PubMed=2427334;  
 RA Weller R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;  
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):  
 RT delineation of conserved and unconerved domains and their  
 RT relationship to the biological activity and antigenicity of NGF.";  
 RL EMBO J. 5:1489-1493(1986).  
 [3]  
 RN FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 RN MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 RN STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 RN EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: Y09566; CAA70759.1; -  
 DR EMBL: M26809; AAA30666.1; -  
 DR PIR: A26312; A26312.  
 DR HSSP: P01139; I8ET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.

DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT MON\_TER 1  
 FT SIGNAL <1 8  
 FT PROPEP 9 111  
 FT CHAIN 112 231  
 FT DISULFID 126 191  
 FT DISULFID 169 219  
 FT DISULFID 179 221  
 FT CARBOHYD 156 156  
 FT CONFLICT 118 118  
 FT CONFLICT 161 161  
 FT CONFLICT 230 231  
 SQ SEQUENCE 231 AA; 25437 MW; 0160509291AA48C CRC64;

Query Match 86.4%; Score 564; DB 1; Length 231;  
 Best Local Similarity 89.6%; Pred. No. 9.9e-54;  
 Matches 103; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVFMGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKRA 61  
 DB 112 SSSHPVLRHGEFSVCDVSVMGDKTATDIDKKEVYLAEVNINSVPROFFETKCD 171  
 OY 62 SNPVSGCGRIGDSKRNNSCTTHTFVKALTDERKQAAFRIRIDPACVLSRK 116  
 DB 172 PNPVDSGCGRIGDSKRNNSCTTHTFVKALTDGKQAAFRIRIDPACVLSRK 226

RESULT 8  
 NGF\_CHICK STANDARD; PRT: 243 AA.  
 AC P05200:  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 GN Gallus.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_Taxid=9031;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=86300646; PubMed=3017695;  
 RA Eberhardt T., Larhammar D., Persson H.;  
 RT "Structure and expression of the chicken beta nerve growth factor  
 RT gene.";  
 RL EMBO J. 5:1483-1487(1986).  
 [2]  
 RN SEQUENCE OF 118-243 FROM N.A.  
 RP MEDLINE=86248129; PubMed=3720959;  
 RA Mion D., Perret C., Frechlin N., Keller A., Behar G., Brechet P.,  
 RA Auffray C.;  
 RT "Molecular cloning of the avian beta-nerve growth factor gene:  
 RT transfection in brain.";  
 RL FEBS Lett. 203:82-86(1986).  
 [3]  
 RN SEQUENCE OF 121-243 FROM N.A.  
 RP MEDLINE=86300647; PubMed=2427334;  
 RA Weller R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;  
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):  
 RT delineation of conserved and unconerved domains and their  
 RT relationship to the biological activity and antigenicity of NGF.";  
 RL EMBO J. 5:1489-1493(1986).  
 [4]  
 RN SEQUENCE OF 181-222 FROM N.A.  
 RP MEDLINE=9122573; PubMed=2025430;  
 RA Hallboeck F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary.";  
 RL Neuron 6:845-858(1991).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL; X04003; CAA27633.1; ALT_INIT.
CC EMBL; X04067; CAA27703.1; -
CC EMBL; M26810; AAA48984.1; -
CC PIR; A24857; A24857.
CC PIR; A26311; A26311.
CC HSSP; P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam; PF00243; NGF_1.
CC PRINTS; PR00268; NGF.
CC PRODOM; PD002052; NGF_1.
CC SMART; SM00140; NGF_1; 1.
CC PROSITE; PS00248; NGF_1; 1.
CC PROSITE; PS50270; NGF_2; 1.
CC Growth factor; Signal.
CC SIGNAL; 1 22 POTENTIAL.
CC PROPEP 23 125
CC CHAIN 126 243 BETA-NERVE GROWTH FACTOR.
CC DISULFID 139 204 BY SIMILARITY.
CC DISULFID 182 232 BY SIMILARITY.
CC DISULFID 192 234 BY SIMILARITY.
CC SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 83.6%; Score 546; DB 1; Length 243;
Best Local Similarity 84.6%; Pred. No. 9, 2e-52;
Matches 99; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 STRPVFMHGEFSCDSVSVWVGDKTTATNDIKGEVTVLAENVNNSVFRQYFETRCRAS 62
DB 126 TAPVYLRHGEFSCDSVSVWVGDKTTATNDIKGEVTVLAENVNNSVFRQYFETRCRAS 185
QY 63 NPVSSGRCGIDSKHNSYCTTHTFEVKALTTDEKQAAARRIRIDTACVLSKRR 119
DB 186 RPVSSGRCGIDSKHNSYCTTHTFEVKALTTDEKQAAARRIRIDTACVLSKRR 242

RESULT 9
NGF_XENLA STANDARD: PRT; 231 AA.
ID NGF_XENLA
AC P31617;
DT 01-MAY-1991 (Rel. 18; Created)
DT 15-DEC-1998 (Rel. 37; Last sequence update)
DT 15-DEC-1998 (Rel. 37; Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campioni M., Cardinali B., Pierandrea-Amaldi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [3]
RP SEQUENCE OF 170-211 FROM N.A.
RC TISSUE=Liver;

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RX MEDLINE=9122573; PubMed=2025430;
RA Haliboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL; X5716; CAA39249.1; ALT_INIT.
CC PIR; S1481; S1481.
CC HSSP; P01139; 1BET.
CC InterPro: IPR002072; NGF.
CC Pfam; PF00243; NGF_1.
CC PRINTS; PR00268; NGF.
CC PRODOM; PD002052; NGF_1.
CC SMART; SM00140; NGF_1; 1.
CC PROSITE; PS00248; NGF_1; 1.
CC PROSITE; PS50270; NGF_2; 1.
CC Growth factor; Signal.
CC SIGNAL; 1 18 POTENTIAL.
CC PROPEP 19 114
CC CHAIN 115 231 NERVE GROWTH FACTOR.
CC DISULFID 128 193 BY SIMILARITY.
CC DISULFID 171 221 BY SIMILARITY.
CC DISULFID 181 223 BY SIMILARITY.
CC CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 231 AA; 26416 MW; 72A04E7D008B58C5 CRC64;

Query Match 81.5%; Score 532; DB 1; Length 231;
Best Local Similarity 84.2%; Pred. No. 2, 8e-50;
Matches 96; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 STRPVFMHGEFSCDSVSVWVGDKTTATNDIKGEVTVLAENVNNSVFRQYFETRCRAS 62
DB 115 TAPVYLRHGEFSCDSVSVWVGDKTTATNDIKGEVTVLAENVNNSVFRQYFETRCRAS 174
QY 63 NPVSSGRCGIDSKHNSYCTTHTFEVKALTTDEKQAAARRIRIDTACVLSKRR 116
DB 175 KPVSSGRCGIDSKHNSYCTTHTFEVKALTTDEKQAAARRIRIDTACVLSKRR 228

RESULT 10
NGF_DABRR STANDARD: PRT; 117 AA.
ID NGF_DABRR
AC P30894;
DT 01-JUL-1993 (Rel. 26; Created)
DT 01-JUL-1993 (Rel. 26; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE Nerve growth factor (NGF).
OS Dabolia russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperae; Viperae; Dabolia.
OX NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;

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RT "Purification and amino-acid sequence of a nerve growth factor from  
 the venom of Vipera russelli russelli".  
 RL Blochm. Biophys. Acta 1160:287-292(1992).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC  
 CC NEURONS IN THE BRAIN.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 DR PIR: S28161; S28161.  
 DR HSSP: P01139; 18ET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF; 1; 1.  
 DR PROSITE: PS0270; NGF; 2; 1.  
 DR Glycoprotein: Growth factor.  
 FT DISULFID 12 77  
 FT DISULFID 55 105 BY SIMILARITY.  
 FT DISULFID 65 107 BY SIMILARITY.  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC...).  
 SQ SEQUENCE 117 AA: 13283 MW: A64559C5EC11F66 CRC64;  
 Query Match 72.7%; Score 475; DB 1; Length 117;  
 Best Local Similarity 73.2%; Pred. No. 1.9e-44;  
 Matches 82; Conservative 17; Mismatches 13; Indels 0; Gaps 0;  
 Oy 5 HPVHMGESVCDSSVWVGDKTTATDICKREYTLAEVNNINSVFRQFFETCKRA 64  
 Db 1 HPVHMGESVCDSSVWVGDKTTATDICKREYTLAEVNNINSVFRQFFETCKRA 60  
 Oy 65 VESGCRGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDACVCVSRK 116  
 Db 61 VPSGCRGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDACVCVSRK 112  
 RESULT 11  
 NGF\_BUNMU STANDARD: PRT; 243 AA.  
 ID NGF\_BUNMU  
 AC P34128;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Nerve growth factor precursor (NGF).  
 OS Bungarus multicinctus (Many-banded krait).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 CC Elapidae; Bungarinae; Bungarus.  
 CC NCBI\_Taxid=8616;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom gland;  
 RA MEDLINE=93192074; PubMed=7916740;  
 RA Danse J.M., Garnier J.M.;  
 RT "Molecular cloning of a cDNA encoding a nerve growth factor precursor  
 from the krait, Bungarus multicinctus".  
 RL Growth factors 8:77-86(1993).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC  
 CC NEURONS IN THE BRAIN.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: S56212; AAB25729.1; .  
 DR HSSP: P01139; 18ET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF; 1; 1.  
 DR PROSITE: PS0270; NGF; 2; 1.  
 DR Growth factor: Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 125  
 FT CHAIN 126 243  
 FT DISULFID 139 204  
 FT DISULFID 182 232  
 FT DISULFID 192 234  
 SQ SEQUENCE 243 AA: 27514 MW: E33F64B142179A08 CRC64;  
 Query Match 72.1%; Score 471; DB 1; Length 243;  
 Best Local Similarity 72.2%; Pred. No. 1.1e-43;  
 Matches 83; Conservative 14; Mismatches 18; Indels 0; Gaps 0;  
 Oy 2 SSTRPFFHMGESVCDSSVWVGDKTTATDICKREYTLAEVNNINSVFRQFFETCKRA 61  
 Db 125 NNRHPPVHMGESVCDSSVWVGDKTTATDICKREYTLAEVNNINSVFRQFFETCKRN 184  
 Oy 62 SPSVSGCRGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDACVCVSRK 116  
 Db 185 PBPVSGCRGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDACVCVSRK 239  
 RESULT 12  
 NGF\_NAJNA STANDARD: PRT; 116 AA.  
 ID NGF\_NAJNA  
 AC P01140;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Nerve growth factor (NGF).  
 OS Naja naja (Indian cobra).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 CC Elapidae; Elapinae; Naja.  
 CC NCBI\_Taxid=35670;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA MEDLINE=91138755; PubMed=1995338;  
 RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;  
 RT "Amino acid sequences of nerve growth factors derived from cobra  
 venoms".  
 RL FEBS Lett. 279:38-40(1991).  
 RN [2]  
 RP PRELIMINARY SEQUENCE.  
 RC TISSUE=Venom;  
 RA MEDLINE=76114772; PubMed=1247508;  
 RA Hogue-Angelietti R.A., Frazier W.A., Jacobs J.W., Nall H.D.,  
 RA Bradshaw R.A.;  
 RT "Purification, characterization, and partial amino acid sequence of  
 nerve growth factor from cobra venom".  
 RL Biochemistry 15:26-34(1976).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC  
 CC NEURONS IN THE BRAIN.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 DR PIR: A01401; NGNXXI.  
 DR PIR: S13927; S13927.





FT CHAIN 80 194 NERVE GROWTH FACTOR.  
 FT DISULFID 90 155 BY SIMILARITY.  
 FT DISULFID 133 183 BY SIMILARITY.  
 FT DISULFID 143 185 BY SIMILARITY.  
 SQ SEQUENCE 194 AA: 21596 MW: 0369E0FA51147AE CRC64;

Query Match 59.7%: Score 390; DB 1; Length 194;  
 Best Local Similarity 66.1%: Pred. No. 4, 9e-35;  
 Matches 72; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 9 HMGESVCDSSVYWGDKTTATDINKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 68  
 DB 83 HMGESVCDSSVYWGDKTTATDINKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 68  
 QY 69 CNGIDSKHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVCLSKA 117  
 DB 143 CNGIDSKHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVCLSKA 117

# RESULT 15

NT7\_CYPCA STANDARD: PRT: 140 AA.

AC 093474:  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurotrophin-7 precursor (NT-7) (Fragment).  
 GN NT7 OR NT7 OR NNT.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=9618228;  
 RA Lai K.-O., Fu W.-Y., Ip F.C.F., Ip N.Y.;  
 RT Cloning and expression of a novel neurotrophin, NT-7, from carp.;  
 RL Mol. Cell. Neurosci. 11:64-76(1998).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 CC EMBL: U94949; AAC25632.1; -  
 DR HSSP: P01139; 1SGF.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor.  
 FT NON\_TER 1  
 FT PROPEP 7  
 FT CHAIN 8 140 BY SIMILARITY.  
 FT DISULFID 21 101 NEUTROPHIN-7.  
 FT DISULFID 64 129 BY SIMILARITY.  
 FT DISULFID 89 131 BY SIMILARITY.  
 FT VARIANT 70 70 I -> V.  
 FT VARIANT 95 95 E -> K.  
 SQ SEQUENCE 140 AA: 15855 MW: 3F5F0BCE2601B0FC CRC64;

Query Match 58.1%: Score 379.5; DB 1; Length 140;  
 Best Local Similarity 56.3%: Pred. No. 4, 7e-34;  
 Matches 71; Conservative 14; Mismatches 26; Indels 15; Gaps 1;

QY 9 HMGESVCDSSVYWGDKTTATDINKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 65  
 DB 14 HMGESVCDSSVYWGDKTTATDINKKEVTVLAEVNINSVFRQYFEETKCRASNPVSG 65  
 QY 66 -----ESGCRGIDSKHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVCL 113  
 DB 74 KPGQGVSGVAKGTSSCGIDNEHNSYCTTHTFVKALTTDEKQAMRFRTIDTACVCL 133  
 QY 114 SRKATR 119  
 DB 134 SRKATR 139

Search completed: December 2, 2002, 15:12:43  
 Job time: 5.96483 secs

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OK protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 18.7245 Seconds  
(without alignments)  
1331.501 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653

Sequence: 1 PSSSTPVPFMGEFVSVCDSVS.....FIRIDTACVLSRKATRRG 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584	89.4	241	4	Q9P208
2	584	89.4	241	4	Q9UKL8
3	584	89.4	241	6	Q9N2F1
4	584	89.4	241	6	Q9N2F0
5	584	89.4	241	6	Q9N2E9
6	577	88.4	294	11	Q91XB4
7	576	88.2	241	4	Q96P60
8	522	79.9	217	6	Q9N1B3
9	478	73.2	241	13	Q90W38
10	471	72.1	241	13	Q9DEZ9
11	424	64.9	87	6	Q9TTC3
12	416	63.7	87	4	Q9P224
13	347.5	53.2	286	13	Q91988
14	335.5	51.4	241	6	Q9N1B2
15	325.5	49.8	153	11	Q9CYL3
16	325.5	49.8	247	6	Q97759

17	325.5	49.8	249	11	Q8VNH4	Q8VNH4 mus musc
18	320.5	49.1	246	13	Q8G76	Q8G76 japalura
19	319.5	48.9	270	13	Q9YH42	Q9YH42 brachyd
20	318.5	48.8	177	13	Q91BL2	Q91BL2 poephila
21	318.5	48.8	246	13	Q8G74	Q8G74 cyclophiops
22	314.5	48.2	246	13	Q8G75	Q8G75 phrynosoma
23	305	46.7	247	13	Q8G77	Q8G77 tylosotrit
24	296.5	45.4	101	6	Q9T722	Q9T722 macaca fusc
25	270	41.3	324	13	Q9YX95	Q9YX95 lampetra f1
26	262.5	40.2	186	12	Q9J5D9	Q9J5D9 fowlipep vlr
27	227	34.8	85	6	Q02790	Q02790 macropus fu
28	227	33.8	85	6	Q13114	Q13114 isodon mac
29	221	33.8	85	6	Q13122	Q13122 tarsipes ro
30	221	33.8	85	6	Q02795	Q02795 ornithorhyn
31	221	33.8	85	6	Q02798	Q02798 petaurus br
32	221	33.8	85	6	Q13104	Q13104 cetartreus
33	221	33.8	85	6	Q02792	Q02792 notoryctes
34	221	33.8	85	6	Q13105	Q13105 dasyrodides
35	221	33.8	85	6	Q02801	Q02801 tachylosus
36	220	33.7	85	6	Q02803	Q02803 trichosurus
37	197	30.2	42	6	Q02794	Q02794 ornithorhyn
38	195	29.9	42	6	Q02802	Q02802 tachylosus
39	194	29.7	42	6	Q02802	Q02802 trichosurus
40	161	24.7	185	11	Q99NV9	Q99NV9 pedetes cap
41	160	24.5	184	6	Q9BRT5	Q9BRT5 tupia mmo
42	160	24.5	185	6	Q9BRT6	Q9BRT6 talpa alai
43	160	24.5	185	6	Q9BRT5	Q9BRT5 condyura c
44	160	24.5	186	6	Q9BRT3	Q9BRT3 choleopus h
45	160	24.5	186	6	Q9BRT2	Q9BRT2 choleopus d

## ALIGNMENTS

## RESULT 1

ID Q9P208 PRELIMINARY; PRT; 241 AA.  
AC Q9P208;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Beta-nerve growth factor (Fragment).  
GN BETA-NGF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kitano T., Kobayakawa H., Saitou N.:  
\*Silver Project.\*  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB037517; BAA90437.1; -  
DR HSSP; P01139; 1BET.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF; 1.  
DR PRINTS: PR00268; NGF.  
DR PRODOM: PD002052; NGF; 1.  
DR SMART: SM00140; NGF; 1.  
DR PROSITE: PS00246; NGF\_1; 1.  
DR PROSITE: PS0270; NGF\_2; 1.  
FT NON\_TER 241 241  
SQ SEQUENCE 241 AA; 26998 MW; D5531ED825D96C14 CRC64;

Query Match 89.4%; Score 584; DB 4; Length 241;  
Best Local Similarity 89.9%; Pred. No. 1.1e-58;  
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVPFMGEFVSVCDSVWVGDKTTATDICKKEVTLAEVINNSVFRQFFETKCR 61  
DB 122 SSTRPVPFMGEFVSVCDSVWVGDKTTATDICKKEVTLAEVINNSVFRQFFETKCR 181  
QY 62 SNPVSQGRGIDSKHNSYCTTHTFYKALTTDEKQANRFRIDTACVLSRKATRR 120

DB 182 PNPVDSGCRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 240

## RESULT 2

ID 09N2E1 PRELIMINARY: PRT: 241 AA.

AC 09N2E1: 01-OCT-2000 (Tremblrel. 13, Created)

DT 01-OCT-2000 (Tremblrel. 13, Last sequence update)

DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)

GN Nerve growth factor B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RM SEQUENCE FROM N.A.

RP MEDLINE=99256269; PubMed=10322959;

RA Tong Y., Wang H., Chen W.;

RT "Cloning and sequencing of the gene for premature beta nerve growth

factor."

RT Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).

RM SEQUENCE FROM N.A.

RA Tong Y., Wang H.;

RT Submited (MAY-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF100960; AAD55975.1; -

DR HSP: P01139; 1BET.

DR InterPro: IPRO02072; NCF.

DR Pfam: PF00243; NCF. 1.

DR PRINTS: PR00268; NCF.

DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.

DR PROSITE: PS00248; NCF. 1.

DR PROSITE: PS50270; NCF. 2; 1.

SO SEQUENCE 241 AA; 26959 MW; 619DFC65EB3B0671 CRC64;

Query Match 89.4%; Score 584; DB 4; Length 241;

Best Local Similarity 89.9%; Pred. No. 1,1e-58;

Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCA 61

DB 122 SSSHPFFHMGESVCDSSVWVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCD 181

QY 62 SNPVEGCGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATR 120

DB 182 PNPVDSGCRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 240

## RESULT 3

ID 09N2E1 PRELIMINARY: PRT: 241 AA.

AC 09N2E1: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)

GN Beta-nerve growth factor (fragment).

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

OX NCBI\_TaxID=9598;

RM SEQUENCE FROM N.A.

RP STRAIN=CHMP-220;

RA Kitano T., Kobayakawa H., Saitou N.;

RT "Silver Project."

RT Submited (JAN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AB037519; BAA90438.1; -

DR HSP: P01139; 1BET.

DR InterPro: IPRO02072; NCF.

DR Pfam: PF00243; NCF. 1.

DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.

DR PROSITE: PS00248; NCF. 1.

DR PROSITE: PS50270; NCF. 2; 1.

FT NON-TER 241

SO SEQUENCE 241 AA; 26915 MW; 6F54D163C384BB34 CRC64;

Query Match 89.4%; Score 584; DB 6; Length 241;

Best Local Similarity 89.9%; Pred. No. 1,1e-58;

Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCA 61

DB 122 SSSHPFFHMGESVCDSSVWVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCD 181

QY 62 SNPVEGCGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATR 120

DB 182 PNPVDSGCRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 240

RESULT 4

ID 09N2E1 PRELIMINARY: PRT: 241 AA.

AC 09N2E1: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)

GN Beta-nerve growth factor (fragment).

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.

OX NCBI\_TaxID=9593;

RM SEQUENCE FROM N.A.

RP STRAIN=GORILLA-01;

RA Kitano T., Kobayakawa H., Saitou N.;

RT "Silver Project."

RT Submited (JAN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AB037519; BAA90439.1; -

DR HSP: P01139; 1BET.

DR InterPro: IPRO02072; NCF.

DR Pfam: PF00243; NCF. 1.

DR ProDom: PD002052; NCF. 1.

DR SMART: SM00140; NCF. 1.

DR PROSITE: PS00248; NCF. 1.

DR PROSITE: PS50270; NCF. 2; 1.

FT NON-TER 241

SO SEQUENCE 241 AA; 26915 MW; 6F54D163C384BB34 CRC64;

Query Match 89.4%; Score 584; DB 6; Length 241;

Best Local Similarity 89.9%; Pred. No. 1,1e-58;

Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCA 61

DB 122 SSSHPFFHMGESVCDSSVWVGDKTTATDIDKKEVTLAEVNNNSVFQYFEETKCD 181

QY 62 SNPVEGCGIDSKHMSYCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATR 120

DB 182 PNPVDSGCRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 240

RESULT 5

ID 09N2E1 PRELIMINARY: PRT: 241 AA.

AC 09N2E1: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

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DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORAN-U1.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RU Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB037520; BAA90440.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 241
SQ SEQUENCE 241 AA; 26876 MW; DFC168E7E4E01F15 CRC64;

Query Match 89.4%; Score 584; DB 6; Length 241;
Best Local Similarity 89.9%; Pred. No. 1,le-58;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVHMGESVCDSSVWVGDKTTATDINGKREVTYLAEVNINSVFRQYFFETKCR 61
DB 122 SSSHPHFHGEFSCDSVSVWVGDKTTATDINGKREVTYLAEVNINSVFRQYFFETKCRD 181
OY 62 SNPESGCGRIGDSKHNNSCTTHTFFVKALTDDEKQAAFRIRIDTACVLSKRAVR 120
DB 182 PNPVDSGCGRIGDSKHNNSCTTHTFFVKALTDGKQAAFRIRIDTACVLSKRAVR 240

RESULT 6
OY 091XB4 PRELIMINARY; PRT; 294 AA.
ID 091XB4
AC 091XB4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Similar to nerve growth factor, beta.
GN NGFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011123; AAH11123.1; -.
DR MGI: MGI:97321; Ngfb.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
SQ SEQUENCE 294 AA; 33326 MW; 9EE7402DAC899229 CRC64;

Query Match 88.4%; Score 577; DB 11; Length 294;
Best Local Similarity 100.0%; Pred. No. 9e-58;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSTRPVHMGESVCDSSVWVGDKTTATDINGKREVTYLAEVNINSVFRQYFFETKCR 61
DB 188 SSTRPVHMGESVCDSSVWVGDKTTATDINGKREVTYLAEVNINSVFRQYFFETKCR 247

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OY 62 SNPESGCGRIGDSKHNNSCTTHTFFVKALTDDEKQAAFRIRIDTACVLSKRAVR 108
DB 248 SNPESGCGRIGDSKHNNSCTTHTFFVKALTDDEKQAAFRIRIDTACVLSKRAVR 294

RESULT 7
OY 096P60 PRELIMINARY; PRT; 241 AA.
ID 096P60
AC 096P60;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Nerve growth factor beta.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RU Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF411526; AL05874.1; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR ProDom: PD002052; NGF. 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 26964 MW; 745216485C21E558 CRC64;

Query Match 88.2%; Score 576; DB 4; Length 241;
Best Local Similarity 88.2%; Pred. No. 9.2e-58;
Matches 105; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVHMGESVCDSSVWVGDKTTATDINGKREVTYLAEVNINSVFRQYFFETKCR 61
DB 122 SSSHPHFHGEFSCDSVSVWVGDKTTATDINGKREVTYLAEVNINSVFRQYFFETKCRD 181
OY 62 SNPESGCGRIGDSKHNNSCTTHTFFVKALTDDEKQAAFRIRIDTACVLSKRAVR 120
DB 182 PNPVDSGCGRIGDSKHNNSCTTHTFFVKALTDGKQAAFRIRIDTACVLSKRAVR 240

RESULT 8
OY 09N183 PRELIMINARY; PRT; 217 AA.
ID 09N183
AC 09N183;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Beta nerve growth factor (fragment).
OS Macaca fasciata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RX MEDLINE-99270338; PubMed-10340513;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and c-fos mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys."
RN J. Comp. Neurol. 408:378-398(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLLOOD;
RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
RU Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF222682; AAF33790.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.

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DR PFAM: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT SEQUENCE 217 AA; 24240 MW; 36A5A201DFCD8DC CRC64;

Query Match
Best Local Similarity 79.9%; Score 522; DB 6; Length 217;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 STHPVFKGEFVCDVSVVWGDTTATDIDKREVTYLAENVINNSVFQYFETKCRPA 61
DB 112 SSSHPIFHNGEFVCDVSVVWGDTTATDIDKREVTYLAENVINNSVFQYFETKCRD 171
OY 62 SVPVSGCGRIGDSKHNNSYCTTHTFYKALITDEKQAMRFIRIDT 107
DB 172 PNPVDSGCRIGDSKHNNSYCTTHTFYKALITDEKQAMRFIRIDT 217

RESULT 9
OY0W38 PRELIMINARY; PRT; 241 AA.
AC 090W38:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative neurotrophic growth factor.
GN NGF.
OS Botryopsis jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID-8726;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-VENOM GLAND;
RA Kashiwa S., Pereira J.O., Astolfi Filho S., Soares A.M.,
RA Gintre A.C.O., Giglio J.R., Franca S.C.;
RT Molecular cloning and cDNA sequence of a nerve growth factor
RT precursor from Bothrops jararacussu venomous gland.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY007318; AAC12169.1;
DR InterPro: IPR002072; NGF.
DR PFAM: PF00243; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR PROSITE: PS00248; NGF_1; UNKNOWN_1.
DR PROSITE: PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CRC64;

Query Match
Best Local Similarity 73.2%; Score 478; DB 13; Length 241;
Matches 83; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

OY 5 HPVFHNGEFVCDVSVVWGDTTATDIDKREVTYLAENVINNSVFQYFETKCRASP 64
DB 125 HPVHNGEFVCDVSVVWANKTTATDIDKREVTYLAENVINNSVFQYFETKCRNP 184
OY 65 VESGCGRIGDSKHNNSYCTTHTFYKALITDEKQAMRFIRIDTACVYSRK 116
DB 185 VPTGCGRIGDSKHNNSYCTTHTFYKALITDEKQAMRFIRIDTACVYSRK 236

RESULT 10
OY0E29 PRELIMINARY; PRT; 241 AA.
AC 090E29:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
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DE Nerve growth factor.
OS Crocalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID-8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-VENOM GLAND;
RA Hayashi M.A.F., Radle-Baptista G., Ymane T., Canargo A.C.M.;
RT Cloning and sequence of a cDNA coding for a rattlesnake (Crotalus
RT durissus terrificus) nerve growth factor.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF306533; AAG30924.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR PFAM: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 27118 MW; 4A261F42C5D6EF3F CRC64;

Query Match
Best Local Similarity 72.1%; Score 471; DB 13; Length 241;
Matches 82; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

OY 5 HPVFHNGEFVCDVSVVWGDTTATDIDKREVTYLAENVINNSVFQYFETKCRASP 64
DB 125 HPVHNGEFVCDVSVVWANKTTATDIDKREVTYLAENVINNSVFQYFETKCRNP 184
OY 65 VESGCGRIGDSKHNNSYCTTHTFYKALITDEKQAMRFIRIDTACVYSRK 116
DB 185 VPTGCGRIGDSKHNNSYCTTHTFYKALITDEKQAMRFIRIDTACVYSRK 236

RESULT 11
OY0TC3 PRELIMINARY; PRT; 87 AA.
AC 090TC3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Beta nerve growth factor (fragment).
GN NGF.
OS Cervus elaphus scotticus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID-109627;
RN [1]
RP SEQUENCE FROM N.A.
RA Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
RA Suttie J.M.;
RT "NGF expression in Antler."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF145043; AAF17235.1;
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR PFAM: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT SEQUENCE 87 AA; 9876 MW; 17E06E49AF7A0A4 CRC64;

Query Match
Best Local Similarity 64.9%; Score 424; DB 6; Length 87;
Matches 77; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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FT NON\_TER 1 1  
 FT NON\_TER 241 241  
 SO SEQUENCE 241 AA; 27803 MW; AB95E457C7B07113 CRC64;

Query Match 51.4%; Score 335.5; DB 6; Length 241;  
 Best Local Similarity 58.0%; Pred. No. 3e-30; 21; Indels 1; Gaps 1;  
 Matches 58; Conservative 20; Mismatches 21

OY 9 HNGEVSVDVSVVWVDKTTATIDIKREVTYLAEVNINNSVPROYFEETKCRASNPVSG 68  
 Db 142 HNGEVSVDSESLWTKSSAIDIRGHQVTLGEIKGNSPKROYFEETKCRARPVKMG 201

OY 69 CRGIDSKHNSCYCTTHTFEVRLTID-EKQAAAFIRIDT 107  
 Db 202 CRGIDSKHNSCYCTTHTFEVRLTID-EKQAAAFIRIDT 241

## RESULT 15

ID 09CYL3 PRELIMINARY; PRT: 153 AA.  
 AC 09CYL3:  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE Brain derived neurotrophic factor.  
 GN BDNF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBryo;  
 RX MEDLINE=21085660; Pubmed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Araiwa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa N., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gasterland T., Gissi C., King B., Kochava H.,  
 Kuehl P., Lewis S., Matsuo Y., Nakai T., Pesole G., Quackenbush J.,  
 Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Ohtsuka T., Furuno M., Aono H., Baldarelli R., Barish G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 Wyshewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,  
 Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RT Nature 409:685-690(2001).  
 RL EMBL: AK017559; BAB30805.1; -  
 DR HSSP: P23560; 1884.  
 DR MGD: MGI:88145; Bdnf.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF. 1; 1.  
 DR PROSITE: PS50270; NGF. 2; 1.  
 SQ SEQUENCE 153 AA; 17519 MW; CA8E8B944CE5B37 CRC64;

Query Match 49.8%; Score 325.5; DB 11; Length 153;  
 Best Local Similarity 54.5%; Pred. No. 2.4e-29;  
 Matches 61; Conservative 16; Mismatches 33; Indels 3; Gaps 2;

OY 11 GEFVCSVSVWV--GKTTATIDIKREVTYLAEVNINNSVPROYFEETKCRASNPVSG 68  
 Db 42 GEFVCSVSVWV--GKTTATIDIKREVTYLAEVNINNSVPROYFEETKCRASNPVSG 101

OY 69 CRGIDSKHNSCYCTTHTFEVRLTID-EKQAAAFIRIDTACVLSRATR 119  
 Db 102 CRGIDSKHNSCYCTTHTFEVRLTID-EKQAAAFIRIDTACVLSRATR 153

Search completed: December 2, 2002, 15:12:01  
 Job time: 18.7245 secs



GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 8.16928 Seconds  
(without alignments)  
425.386 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653

Sequence: 1 PSSSTHVFHMGESFVSCDSVS.....FTRIDTACVLSRKATRRG 121

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/ptodata/1/laa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/laa/5B.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/laa/5A.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/laa/5B.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/laa/PTC10S.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	653	100.0	121	4	US-09-675-503-3
2	646	98.9	120	1	US-08-440-049-1
3	646	98.9	120	2	US-08-441-513A-1
4	646	98.9	120	3	US-08-970-865-3
5	646	98.9	120	4	US-09-363-573-3
6	646	98.9	120	5	PCT-US93-08918-1
7	618	94.6	120	1	US-07-879-630-1
8	618	94.6	120	5	PCT-US93-11292-1
9	594	91.0	121	4	US-09-675-503-2
10	587	89.9	120	3	US-08-970-865-2
11	587	89.9	120	4	US-09-363-573-2
12	584	89.4	120	1	US-08-440-049-3
13	584	89.4	120	2	US-08-441-513A-3
14	584	89.4	120	3	US-08-581-662-31
15	584	89.4	120	4	US-08-845-541B-1
16	584	89.4	120	4	US-09-066-065A-1
17	584	89.4	120	4	US-09-447-356-1
18	584	89.4	120	4	US-09-664-295-31
19	584	89.4	120	5	PCT-US95-06918-3
20	584	89.4	241	1	US-08-266-080B-4
21	584	89.4	241	1	US-08-451-947-5
22	584	89.4	241	1	US-08-424-826A-5
23	584	89.4	241	2	US-08-595-043A-75
24	584	89.4	241	3	US-08-970-865-1
25	584	89.4	241	3	US-08-928-694-5
26	584	89.4	241	4	US-09-363-573-1
27	584	89.4	241	4	US-09-447-356-3

28	584	89.4	241	5	PCT-US91-06950-5	Sequence 5, Appl 1
29	584	89.4	241	5	PCT-US95-05423-4	Sequence 4, Appl 1
30	584	89.4	242	4	US-09-675-503-1	Sequence 1, Appl 1
31	579	88.7	119	3	US-08-753-642-2	Sequence 2, Appl 1
32	579	88.7	153	4	US-09-675-922-2	Sequence 4, Appl 1
33	579	88.7	157	4	US-09-675-922-4	Sequence 4, Appl 1
34	579	88.7	163	4	US-09-675-922-6	Sequence 6, Appl 1
35	579	88.7	167	4	US-09-675-922-8	Sequence 8, Appl 1
36	570	87.3	120	4	US-08-845-541B-3	Sequence 3, Appl 1
37	570	87.3	120	4	US-09-066-065A-3	Sequence 3, Appl 1
38	567	86.8	120	4	US-08-845-541B-4	Sequence 4, Appl 1
39	567	86.8	120	4	US-09-066-065A-4	Sequence 4, Appl 1
40	562	86.1	120	4	US-08-845-541B-12	Sequence 12, Appl 1
41	562	86.1	120	4	US-09-066-065A-12	Sequence 12, Appl 1
42	561	85.9	120	4	US-08-845-541B-17	Sequence 17, Appl 1
43	561	85.9	120	4	US-08-845-541B-20	Sequence 20, Appl 1
44	561	85.9	120	4	US-09-066-065A-17	Sequence 17, Appl 1
45	561	85.9	120	4	US-09-066-065A-20	Sequence 20, Appl 1

## ALIGNMENTS

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RESULT 1
US-09-675-503-3
; Sequence 3, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmeltzer, Charles H.
; TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS
; TITLE OF INVENTION: USING HYDROPHOBIC INTERACTION CHROMATOGRAPHY
; FILE REFERENCE: GENE 037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-09-675-503-3
; Sequence 1, Application US/08440049
; Sequence 1, Application US/08440049
```

Patent No. 5728803  
GENERAL INFORMATION:  
APPLICANT: Ureter, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John M.  
TITLE OF INVENTION: PANTHROPIC NEUTROTROPIC FACTORS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipain (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,049  
FILING DATE: 12-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-440-049-1  
Query Match 98.9%; Score 646; DB 1; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.5e-72;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SSTRPVFMHGEFSCDSVSVWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFEETKRA 61  
DB 1 SSTRPVFMHGEFSCDSVSVWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFEETKRA 60  
QY 62 SNPEVSGCGIDSKHWNSTCTTHTFVAKLTDEKQAAAFRIRIDTACVCLSRKATRRG 121  
DB 61 SNPEVSGCGIDSKHWNSTCTTHTFVAKLTDEKQAAAFRIRIDTACVCLSRKATRRG 120  
RESULT 3  
US-08-441-513A-1  
Sequence 1, Application US/08441513A  
GENERAL INFORMATION:  
APPLICANT: Ureter, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John M.  
TITLE OF INVENTION: Panthropic Neutrotrophic Factors  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipain (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,513A  
FILING DATE: 15-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, P.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-441-513A-1  
Query Match 98.9%; Score 646; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.5e-72;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SSTRPVFMHGEFSCDSVSVWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFEETKRA 61  
DB 1 SSTRPVFMHGEFSCDSVSVWVGDKTTATDIDKGEVTVLAEVNINNSVFRQYFEETKRA 60  
QY 62 SNPEVSGCGIDSKHWNSTCTTHTFVAKLTDEKQAAAFRIRIDTACVCLSRKATRRG 121  
DB 61 SNPEVSGCGIDSKHWNSTCTTHTFVAKLTDEKQAAAFRIRIDTACVCLSRKATRRG 120  
RESULT 4  
US-08-970-865-3  
Sequence 3, Application US/08970865  
Patent No. 6005081  
GENERAL INFORMATION:  
APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck  
TITLE OF INVENTION: Purification of NGF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipain (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,865  
FILING DATE: 14-No. 6005081-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030838  
FILING DATE: 11/15/1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, P.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1063R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881  
: INFORMATION FOR SEQ ID NO: 3:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 120 amino acids  
: TYPE: Amino Acid  
: TOPOLOGY: Linear  
US-08-970-865-3

Query Match 98.9%; Score 646; DB 3; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.5e-72;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 61  
Db 1 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 60  
Qy 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRKATRG 121  
Db 61 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRKATRG 120

RESULT 5  
US-09-363-573-3  
: Sequence 3, Application US/09363573  
: Patent No. 6184360

GENERAL INFORMATION:  
: APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck  
: TITLE OF INVENTION: Purification of NGF  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 1 DNA Way  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080

COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: WinPatIn (Genentech)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/363,573  
: FILING DATE:

CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/970,865  
: FILING DATE: 14-No. 6184360-1997  
: APPLICATION NUMBER: 60/030838  
: FILING DATE: 11/15/1996  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 60/047855  
: FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:  
: NAME: Torchia, Ph.D., Timothy E.  
: REGISTRATION NUMBER: 36,700  
: REFERENCE/DOCKET NUMBER: P1063R2  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 650/225-8674  
: TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 120 amino acids  
: TYPE: Amino Acid  
: TOPOLOGY: Linear  
US-09-363-573-3

Query Match 98.9%; Score 646; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.5e-72;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 61  
Db 1 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 60

Db 1 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 60  
Qy 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRKATRG 121  
Db 61 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRKATRG 120

RESULT 6  
PCT-US95-06918-1  
: Sequence 1, Application PC/TUS9506918  
: Patent No. 5488099

GENERAL INFORMATION:  
: APPLICANT: Genentech, Inc.  
: TITLE OF INVENTION: PANTROPIC NEUROTROPHIC FACTORS  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 460 Point San Bruno Blvd  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080

COMPUTER READABLE FORM:  
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatIn (Genentech)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: PCT/US95/06918  
: FILING DATE:

CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Torchia, Timothy E.  
: REGISTRATION NUMBER: 36,700  
: REFERENCE/DOCKET NUMBER: 905PCT

TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 415/225-8674  
: TELEFAX: 415/952-9881  
: TELE: 910/371-7168  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 120 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
PCT-US95-06918-1

Query Match 98.9%; Score 646; DB 5; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.5e-72;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 61  
Db 1 SSTRPVFMHGEFVSVCDSVSVWVGDKTTATDICKGEVTVLAEVNINNSVPROYFEETKRA 60  
Qy 62 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRKATRG 121  
Db 61 SNPVESGCGIDSKHNSYCTTHTFVKALTTDEKQAAMRFIRIDPACVLSRKATRG 120

RESULT 7  
US-07-979-630-1  
: Sequence 1, Application US/07979630  
: Patent No. 5488099

GENERAL INFORMATION:  
: APPLICANT: Person, et al  
: TITLE OF INVENTION: Multifunctional Neurotrophic Factors  
: NUMBER OF SEQUENCES: 3  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
: STREET: 777 Old Saw Mill River Road  
: CITY: Tarrytown

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/979,630  
FILING DATE: 20-NOV-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,369  
FILING DATE: 06-MAR-1992  
NAME:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempier Ph.D., Gall M.  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 41  
TELEPHONE: 914-347-7000  
TELEFAX: 914-347-2113  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-07-979-630-1

Query Match 94.6%; Score 618; DB 1; Length 120;  
Best Local Similarity 94.2%; Pred. No. 4,4e-69;  
Matches 113; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVEHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFQYFEETKRA 61  
DB 1 SSTRPVEHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFQYFEETKRA 60  
OY 62 SNPEVSGCGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 121  
DB 61 PNPEVSGCGIDSKHNSCTTHTFVKALTTDDKQAMRFIRIDTACVLSRKATRRG 120

RESULT 8  
PCT-US93-11292-1  
Sequence 1, Application PC/TUS9311292  
GENERAL INFORMATION:  
APPLICANT: Persson, et al.  
TITLE OF INVENTION: Multifunctional Neurotrophic Factors  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11292  
FILING DATE: 19-NOV-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,369  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempier Ph.D., Gall M.

REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 41  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-347-7000  
TELEFAX: 914-347-2113  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US93-11292-1

Query Match 94.6%; Score 618; DB 5; Length 120;  
Best Local Similarity 94.2%; Pred. No. 4,4e-69;  
Matches 113; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSTRPVEHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFQYFEETKRA 61  
DB 1 SSTRPVEHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFQYFEETKRA 60  
OY 62 SNPEVSGCGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 121  
DB 61 PNPEVSGCGIDSKHNSCTTHTFVKALTTDDKQAMRFIRIDTACVLSRKATRRG 120

RESULT 9  
US-09-675-503-2  
Sequence 2, Application US/09675503  
Patent No. 6423831  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A  
TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS  
FILE REFERENCE: GEMT.037C2  
CURRENT APPLICATION NUMBER: US/09/675,503  
CURRENT FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTED for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-675-503-2

Query Match 91.0%; Score 594; DB 4; Length 121;  
Best Local Similarity 90.8%; Pred. No. 4,2e-66;  
Matches 109; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PSSTRPVEHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFQYFEETKRA 60  
DB 1 PSSSTRPVEHMGESVCDSSVWVGDKTTATDIDKGEVYLAEVNINNSVFQYFEETKRA 60  
OY 61 ASNPVSGCGIDSKHNSCTTHTFVKALTTDEKQAMRFIRIDTACVLSRKATRRG 120  
DB 61 DNPEVSGCGIDSKHNSCTTHTFVKALTTDDKQAMRFIRIDTACVLSRKATRRG 120

RESULT 10  
US-08-970-865-2  
Sequence 2, Application US/08970865



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TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-8674
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 120 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
US-08-440-049-3

Query Match      89.4%; Score 584; DB 1; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVEFMGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPIFHRGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKCRD 60

OY 62 SNPVESGCRGIDSKHNNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

RESULT 13
US-08-441-513A-3
: Sequence 3, Application US/08441513A
: Patent No. 5981480
: GENERAL INFORMATION:
: APPLICANT: Ufer, Roman
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: 'Panotropic Neurotrophic Factors
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/441,513A
: FILING DATE: 15-May-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/253937
: FILING DATE: 03-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Phd., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P0905C3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 120 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
US-08-441-513A-3

Query Match      89.4%; Score 584; DB 2; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVEFMGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPIFHRGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKCRD 60
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DB 1 SSSHPIFHRGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKCRD 60
OY 62 SNPVESGCRGIDSKHNNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

RESULT 14
US-08-581-662-31
: Sequence 31, Application US/08581662
: Patent No. 6121235
: GENERAL INFORMATION:
: APPLICANT: Gao, Wei-Oliang
: TITLE OF INVENTION: Treatment of Balance Impairments
: FILE REFERENCE: P0981
: CURRENT APPLICATION NUMBER: US/08/581,662
: CURRENT FILING DATE: 1995-12-29
: NUMBER OF SEQ ID NOS: 36
: SEQ ID NO 31
: LENGTH: 120
: TYPE: PRT
: ORGANISM: Homo sapiens
:
US-08-581-662-31

Query Match      89.4%; Score 584; DB 3; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVEFMGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPIFHRGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKCRD 60

OY 62 SNPVESGCRGIDSKHNNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

RESULT 15
US-08-845-541B-1
: Sequence 1, Application US/08845541B
: Patent No. 633310
: GENERAL INFORMATION:
: APPLICANT: Presta, Leonard
: APPLICANT: Ufer, Roman
: APPLICANT: Winslow, John
: TITLE OF INVENTION: NGF VARIANTS
: FILE REFERENCE: GENENT-039A
: CURRENT APPLICATION NUMBER: US/08/845,541B
: CURRENT FILING DATE: 1999-04-25
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 120
: TYPE: PRT
: ORGANISM: homo sapien
:
US-08-845-541B-1

Query Match      89.4%; Score 584; DB 4; Length 120;
Best Local Similarity 89.9%; Pred. No. 7.2e-65;
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 SSTRPVEFMGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKRA 61
DB 1 SSSHPIFHRGEFSVCDVSVMVGDKTTATDINKGEVTVLAEVNINNSVFRQYFETKCRD 60

OY 62 SNPVESGCRGIDSKHNNSYCTTHTFVKALTTDEKQAMRFIRIDTACVCLSKRAVR 120
DB 61 PNPVDSGCRGIDSKHNNSYCTTHTFVKALTTMDGKQAMRFIRIDTACVCLSKRAVR 119

Search completed: December 2, 2002, 15:09:43
Job time : 9.36928 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 4.25557 Seconds

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452.778 Million cell updates/sec

Title: US-10-072-681-3

Perfect score: 653  
Sequence: 1 PSSSTHPVFHNGEFSVCDVS.....FIRIDACVLSRKATRRG 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEM\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	121	12 US-10-072-681-3	Sequence 3, Appl1
2	584	91.0	121	12 US-10-072-681-2	Sequence 2, Appl1
3	584	89.4	241	8 US-08-450-842-5	Sequence 5, Appl1
4	584	89.4	241	10 US-09-822-263-16	Sequence 16, Appl1
5	584	89.4	242	12 US-10-072-681-1	Sequence 1, Appl1
6	579	88.7	153	10 US-09-798-338-2	Sequence 2, Appl1
7	579	88.7	153	10 US-09-798-338-4	Sequence 4, Appl1
8	579	88.7	153	10 US-09-798-338-6	Sequence 6, Appl1
9	579	88.7	153	10 US-09-798-338-8	Sequence 8, Appl1
10	573	88.7	167	10 US-09-798-338-8	Sequence 9, Appl1
11	435	66.6	142	8 US-08-450-842-52	Sequence 52, Appl1
12	378.5	58.0	120	10 US-09-745-032-1	Sequence 1, Appl1
13	378.5	58.0	120	10 US-09-742-600-1	Sequence 1, Appl1
14	378.5	58.0	120	10 US-09-872-090-1	Sequence 1, Appl1
15	378.5	58.0	257	8 US-08-450-842-4	Sequence 4, Appl1
16	377.5	57.8	119	10 US-09-745-032-6	Sequence 6, Appl1
17	377.5	57.8	119	10 US-09-742-600-6	Sequence 6, Appl1
18	377.5	57.8	119	10 US-09-872-090-6	Sequence 6, Appl1
19	377.5	57.8	120	10 US-09-745-032-3	Sequence 3, Appl1

20	377.5	57.8	120	10 US-09-742-600-3	Sequence 3, Appl1
21	377.5	57.8	120	10 US-09-872-090-3	Sequence 3, Appl1
22	375.5	57.5	117	10 US-09-745-032-7	Sequence 7, Appl1
23	375.5	57.5	117	10 US-09-742-600-7	Sequence 7, Appl1
24	375.5	57.5	117	10 US-09-872-090-7	Sequence 7, Appl1
25	375.5	57.5	118	10 US-09-745-032-5	Sequence 5, Appl1
26	375.5	57.5	118	10 US-09-742-600-5	Sequence 5, Appl1
27	375.5	57.5	118	10 US-09-872-090-5	Sequence 5, Appl1
28	370.5	56.7	120	9 US-09-813-398-11	Sequence 11, Appl1
29	368.5	56.4	120	12 US-10-072-681-5	Sequence 5, Appl1
30	345	52.8	72	10 US-08-450-842-21	Sequence 21, Appl1
31	326.5	50.0	130	8 US-08-450-842-47	Sequence 8, Appl1
32	325.5	49.8	120	10 US-09-745-032-8	Sequence 8, Appl1
33	325.5	49.8	120	10 US-09-745-032-10	Sequence 10, Appl1
34	325.5	49.8	120	10 US-09-742-600-8	Sequence 8, Appl1
35	325.5	49.8	120	10 US-09-742-600-10	Sequence 10, Appl1
36	325.5	49.8	247	8 US-08-450-842-3	Sequence 47, Appl1
37	324.5	49.7	120	10 US-09-745-032-9	Sequence 9, Appl1
38	324.5	49.7	120	10 US-09-742-600-9	Sequence 9, Appl1
39	319.5	48.9	120	9 US-09-813-398-10	Sequence 10, Appl1
40	314.5	48.2	130	8 US-08-450-842-23	Sequence 23, Appl1
41	312.5	47.9	130	8 US-08-450-842-22	Sequence 22, Appl1
42	312.5	47.9	131	9 US-09-813-398-12	Sequence 12, Appl1
43	312.5	47.9	158	8 US-08-450-842-6	Sequence 6, Appl1
44	312.5	47.9	210	8 US-08-450-842-2	Sequence 2, Appl1
45	311.5	47.7	130	8 US-08-450-842-60	Sequence 60, Appl1

## ALIGNMENTS

RESULT 1  
US-10-072-681-3

Sequence 3, Application US/10072681  
Patent No. US20020137893A1

GENERAL INFORMATION:

APPLICANT: Burton, Louis E.

APPLICANT: Beck, Joanne T.

TITLE OF INVENTION: PURIFICATION OF NGF

QY 1 PSSSTHPVFHNGEFSVCDVSVMWGDKTTATDIDKREVTVAEVMNINSVTFROFEETKCR 60  
DB 1 PSSSTHPVFHNGEFSVCDVSVMWGDKTTATDIDKREVTVAEVMNINSVTFROFEETKCR 60  
QY 61 ASNPVSGCGIDSKMNSICTTTFYKALTTDEKQAMFFIRIDACVLSRKATRR 120  
DB 61 ASNPVSGCGIDSKMNSICTTTFYKALTTDEKQAMFFIRIDACVLSRKATRR 120

OY 121 G 121  
Db 121 G 121

## RESULT 2

US-10-072-681-2  
Sequence 2, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmelzer, Charles H.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: PURIFICATION OF NCF  
FILE REFERENCE: GENE.037C3  
CURRENT APPLICATION NUMBER: US/10/072.681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675,503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-072-681-2

Query Match 91.0%; Score 594; DB 12; Length 121;  
Best Local Similarity 90.8%; Pred. No. 3e-61;  
Matches 109; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 PSSHTPVFMHGEFSCVDSVYWGDKTTATDTDKGKAVYLAENVRIINNSVFQYFETKCR 60  
Db 1 PSSHPFPHHGEFSCVDSVYWGDKTTATDTDKGKAVYLAENVRIINNSVFQYFETKCR 60  
OY 61 ASNVESGCGIDSKHNSYCTTHTTFVKALTTDEKQAAARFIRIDTACVCLSRKATRR 120  
Db 61 PNPVDSGCGIDSKHNSYCTTHTTFVKALTTDEKQAAARFIRIDTACVCLSRKAVRR 120

## RESULT 3

US-08-450-842-5  
Sequence 5, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25 Inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patlin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,770  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
US-08-450-842-5

Query Match 89.4%; Score 584; DB 8; Length 241;  
Best Local Similarity 89.9%; Pred. No. 9.4e-60;  
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 STHPVFMHGEFSCVDSVYWGDKTTATDTDKGKAVYLAENVRIINNSVFQYFETKCR 61  
Db 122 SSSHPFPHHGEFSCVDSVYWGDKTTATDTDKGKAVYLAENVRIINNSVFQYFETKCR 181  
OY 62 SNPVESGCGIDSKHNSYCTTHTTFVKALTTDEKQAAARFIRIDTACVCLSRKATRR 120  
Db 182 PNPVDSGCGIDSKHNSYCTTHTTFVKALTTDEKQAAARFIRIDTACVCLSRKAVRR 240

## RESULT 4

US-03-822-263-16  
Sequence 16, Application US/09822263  
Patent No. US20020036598A1  
GENERAL INFORMATION:  
APPLICANT: Prayaga, Sudhidas  
APPLICANT: Vernet, Corine  
APPLICANT: Shinkets, Richard A  
APPLICANT: Burgess, Catherine  
APPLICANT: Spytek, Kimberly  
APPLICANT: Tcherny, Velliar T  
TITLE OF INVENTION: NO. US20020036598A1el Polynucleotides and Polypeptides Encoded  
FILE REFERENCE: 15966-572 CIP1  
CURRENT APPLICATION NUMBER: US/09/822,263  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 09/672,665  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 60/156,745  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 60/158,942  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: 60/159,248  
PRIOR FILING DATE: 1999-10-13  
PRIOR APPLICATION NUMBER: 60/169,344  
PRIOR FILING DATE: 1999-12-06  
PRIOR APPLICATION NUMBER: 60/215,048  
PRIOR FILING DATE: 2000-06-29  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 16  
LENGTH: 241  
TYPE: PRT  
ORGANISM: Homo sapiens



US-09-822-263-16

Query Match 89.4%; Score 584; DB 10; Length 241;  
Best Local Similarity 89.9%; Pred. No. 9.4e-60;  
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRA 61  
DB 122 SSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRD 181  
QY 62 SNPVESGCRGIDSKHNSICTTHTFVKALTTDEKQAAFRIRIDTACVCLSRKATRR 120  
DB 182 PNPVDSGCRGIDSKHNSICTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 240

RESULT 5

US-10-072-681-1  
Sequence 1, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmeisler, Charles H.  
APPLICANT: Beck, Joanne T.  
FILE REFERENCE: GENEENT.037C3  
CURRENT FILING DATE: 2002-02-08  
PRIOR FILING DATE: 1996-11-15  
PRIOR FILING DATE: 1997-05-29  
PRIOR FILING DATE: 1997-05-29  
PRIOR FILING DATE: 1997-11-14  
PRIOR FILING DATE: 1999-07-29  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-072-681-1

Query Match 89.4%; Score 584; DB 12; Length 242;  
Best Local Similarity 89.9%; Pred. No. 9.4e-60;  
Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRA 61  
DB 123 SSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRD 182  
QY 62 SNPVESGCRGIDSKHNSICTTHTFVKALTTDEKQAAFRIRIDTACVCLSRKATRR 120  
DB 183 PNPVDSGCRGIDSKHNSICTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 241

RESULT 6

US-09-798-338-2  
Sequence 2, Application US/09798338  
Patent No. US20010020086A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schenase, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT FILING DATE: 2001-03-02  
PRIOR FILING DATE: 1998-08-27

NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 153  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Artificial  
US-09-798-338-2

Query Match 88.7%; Score 579; DB 10; Length 153;  
Best Local Similarity 89.8%; Pred. No. 2.1e-59;  
Matches 106; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRA 61  
DB 35 SSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRD 94  
QY 62 SNPVESGCRGIDSKHNSICTTHTFVKALTTDEKQAAFRIRIDTACVCLSRKATRR 119  
DB 95 PNPVDSGCRGIDSKHNSICTTHTFVKALTMGKQAAFRIRIRIDTACVCLSRKAVRR 152

RESULT 7

US-09-798-338-4  
Sequence 4, Application US/09798338  
Patent No. US20010020086A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schenase, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT FILING DATE: 2001-03-02  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 157  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Artificial  
US-09-798-338-4

Query Match 88.7%; Score 579; DB 10; Length 157;  
Best Local Similarity 89.8%; Pred. No. 2.1e-59;  
Matches 106; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPFFHMGESVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRA 61  
DB 39 SSSHPIFRHGEFSVCDSSVWVGDKTTATDIDKGEVTVLAEVNINNSVPROFEETKRD 98  
QY 62 SNPVESGCRGIDSKHNSICTTHTFVKALTTDEKQAAFRIRIDTACVCLSRKATRR 119  
DB 99 PNPVDSGCRGIDSKHNSICTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 156

RESULT 8

US-09-798-338-6  
Sequence 6, Application US/09798338  
Patent No. US20010020086A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schenase, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT FILING DATE: 2001-03-02  
PRIOR FILING DATE: 1998-08-27

FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798,338  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141,153  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6  
LENGTH: 163  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Artificial  
US-09-798-338-6

Query Match 88.7% Score 579; DB 10; Length 163;  
Best Local Similarity 89.8% Pred. No. 2,2e-59;  
Matches 106; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVFMGEFVSVCDSVSWVGDKTTATDINGKEVTLAEVNNINSVFRQYFETCR 61  
DB 45 SSSHPHFHREGFVSVCDSVSWVGDKTTATDINGKEVTLAEVNNINSVFRQYFETCR 104  
QY 62 SNPEVSGCGIDSKHNNSCYCTTHTFVKALTTDERQAAFRIRIDTACVCLSKRAVR 119  
DB 105 PNPVDSGCRGIDSKHNNSCYCTTHTFVKALTDGQAAFRIRIDTACVCLSKRAVR 162

RESULT 9  
US-09-798-338-8  
Sequence 8. Application US/09798338  
Patent No. US20010020086A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey A.  
APPLICANT: Schense, Jason C.  
APPLICANT: Sakiyama, Shelly E.  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE  
FILE REFERENCE: 87662-68879  
CURRENT APPLICATION NUMBER: US/09/798,338  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/141,153  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 8  
LENGTH: 167  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Artificial  
US-09-798-338-8

Query Match 88.7% Score 579; DB 10; Length 167;  
Best Local Similarity 89.8% Pred. No. 2,3e-59;  
Matches 106; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SSTRPVFMGEFVSVCDSVSWVGDKTTATDINGKEVTLAEVNNINSVFRQYFETCR 61  
DB 49 SSSHPHFHREGFVSVCDSVSWVGDKTTATDINGKEVTLAEVNNINSVFRQYFETCR 108  
QY 62 SNPEVSGCGIDSKHNNSCYCTTHTFVKALTTDERQAAFRIRIDTACVCLSKRAVR 119  
DB 109 PNPVDSGCRGIDSKHNNSCYCTTHTFVKALTDGQAAFRIRIDTACVCLSKRAVR 166

RESULT 10  
US-09-813-398-9  
Sequence 9. Application US/09813398  
Patent No. US20020169292A1  
GENERAL INFORMATION:

APPLICANT: Bruce D. Weintraub  
APPLICANT: Mariusz W. Szuljanski  
APPLICANT: University of Maryland  
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: UOFPD.003C1  
CURRENT APPLICATION NUMBER: US/09/813,398  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US98/19772  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 121  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-09-813-398-9

Query Match 87.7% Score 573; DB 9; Length 121;  
Best Local Similarity 87.3% Pred. No. 7,6e-59;  
Matches 105; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 PSSTPVFMGEFVSVCDSVSWVGDKTTATDINGKEVTLAEVNNINSVFRQYFETCR 60  
DB 1 PSSHPHFHREGFVSVCDSVSWVGDKTTATDINGKEVTLAEVNNINSVFRQYFETCR 60  
QY 61 ASNPVSGCGIDSKHNNSCYCTTHTFVKALTTDERQAAFRIRIDTACVCLSKRAVR 120  
DB 61 DNPVDSGCRGIDSKHNNSCYCTTHTFVKALTDGQAAFRIRIDTACVCLSKRAVR 120

RESULT 11  
US-08-450-842-52  
Sequence 52. Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patcin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA: 07/648482  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 66622C1D3

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/953-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 142 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

Query Match	66.68;	Score 435;	DB 8;	Length 142;
Best Local Similarity	61.78;	Pred. NO. 6.2e-43;		
Matches 87;	Conservative 12;	Mismatches 20;	Indels 22;	Gaps 41;

```

0y      2 SSTRHVFHMGEFEFVCSOSVYMWGDKTTATDICKGEVTVLAEVINNSY----- 49
        ||::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 SSHPHFHGRGEFSVCDSVSVMWGDKTTATDICKGEYMWLGEVINNSVTLGEYPAGGSP 60

```

0y 50 FROFFETCKRASNPVE-----SGRGIDSKHNSYCTTHTEFKALTTD-EKQAAVR 101  
 |||||:| | |||:| | | :|:| | | : |  
 Db 61 LRQFFETCKADNMEEGCPAGGGGCRGVDRRHVSECKAKQSVYRALTADAGRGVGR 120

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Oy      102 FIRIDTA--CVCVLSRKATR 120
          :|||||  ||| |||||  ||
Db      121 WIRIDTACVCVCVLSRKAVR 141

```

RESULT 12  
US-09-745-032-1  
; Sequence 1, Application US/09745032  
; Patent No. US20010027170A1

```

1  APPLICANT: Boone, Thomas C.
2  APPLICANT: Cheung, Ellen M.
3  APPLICANT: Hersthenson, Susan I.
4  APPLICANT: Young, John D.
5  TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
6  FILE REFERENCE: A-411a US Revised073100
7  CURRENT APPLICATION NUMBER: 05/09/745,032
8  PRIOR FILING DATE: 2000-12-19
9  PRIOR APPLICATION NUMBER: 09/214,214
10 PRIOR FILING DATE: 1998-12-23
11 PRIOR APPLICATION NUMBER: US 08/684,353
12 PRIOR FILING DATE: 1996-07-19
13 NUMBER OF SEQ ID NOS: 14
14 SOFTWARE: PatentIn Ver. 2.1
15 SEQ ID NO 1
16 LENGTH: 120
17 TYPE: PRT
18 ORGANISM: Human
19 OS-09-745-032-1

```

Query Match	58.0%;	Score 378.5;	DB 10;	Length 120;
Best Local Similarity	58.9%;	Pred. No. 1.5e-36;		
Matches 66; Conservative	21;	Mismatches 24;	Indels .1;	Gaps 1

[illegible]

0y 69 CRGIDSKHMSYCTTHTFYALTTD-EKQAAWRFIRIDTACVLSRKATR 119  
 ||||| ||||| | : : : ||||| : | ||: ||||| : |||||  
 Db 68 CRGIDSKHMSOCTTSOTYVRYALTSENKLVGWRMRIRIDTSCVALSRKIGR 119

RESULT 13  
US-09-742

```

; Sequence 1, Application US/09742600
; Patent No. US20020010135A1
;
GENERAL INFORMATION:

```

```

; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.

```

```

1  APPLICANT:  Hershenson, Susan I.
2  APPLICANT:  Young, John D.
3  TITLE OF INVENTION:  ANALOGS OF CATIONIC PROTEININS
4  FILE REFERENCE:  A-411a US Revised073100
5  CURRENT APPLICATION NUMBER:  US/09/742,600
6  CURRENT FILING DATE:  2000-12-19
7  PRIOR APPLICATION NUMBER:  09/214,214
8  PRIOR FILING DATE:  1998-12-23
9  PRIOR APPLICATION NUMBER:  US 08/684,353
10 PRIOR FILING DATE:  1996-07-19
11 NUMBER OF SEQ ID NOS:  12
12 SOFTWARE:  PatentIn Ver. 2.1
13 SEQ ID NO 1
14 LENGTH:  130
15 TYPE:  PRT
16 ORGANISM:  Human
17 US-09-742-600-1

```

Query Match	58.08;	Score 378.5;	DB 10;	Length 120;
Best Local Similarity	58.90;	Pred. No. 1.5e-36;		
Matches 66;	Conservative 21;	Mismatches 24;	Indels 1;	Gaps 1

D6  
8 HRGELSYCDSESLWTDKSSAIDIRGHQVYVLGEIKTGNSPVQRYFYETRECKEARPVKNG 67

```

09 69 CRGIDSKHWNSTCTTHTFVKALTTD-EKQAMAFIRIDTACVCLSRKATR 119
      ||||| ||||| : : : ||| : : ||| ||||| ||| ||| |
Db 68 CRGIDDKHWNSTCTTHTFVKALTTD-EKQAMAFIRIDTACVCLSRKATR 119

```

## RESULT 14

Sequence 1, Application No. US09872090  
Patent No. US20020052488A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen Mei Yin  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: Analogs of NT-3 (As Amended)  
FILE REFERENCE: A-411B  
CURRENT APPLICATION NUMBER: US/09/872,090  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 02/255,953  
PRIOR FILING DATE: 1999-02-23  
PRIOR APPLICATION NUMBER: 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ. ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ. ID NO. 1  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
IS-09-872-090-1

Query Match	58.00;	Score 378.5;	DB 10;	Length 120;
Best local Similarity	58.98;	Pred. No.1.5e-36;		
Matches 66;	Conservative 21;	Mismatches 24;	Indels 1;	Gaps 1

OY HMGEEFSCDSVWVGDKTTATDIDKRETVLAEVINNSVFROYEFETCKRASNPEVSG 68  
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :  
Db HRGEYSVCDESMTWDKSSAIDIRGHQVTVLGELTKTGNSPVKRYEFTETCKEARPVKNG 67

QY 69 CRGIDSKHNSYCCTTHTEFVALTID-EKQAAHREIRIDTACVLSRKATR 119  
 ||||| ||||| | : : : ||||| : | ||:||||| :||| ||| |  
 Db 68 CRGIDOKHNSQCKTSQTYYRALTSENKLVGHRMIRIDTSCVALSRKIGR 119

RESULT 15

US-06-430-842-4  
: Sequence 4, Application US/08450842  
: Patent No. US20020045576A1

Mon Dec 2 15:36:37 2002

us-10-072-681-3.rapb

Page 6

GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/852-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-4

Query Match 58.0%; Score 378.5; DB 8; Length 257;  
Best Local Similarity 58.9%; Pred. No. 3.8e-36;  
Matches 66; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

OY 9 HMGFSVCDVSVMVCDTATDINKREVTLAEVINNSVPROFFETKCRASNPVPSG 68  
DB 145 HRGEYSVCDSSSLMTWDKSSALDIRHQVTYLGKRTGNSPVKQYFETRKCKEARPYKNG 204  
OY 69 CRGIDSKHMSYCTTTFYKALTD-EKQAAHFRIRIDTACVCYLSKRAIR 119  
DB 205 CRGIDSKHMSYCTTTFYKALTD-EKQAAHFRIRIDTACVCYLSKRAIR 256

Search completed: December 2, 2002, 15:14:34  
Job time : 4.25557 secs



XX Beck JT, Burton LE, Schmelzer CH;  
PI WPI: 1998-322333/28.  
DR  
XX  
XX Isolation of neurotrophin(s) from, e.g. mla-folded or glycosylated  
PT variant(s) - using hydrophobic interaction chromatography,  
PT optionally in combination with high performance cation exchange  
chromatography  
PS  
XX Disclosure: page 37: 59pp: English.  
CC This polypeptide comprises brain-derived neurotrophic factor  
CC (BDNF). Methods are provided for large-scale purification of  
CC neurotrophins, including mature BDNF, suitable for clinical use. A  
CC claimed method comprises: (1) separating the neurotrophin from the  
CC other proteins using a hydrophobic interaction chromatography resin  
CC (HICR); and optionally (2) separating the neurotrophin from a  
CC chemical variant by high performance cation exchange chromatography  
CC (HPEC). The processes can also be used for purification of e.g.  
CC human nerve growth factor (NGF) (see AAM48886), mouse NGF (see  
CC AAM48887), neurotrophin-4/5 (see AAM48890) and neurotrophin-3 (see  
CC AAM48889). The processes allow separation of neurotrophins from  
CC various undesirable misprocessed, misfolded, size, glycosylated or  
CC charge forms. They allow selective separation from variants and  
CC other molecules, and from other polypeptides with high pi. The  
CC processes are applicable to starting materials from various  
CC sources, including fermentation broths or lysed bacterial or  
CC mammalian cells.  
SQ Sequence 118 AA:  
Query Match 98.9%; Score 633; DB 19; Length 118;  
Best Local Similarity 100.0%; Pred. No. 5.4e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 HSDPARGELSYVDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 61  
DB 1 HSDPARGELSYVDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 60  
QY 62 MGYTKKRCRGIDKRHNNSOCRTQSYVRLTMDSKKRIGMRIRIDTSCVLTIRGR 119  
DB 61 MGYTKKRCRGIDKRHNNSOCRTQSYVRLTMDSKKRIGMRIRIDTSCVLTIRGR 118  
RESULT 2  
AAB29114  
ID AAB29114 standard; Protein: 118 AA.  
XX  
XX AAB29114:  
AC  
XX  
XX 02-FEB-2001 (first entry)  
DT  
XX  
XX Brain derived neurotrophic factor.  
DE  
XX  
XX Neurotrophin: trkB; trkC; ototoxicity-related balance impairment;  
XX Meniere's syndrome; myringitis; otitis media;  
XX acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;  
XX middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US6121235-A.  
PN  
XX  
XX 19-SEP-2000.  
PD  
XX  
XX 29-DEC-1995; 95US-0581662.  
PF  
XX  
XX 29-DEC-1995; 95US-0581662.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Gao W;  
PI

XX  
DR WPI: 2000-618200/59.  
XX  
XX Treating ototoxin-induced neuronal-related balance impairment and  
PT promoting vestibular ganglion neuron survival prior to, upon or after  
PT exposure to an ototoxin, comprises administering a trkB or trkC agonist  
PT  
PS Disclosure: Column 49-50; 40pp: English.  
XX  
XX The present invention relates to treating ototoxin-induced  
CC neuronal-related balance impairment in a mammal by administering a  
CC trkB or trkC agonist, particularly neurotrophin-4/5 (NT-4/5).  
CC ototoxicity-related balance impairments include Meniere's syndrome,  
CC myringitis, otitis media, acute vestibular neuronitis, herpes zoster  
CC oticus, labyrinthitis, middle or labyrinthine tumours, petrositis and  
CC otosclerosis. NT-4/5 may also be used to treat diseases  
CC induced by gram positive, gram negative and acid-fast bacteria. The  
CC present sequence is a protein used in the invention.  
SQ Sequence 118 AA:  
Query Match 98.9%; Score 633; DB 21; Length 118;  
Best Local Similarity 100.0%; Pred. No. 5.4e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 HSDPARGELSYVDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 61  
DB 1 HSDPARGELSYVDSISEVNTAADKKTAVDMSGCTVTVLEKVPVSKGLKQYFETKCNP 60  
QY 62 MGYTKKRCRGIDKRHNNSOCRTQSYVRLTMDSKKRIGMRIRIDTSCVLTIRGR 119  
DB 61 MGYTKKRCRGIDKRHNNSOCRTQSYVRLTMDSKKRIGMRIRIDTSCVLTIRGR 118  
RESULT 3  
AAR29494  
ID AAR29494 standard; Protein: 119 AA.  
XX  
XX AAR29494:  
AC  
XX  
XX 22-APR-1993 (first entry)  
DT  
XX  
XX BDNF, mouse.  
DE  
XX  
XX Neurotrophin; NT: nerve growth factor; NGF;  
XX Brain-derived neurotrophic factor; BDNF.  
XX  
XX Mus musculus.  
OS  
XX  
XX WO9220365-A.  
PN  
XX  
XX 26-NOV-1992.  
PD  
XX  
XX 20-MAY-1992; 92MO-US04266.  
PF  
XX  
XX 21-MAY-1991; 91US-0703450.  
PR  
XX 12-JUL-1991; 91US-0729253.  
PR 23-JUL-1991; 91US-0734422.  
PR 28-AUG-1991; 91US-0751356.  
PR 20-SEP-1991; 91US-0762674.  
PR 14-NOV-1991; 91US-0791924.  
XX  
XX (REGG-) REGENERON PHARM INC.  
PA  
XX  
XX Halibook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD;  
PI WPI: 1992-415468/50.  
DR  
XX  
XX Use of neurotrophin-4 for promoting growth and survival of nerve  
PT cells - useful in treating neurological, fertility and  
PT immunological disorders and in diagnosis  
XX

PS Disclosure: Page 106 + Fig 4B: 180pp: English.  
XX A comparison of the mature NT-4 protein (Xenopus) to the mature  
CC NRP, BDNF, and NT-3 proteins from mouse revealed 51%, 60% and 58%  
CC amino acid identity respectively. See sequences AAR29491 and  
CC AAR29493-95.  
XX

SQ Sequence 119 AA:

Query Match 97.3%: Score 622.5; DB 13; Length 119;  
Best Local Similarity 99.2%: Pred. No. 7,8e-61;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVDSISEWYTAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61  
DB 1 HSDPARRGELSYVDSISEWYTAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 60  
OY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRLATMDSKRRIGMRIRIDTSCV-TLTIKRGR 119  
DB 61 MGYTKEGCGIDKRRHNSOCRTTOSYVRLATMDSKRRIGMRIRIDTSCV-TLTIKRGR 119

RESULT 4

AAR76814  
ID AAR76814 standard; Protein: 119 AA.

AC AAR76814;

DT 07-DEC-1995 (first entry)

DE Porcine BDNF mature protein.

KM Brain derived neurotrophic factor; BDNF; neuron; Alzheimer's disease;  
KM trauma; Parkinson's disease.

OS Sus scrofa.

PN US5438121-A.

PD 01-AUG-1995.

PF 30-AUG-1989; 89US-0400591.

PR 25-APR-1991; 91US-0691612.

PR 30-AUG-1989; 89US-0400591.

PR 20-AUG-1990; 90US-0570657.

PA (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.  
(REGE-) REGENERON PHARM INC.

XX Barde Y, Edgar D, Leibel J, Lottspeltch F, Thoenen H;  
PI Yancopoulos G;  
PI WPI: 1995-274920/36.

DR WPI: 1995-274920/36.

XX New brain derived neurotrophic factor proteins sustain survival of CNS  
PT dopaminergic and cholinergic neurons - used in the diagnosis and  
PT treatment of neurological disorders, eg. trauma, Alzheimer's disease,  
etc.

XX Claim 2: Column 89; 100pp: English.

XX Mature BDNF proteins isolated from pig brain are given in AAR76813-15.  
CC They are used to isolate nucleic acids encoding BDNF and to develop  
CC antibodies and other prods. useful in the diagnosis and treatment of  
CC neurological disorders.

SQ Sequence 119 AA:

Query Match 97.3%: Score 622.5; DB 16; Length 119;  
Best Local Similarity 99.2%: Pred. No. 7,8e-61;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVDSISEWYTAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61  
DB 1 HSDPARRGELSYVDSISEWYTAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 60  
OY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRLATMDSKRRIGMRIRIDTSCV-TLTIKRGR 119  
DB 61 MGYTKEGCGIDKRRHNSOCRTTOSYVRLATMDSKRRIGMRIRIDTSCV-TLTIKRGR 119

RESULT 5  
AAB35945

ID AAB35945 standard; Protein: 119 AA.

AC AAB35945;

DT 26-FEB-2001 (first entry)

DE BDNF amino acid sequence.

KM Heparin binding; vascular graft; matrix; cell adhesion; growth factor;  
KM wound healing; dermal wound; wound healing; BDNF.

OS Unidentified.

PN WO20064481-A1.

PD 02-NOV-2000.

PF 22-APR-1999; 99WO-1B00800.

PR 22-APR-1999; 99WO-1B00800.

PA (ETH2-) ETH ZURICH & UNIV ZURICH.

XX Sakiyama SE, Hubbard JA;

PI WPI: 2001-024627/03.

XX Matrix for controlled release of growth factor for wound healing, has  
PT substrate that attaches heparin binding peptide, protein growth factor  
PT that bind heparin with low affinity, and heparin or heparin-like  
PT polymer

PS Example 5; Page 21; 48pp: English.

XX This invention relates to a matrix comprising a substrate capable of  
CC providing attachment of a heparin binding peptide (HBP), a peptide  
CC comprising a binding domain which binds heparin with high affinity,  
CC heparin or heparin-like polymer, and a protein growth factor or peptide  
CC fragment which has a domain that binds heparin with low affinity.  
CC which is capable of supporting cell adhesion. The matrix is used for  
CC delivering low heparin binding affinity growth factor proteins or  
CC peptides in a controlled manner suitable for wound healing. The matrix  
CC can be used in an article for treating dermal wounds, and in an  
CC implantable sterilized composition capable of supporting cell adhesion.  
CC The present sequence represents a growth factor protein. The protein is  
CC used in an example illustrating that non-heparin binding growth factors  
CC can be released in a controlled manner from heparin-based drug delivery  
CC systems based on their low affinity for heparin.

SQ Sequence 119 AA:

Query Match 97.3%: Score 622.5; DB 22; Length 119;  
Best Local Similarity 99.2%: Pred. No. 7,8e-61;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVDSISEWYTAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 61  
DB 1 HSDPARRGELSYVDSISEWYTAADKTAVDMSGCTVLEKVPVSKGOLKQYFETKCNP 60  
OY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRLATMDSKRRIGMRIRIDTSCV-TLTIKRGR 119  
DB 61 MGYTKEGCGIDKRRHNSOCRTTOSYVRLATMDSKRRIGMRIRIDTSCV-TLTIKRGR 119





PF 29-AUG-1990; 90MO-US04915.  
 XX 20-AUG-1990; 90US-0570657.  
 PR 30-AUG-1989; 89US-0400591.  
 XX (PLAC) MAX PLANCK GES WISSENSCH.  
 PA (REGE-) REGENERON PHARM INC.  
 XX Hyman C, Alderson R, Yancopoulos G, Barde YA, Thoenen HE;  
 PI Horn A, Lottspeich F, Lindsay RM;  
 DR WPI: 1991-102083/14.  
 N-PSDB: AAQ11204.  
 XX Brain derived neurotrophic factor and DNA encoding it - for  
 PT diagnosis and treatment of neurological disorders, eg  
 PT Parkinson's disease and retinal degeneration  
 XX Claim 25: Page 154; 229pp; English.  
 XX A portion of the coding sequence for mature human BDNF was  
 CC amplified by PCR and the sequence determined. The deduced amino  
 CC acid sequence for the region of at least amino acids 28 to 111 was  
 CC identical to that of porcine BDNF. The BDNF can be used to sustain  
 CC the survival of dopaminergic and cholinergic neurons of the CNS, to  
 CC suppress the proliferation of astroglial cells, to inhibit the uptake  
 CC of GABA into neurons and to upregulate the expression of NGF receptor  
 CC on the cell surface.  
 CC See also AAQ11203, AAQ11205-6 and AAQ11604.  
 XX Sequence 247 AA:  
 SQ  
 Query Match 97.3%; Score 622.5; DB 12; Length 247;  
 Best Local Similarity 99.2%; Pred. No. 1.9e-60;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 OY 2 HSDPARRGELSYCDISSEVMTADKKTAVDMSGGTVLEKVPVSKGOLKQYFETKCNP 61  
 DB 129 HSDPARRGELSYCDISSEVMTADKKTAVDMSGGTVLEKVPVSKGOLKQYFETKCNP 188  
 OY 62 MGYTEGCGIDKRRHNSCQRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 119  
 DB 189 MGYTEGCGIDKRRHNSCQRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 247  
 RESULT 9  
 AAR37798  
 ID AAR37798 standard; Protein: 247 AA.  
 XX AAR37798;  
 AC  
 DT 29-SEP-1993 (first entry)  
 DE Human BDNF.  
 XX Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;  
 KM BDNF; chimeric; fusion; mouse; nerve growth factor.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 1..128  
 FT /note- "Prepro region"  
 FT Protein 129..247  
 FT /note- "Mature BDNF"  
 XX MO9310150-A.  
 XX 27-MAY-1993.  
 XX 13-NOV-1992; 92MO-US09792.  
 XX 14-NOV-1991; 91US-0792492.

XX (AMGE-) AMGEN.  
 PA (REGE-) REGENERON PHARM INC.  
 XX Giles D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;  
 DR WPI: 1993-182492/22.  
 N-PSDB: AAQ42570.  
 XX Eukaryotic expression of neurotrophins - using prepro region of a  
 PT different neurotrophin for more efficient post-translational  
 PT processing  
 XX Disclosure; Fig 3; 80pp; English.  
 XX This sequence represents human brain-derived neurotrophic factor  
 CC (BDNF). The protein encoded by this sequence promotes the survival  
 CC of dorsal root ganglions. BDNF is a highly basic protein (isoelectric  
 CC point, pI 10.1) which has a molecular weight of 12.3 kD. These  
 CC characteristics are very similar to the nerve growth factor (NGF).  
 CC The cDNA encoding this protein may be used in the construction of a  
 CC chimeric nucleic acid molecule to encode a preproNGF/BDNF chimera  
 CC (see also AAQ42568-69).  
 XX Sequence 247 AA:  
 SQ  
 Query Match 97.3%; Score 622.5; DB 14; Length 247;  
 Best Local Similarity 99.2%; Pred. No. 1.9e-60;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 OY 2 HSDPARRGELSYCDISSEVMTADKKTAVDMSGGTVLEKVPVSKGOLKQYFETKCNP 61  
 DB 129 HSDPARRGELSYCDISSEVMTADKKTAVDMSGGTVLEKVPVSKGOLKQYFETKCNP 188  
 OY 62 MGYTEGCGIDKRRHNSCQRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 119  
 DB 189 MGYTEGCGIDKRRHNSCQRTQSYVRALTMDSKKRIGMFRIDTSCV-TLTIRGR 247  
 RESULT 10  
 AAR44917  
 ID AAR44917 standard; Protein: 247 AA.  
 XX AAR44917;  
 AC  
 DT 18-OCT-1994 (first entry)  
 DE Human BDNF.  
 XX BDNF; brain derived nerve factor; promotor; expression; vector.  
 KM  
 XX Homo sapiens.  
 OS  
 PN JP05317049-A.  
 XX 03-DEC-1993.  
 PD  
 PF 01-JUN-1992; 92JP-0140570.  
 XX 31-MAY-1991; 91JP-0129666.  
 PR (TAKE) TAKEDA CHEM IND LTD.  
 PA WPI: 1994-011018/02.  
 DR N-PSDB: AA054374.  
 XX Expression promoter contg. 142 specified bases - is used in  
 PT prepn. of diseased model animal and drug screening system  
 XX Claim 1; Fig 1; 15pp; Japanese.  
 CC The sequence (AA054374) encodes a human brain derived nerve nutrient  
 CC factor. This is also transformed into a bacterium using the vector

CC shown in sequence (AA054375). The factor can be used for the  
 CC preparation of animal models of diseases and their treatment as  
 CC well as establishing a drug screening system.

XX Sequence 247 AA:

Query Match 97.3% Score 622.5; DB 15; Length 247;  
 Best Local Similarity 99.2% Pred. No. 1.9e-60;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRELISVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQYETKCNP 61  
 DB 129 HSDPARRELISVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQYETKCNP 188  
 OY 62 MGYTEGCGIGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119  
 DB 189 MGYTEGCGIGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 247

RESULT 11

AA076817  
 ID AA076817 standard; Protein: 247 AA.

XX AA076817;  
 AC 07-DEC-1995 (first entry)  
 XX  
 DE Human prepro-BDNF.  
 XX  
 KW Brain derived neurotrophic factor: BDNF; neuron; Alzheimer's disease;  
 KW trauma; Parkinson's disease.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Active-site 1..128  
 FT /label= prepro-peptide

XX US0438121-A.

XX 01-AUG-1995.

XX 30-AUG-1989; 89US-0400591.

XX 25-APR-1991; 91US-0691612.

XX 30-AUG-1989; 89US-0400591.

XX 20-AUG-1990; 90US-0570657.

XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX (REGC-) REGENERON PHARM INC.

XX Barde Y, Edgar D, Leibrock J, Lottspeltch F, Thoenen H;  
 PI Yancopoulos G;

XX WPI: 1995-274920/36.

XX N-PSDB: AA093135.

XX New brain derived neurotrophic factor proteins sustain survival of CNS  
 PT dopaminergic and cholinergic neurons - used in the diagnosis and  
 PT treatment of neurological disorders, eg. trauma, Alzheimer's disease,  
 PT etc.

XX Disclosure: Fig. 4B-H; 100pp; English.

XX An adult human retina cDNA library was screened using a probe  
 CC based on pig BDNF to obtain a clone, pBDNF-C-1, that encoded  
 CC prepro-BDNF.

XX Sequence 247 AA:

Query Match 97.3% Score 622.5; DB 16; Length 247;  
 Best Local Similarity 99.2% Pred. No. 1.9e-60;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRELISVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQYETKCNP 61

DB 129 HSDPARRELISVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQYETKCNP 188

OY 62 MGYTEGCGIGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119

DB 189 MGYTEGCGIGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 247

RESULT 12

AA076238  
 ID AA076238 standard; Protein: 247 AA.

XX AA076238;  
 AC 16-MAR-1998 (first entry)  
 XX  
 DE Human preproBDNF.  
 XX  
 KW Fusion protein: hydrophilic spacer; recombinant; expression system;  
 KW carboxypeptidase; preproNGF.  
 XX  
 OS Homo sapiens.

XX W09728272-A1.

XX 07-AUG-1997.

XX 31-JAN-1997; 97WO-US01470.

XX 31-JAN-1996; 96US-0595043.

XX (TECH-) TECHNOLOGENE INC.

XX Sgarlato GD;

XX WPI: 1997-402624/37.

XX N-PSDB: AAT80163.

XX Recombinant protein expression system for fusion protein production  
 PT - useful for high quantity production of authentic recombinant  
 PT proteins

XX Example 6; Page 142-143; 194pp; English.

XX A novel recombinant vector has been developed which comprises a  
 CC nucleotide sequence encoding a fusion protein. The fusion protein  
 CC comprises three domains joined together in order, from N-terminus to  
 CC C-terminus, of a first domain comprising a protein of interest, a second  
 CC domain comprising a hydrophilic spacer and an affinity domain, each  
 CC domain comprising amino acid residues. The present sequence represents  
 CC human preproBDNF, used in example 6 of the present invention. The  
 CC recombinant vector is used for the production of authentic recombinant  
 CC proteins of interest. The method of the invention is useful for the  
 CC expression of fusion proteins capable of isolation by affinity  
 CC chromatography in pro- or eukaryotic cells. This method allows  
 CC for the efficient cleavage and generation of authentic proteins of  
 CC interest that do not contain extraneous (i.e. non-naturally occurring)  
 CC amino acids.

XX Sequence 247 AA:

Query Match 97.3% Score 622.5; DB 18; Length 247;  
 Best Local Similarity 99.2% Pred. No. 1.9e-60;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRELISVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQYETKCNP 61

DB 129 HSDPARRELISVCSISISMTAAADKTAVDMSGGTIVLEKVPVSKGOLKQYETKCNP 188

OY 62 MGYTEGCGIGIDKRRHNSOCRTTOSYVRLTMDSKKRIGRFRIDTSCV-TLTIRGR 119

Db 189 MGTYREGCGIDKRRHNSCRRTOSTYVRALTMDSKKRIGMRFRIDTSCVCTLTIRKGR 247

RESULT 13  
AAM50846  
ID AAM50846 standard; Protein: 247 AA.  
XX  
XX AAM50846:  
XX  
XX 01-MAY-2002 (first entry)  
XX  
XX Human recombinant brain-derived growth factor.  
XX  
XX Brain-derived growth factor: BDNF; human; neurotrophic factor; NTF;  
XX Huntington's disease; Parkinson's disease; Alzheimer's disease;  
XX amyotrophic lateral sclerosis; neurodegenerative disease; cancer;  
XX neuroprotective; nootropic; anticonvulsant; antiparkinsonian;  
XX cytostatic; therapy.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..18  
XX /label= Signal\_peptide  
XX Peptide 19..128  
XX /label= Propeptide  
XX Protein 129..247  
XX /label= Mature\_protein  
XX Disulfide-bond 141..208  
XX Disulfide-bond 186..237  
XX Disulfide-bond 196..237  
XX Disulfide-bond 196..239  
XX Misc-difference 66  
XX /note= "may be replaced by Met"  
XX  
XX W020203071-A2.  
XX  
XX 10-JAN-2002.  
XX  
XX 05-JUL-2001: 2001MO-US21472.  
XX  
XX 05-JUL-2000: 2000US-215778P.  
XX  
XX (PANG-) PANGENE CORP.  
XX  
XX Bates AT:  
XX  
XX WPI: 2002-179638/23.  
XX  
XX Screening for a neurotrophic factor mimetic, useful for treating, e.g.,  
XX cancer and Alzheimer's, comprises combining a candidate mimetic with a  
XX fragment of a tyrosine kinase protein -  
XX  
XX Disclosure: Fig 6: 107pp; English.  
XX  
XX The present sequence is that of human recombinant brain-derived  
XX growth factor (BDNF), a neurotrophic factor (NTF) that binds to TrkB  
XX receptor tyrosine kinase. The invention concerns Trks and their  
XX ligands that modulate cell growth, differentiation and survival.  
XX Trk proteins are known to mediate the activities of neurotrophins  
XX and are also known proto-oncogenes. Methods are claimed for screening  
XX for small molecule NTF mimetics, such as the cyclic peptide given  
XX in AAM50844, capable of binding to a Trk protein or of modulating  
XX the binding of a neurotrophin to a Trk protein. Also claimed are  
XX medicaments comprising a small molecule NTF mimetic and their use  
XX in claimed methods for treatment of cancer or a neurodegenerative  
XX disease selected from Huntington's disease, Parkinson's disease,  
XX Alzheimer's disease and amyotrophic lateral sclerosis.  
XX  
XX Sequence 247 AA:  
XX  
XX Query Match 97.3%; Score 622.5; DB 23; Length 247;  
XX Best Local Similarity 99.2%; Pred. No. 1.9e-60;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYVDSISPMYTAADKTAADMSSGTYVLEKRVSGOLKQFYETKCP 61  
DB 129 HSDPARRGELSYVDSISPMYTAADKTAADMSSGTYVLEKRVSGOLKQFYETKCP 188  
OY 62 MGTYREGCGIDKRRHNSCRRTOSTYVRALTMDSKKRIGMRFRIDTSCV-TLTIRKGR 119  
DB 189 MGTYREGCGIDKRRHNSCRRTOSTYVRALTMDSKKRIGMRFRIDTSCVCTLTIRKGR 247

RESULT 14  
AAR11365  
ID AAR11365 standard; Protein: 249 AA.  
XX  
XX AAR11365:  
XX  
XX 31-MAY-1991 (first entry)  
XX  
XX Rat prepro-Brain Derived Neurotrophic Factor.  
XX  
XX BDNF; Parkinson's disease; Huntington's chorea; Alzheimer's Disease;  
XX neuroblastoma; Parkinson plus Syndrome.  
XX  
XX Rattus rattus.  
XX  
XX Key Location/Qualifiers  
XX Protein 131..249  
XX /label= mature rat BDNF  
XX Peptide 1..130  
XX /label= pre-pro-sequence  
XX  
XX W09103568-A.  
XX  
XX 21-MAR-1991.  
XX  
XX 29-AUG-1990: 90MO-US04915.  
XX  
XX 20-AUG-1990: 90US-0570657.  
XX 30-AUG-1989: 89US-0400591.  
XX  
XX (PLAC ) MAX PLANCK GES WISSENSCH.  
XX (REG-) REGENERON PHARM INC.  
XX  
XX Hyman C, Alderson R, Yancopoulos G, Barde YA, Thoenen HF;  
XX Hohn A, Lottspeich F, Lindsay RM;  
XX  
XX WPI: 1991-102083/14.  
XX N-PSDB: AAO11205.  
XX  
XX Brain derived neurotrophic factor and DNA encoding it - for  
XX diagnosis and treatment of neurological disorders, eg  
XX Parkinson's disease and retinal degeneration  
XX  
XX Claim 30; Page 155; 229pp; English.  
XX  
XX A portion of the coding sequence for mature rat BDNF was  
XX amplified by PCR and the sequence determined. The sequence contains  
XX a number of conservative changes from the porcine BDNF gene  
XX although the deduced amino acid sequence for the region of at least  
XX amino acids 28 to 111 was identical to that of porcine BDNF.  
XX The BDNF can be used to sustain the survival of dopaminergic and  
XX cholinergic neurons of the CNS, to suppress the proliferation of  
XX astroglial cells, to inhibit the uptake of GABA into neurons and to  
XX upregulate the expression of NGF receptor on the cell surface.  
XX See also AAO11205-4, AAO11206 and AAO11604.  
XX  
XX Sequence 249 AA:  
XX  
XX Query Match 97.3%; Score 622.5; DB 12; Length 249;  
XX Best Local Similarity 99.2%; Pred. No. 2e-60;  
XX Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	Db	Qy	Db
2	131	62	191
HSDPARGELTSLVCDSTISEMVTAAADKTVADVSGGTYVLEAVPAKSQLQYETFRKCP	HSDPARGELTSLVCDSTISEMVTAAADKTVADVSGGTYVLEAVPAKSQLQYETFRKCP	MGATKECCRCIDRRHNSCORTTOSVVALTMDSKRRIGAFETFDPSCTLTIRGR	MGATKECCRCIDRRHNSCORTTOSVVALTMDSKRRIGAFETFDPSCTLTIRGR
61	19	119	249

RESULT 15  
ABR57117

ID ABB57117 standard; Protein: 249 AA.

AC AB857117;

DT 07-MAR-2002 (first entry)

DE Mouse ischaemic condition related protein sequence SEQ ID NO:266.

KM Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KM vasospastic ischaemia; ischaemic condition; ischaemic disease

**Mus musculus.**

PN HQ200188188-A2.

PD 22-NOV-2001.

PF 18-MAY-2001; 2001WO-JP04192

PR 18-MAY-2000; 2000JP-0145977.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

DR WPI: 2002-034733/04.

DR N-PSDB; ABI99369.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes -

PS Claim 2; Page 748-749; 2690pp; English

The present invention describes a method for examining ischemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischemic condition (e.g. compressive ischemia, occlusive ischemia or vasospastic ischemia), by measuring expression levels of particular genes (AB199202 to AB199912), encoding the protein sequences in AB857020 to AB857314) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischemic condition-improving drugs or therapeutics for ischemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischemic condition related sequence which are used in the exemplification of the present invention.

**Sequence** **249 AA:**

Query Match	97.3%	Score 622.5;	DB 23;	Length 249;

Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1.

```
QY      2 HSDPARBELSVCOSISEWTTADKKTAAMDGGVYVLEKVPKSGOLKOFEYTEKNP   61
|||||
Db      131 HSDPARBELSVCOSISEWTTADKKTAAMDGGVYVLEKVPKSGOLKOFEYTEKNP   190
|||||
QY      62 MGYTEGCGRGIDKRHNSSCQTQSIVRALTMDSKKRIGRFRIPTSCV-TLTIKGR   119
|||||
```

Db 191 MGYTKEGCRGIDKRHWNSQCTTQSYVRALTMDSKRRIGRFRIRIDTSCVCTLTIRGR 249

Search completed: December 2, 2002, 15:08:39  
Job time : 24.7163 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 9.48652 Seconds  
(without alignments)  
1205.921 Million cell updates/sec

Title: US-10-072-681-4

Sequence: 1 PHSDPARGELSYCVSDISEM.....GWRFRIDTSCVTITIKRGR 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	97.3	247	2 A40304	brain-derived neur
2	622.5	97.3	249	2 S12555	brain-derived neur
3	622.5	97.3	249	2 B40304	brain-derived neur
4	622.5	97.3	252	2 A30361	brain-derived neur
5	613.5	95.9	248	2 UC6183	brain-derived neur
6	594	92.8	114	2 I84765	brain-derived neur
7	570.5	89.1	269	2 I51708	brain-derived neur
8	564	88.1	114	2 I50606	brain-derived neur
9	559	87.3	114	2 I51599	brain-derived neur
10	375.5	58.7	236	2 JH0400	neurotrophin-3 pre
11	344.5	53.8	257	2 C40304	neurotrophin-3 pre
12	344.5	53.8	257	2 S09135	neurotrophin-3 pre
13	344.5	53.8	258	2 A35781	neurotrophin-3 pre
14	344.5	53.8	258	2 A35781	neurotrophin-3 pre
15	336.5	52.6	209	2 B42687	neurotrophin-4 pre
16	332.5	52.0	210	2 A42687	neurotrophin-4 pre
17	317	49.5	229	2 I46614	neurotrophin-4 pre
18	317	49.5	229	2 I46614	neurotrophin-4 pre
19	313	48.9	125	2 A26311	nerve growth facto
20	311.5	48.7	125	2 A26311	nerve growth facto
21	310	48.4	303	1 NGRHBM	nerve growth facto
22	308.5	48.2	235	2 S14481	nerve growth facto
23	308.5	48.2	235	2 S14481	nerve growth facto
24	308.5	48.2	307	1 NGMSMG	nerve growth facto
25	306.5	47.9	241	2 J10097	nerve growth facto
26	301.5	47.1	243	2 S11193	nerve growth facto
27	300.5	47.0	117	2 S28161	nerve growth facto
28	298	46.6	116	1 NGMNXI	nerve growth facto
29	295.5	46.2	116	2 A58566	nerve growth facto

30	295.5	46.2	246	2 A59218	nerve growth facto
31	254	39.7	286	2 S50855	neurotrophin-6
32	253.5	39.6	194	2 S11709	nerve growth facto
33	74	11.6	796	2 H82406	probable lipase VC
34	69.5	10.9	184	2 G83521	hypothetical prote
35	69	10.8	476	2 T79463	hypothetical prote
36	69	10.8	481	2 H75198	hypothetical prote
37	69	10.8	1006	2 T13331	probable tail prot
38	68	10.6	195	2 S77401	hypothetical prote
39	68	10.6	245	1 PSHUAM	14-3-3 protein zet
40	68	10.6	245	2 A47389	14-3-3 protein zet
41	68	10.6	245	2 S65013	14-3-3 protein zet
42	68	10.6	294	2 T34159	hypothetical prote
43	68	10.6	347	2 S60428	hypothetical prote
44	68	10.6	479	2 A97027	hydrolyase of alpha
45	67.5	10.5	1039	2 C87083	C-term 19ey1-cRNA

#### ALIGNMENTS

##### RESULT 1

A40304 brain-derived neurotrophic factor precursor - human

C:Species: Homo sapiens (man)

C:Date: 03-Apr-1992 sequence, revision 30-Sep-1993 text change 21-Jul-2000

C:Accession: B36208; A60536; A40304; A37218; A61115; I38072

R:Jones, R.R.; Reichardt, L.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A:Title: Molecular cloning of a human gene that is a member of the nerve growth facto

A:Reference number: A36208; MUID:91045537; PMID:2236018

A:Accession: B36208

A:Molecule type: DNA

A:Residues: 1-247 <CON>

A:Cross-references: GB:M1762; MID:9179402; PIDN:AAA51820.1; PID:9179403

R:Rancopulos, G.D.; Malsompliere, P.C.; IP, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul

Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990

A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways

A:Reference number: A60536; MUID:9211157; PMID:1966766

A:Accession: A60536

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-65, 'M', 67-247 <YAN>

R:Malsompliere, P.C.; Le Beau, M.N.; Espinosa III, R.; IP, N.Y.; Belluscio, L.; de la

Genomics 10, 558-568, 1991

A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str

A:Reference number: A40304; MUID:91365361; PMID:189806

A:Accession: A40304

A:Molecule type: mRNA

A:Residues: 1-247 <MAN>

A:Cross-references: GB:M1176; MID:9179404; PIDN:AAA69805.1; PID:9896463

A:NOTE: the sequence in Genbank entry HUMBNFB, release 106.0. (PID:9896463) begins c

R:Ramamo, H.; Gurney, M.E.

J. Neurosci. 10, 3469-3478, 1990

A:Title: Human platelets contain brain-derived neurotrophic factor.

A:Reference number: A37218; MUID:91038253; PMID:2230938

A:Accession: A37218

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 138-236 <YAN>

R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Martin, E.; Burton, L.E.; Shih, A.; Laram

Endocrinology 129, 1289-1294, 1991

A:Title: Primary structure and biological activity of human brain-derived neurotrophin

A:Reference number: A61115; MUID:9139743; PMID:1874171

A:Accession: A61115

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-65, 'M', 67-247 <ROS>

R:Shintani, A.; Ono, Y.; Kaisho, Y.; Igarashi, K.

Biochem. Biophys. Res. Commun. 187, 325-332, 1992

A:Title: Characterization of the 5'-flanking region of the human brain-derived neurot

A:Reference number: I38072; MUID:92118032; PMID:1339267

A:Accession: I38072

A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-247 <SH1>  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 03-Apr-1992 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999  
 A:Cross-references: EMBL:X60201; NID:g9328269; PIDD:CAA4761.1; PID:g496626  
 A:Notes: the authors do not discuss this mRNA sequence in this reference; attribution is  
 C:Genetics:  
 A:Gene: GDB:BNF  
 A:Cross-references: GDB:125916; OMIM:113505  
 A:Map position: 11p13-11p13  
 A:Superfamily: nerve growth factor beta chain  
 C:Key words: dimer; glycoprotein  
 F:1-16/Domain: signal sequence; status predicted <SIG>  
 F:117-128/Domain: propeptide; status predicted <PRO>  
 F:129-247/Product: brain-derived neurotrophic factor; status predicted <MAT>  
 F:121/Binding site: carbohydrate (Asn) (covalent); status experimental

Query Match 97.3%; Score 622.5; DB 2; Length 247;  
 Best Local Similarity 99.2%; Pred. No. 1,1e-56;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISISMTADKTAADKTAADMSGCTVLEKVPVSKGOLKQYFETKCNP 61  
 |||||||  
 DB 129 HSDPARRGELSYCDISISMTADKTAADKTAADMSGCTVLEKVPVSKGOLKQYFETKCNP 188  
 |||||||  
 OY 62 MGYTEGCGIDKRRHNSOCTTOSYVRAALTMDSKRRIGRFRIDTSCV-TLTIKRR 119  
 |||||||  
 DB 189 MGYTEGCGIDKRRHNSOCTTOSYVRAALTMDSKRRIGRFRIDTSCV-TLTIKRR 247

## RESULT 2

S12555 brain-derived neurotrophic factor - mouse

N:Alternate names: BDNF protein

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

A:Accession: S12555; S1180; S51181

R:Hofer, M.; Pegliusi, S. R.; Kohn, A.; Leibrock, J.; Barde, Y. A.

EMBO J. 9, 2459-2464, 1990

A:Title: Regional distribution of brain-derived neurotrophic factor mRNA in the adult mouse

A:Reference number: S12555; MUID:9016101; PMID:2369858

A:Accession: S12555

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-249 <NOF>

A:Cross-references: GB:X55573; NID:g287898; PIDD:CAA39159.1; PID:g287899

R:Kolbeck, R.; Jungbluth, S.; Barde, Y. A.

Eur. J. Biochem. 225, 995-1003, 1994

A:Title: Characterisation of neurotrophin dimers and monomers.

A:Reference number: S51179; MUID:95045576; PMID:7957235

A:Accession: S51180

A>Status: preliminary

A:Molecule type: Protein

A:Residues: 131-135 <KOL>

A:Accession: S51181

A>Status: preliminary

A:Molecule type: Protein

A:Residues: 117-121 <KOZ>

C:Superfamily: nerve growth factor beta chain

Query Match 97.3%; Score 622.5; DB 2; Length 249;  
 Best Local Similarity 99.2%; Pred. No. 1,1e-56;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISISMTADKTAADKTAADMSGCTVLEKVPVSKGOLKQYFETKCNP 61  
 |||||||  
 DB 131 HSDPARRGELSYCDISISMTADKTAADKTAADMSGCTVLEKVPVSKGOLKQYFETKCNP 190  
 |||||||  
 OY 62 MGYTEGCGIDKRRHNSOCTTOSYVRAALTMDSKRRIGRFRIDTSCV-TLTIKRR 119  
 |||||||  
 DB 191 MGYTEGCGIDKRRHNSOCTTOSYVRAALTMDSKRRIGRFRIDTSCV-TLTIKRR 249

## RESULT 3

B40304 brain-derived neurotrophic factor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Apr-1992 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999

A:Accession: B40304; S24955; 160275; 160545

R:Yancopoulos, G. D.; Malsomplere, P. C.; Ip, N. Y.; Aldrich, T. H.; Belluscio, L.; Boul

Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990

A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways

A:Reference number: B40304; MUID:92111157; PMID:1966766

A:Accession: B40304

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-249 <YAN>

R:Malsomplere, P. C.; Le Beau, M. M.; Espinosa III, R.; Ip, N. Y.; Belluscio, L.; de la

Genomics 10, 558-568, 1991

A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str

A:Reference number: B40304; MUID:91365361; PMID:1889806

A:Accession: B40304

A:Molecule type: mRNA

A:Residues: 1-249 <MAT>

A:Cross-references: GB:M61175; NID:g203122; PIDD:AAA16841.1; PID:g203123

R:Meis, M.

submitted to the EMBL Data Library, June 1992

A:Reference number: S24955

A:Accession: S24955

A:Molecule type: mRNA

A:Residues: 8-249 <MEP>

A:Cross-references: EMBL:X67108; NID:g55820; PIDD:CAA47481.1; PID:g55821

R:Ohara, O.; Gahara, Y.; Terakawa, H.; Kitamura, T.

Gene 121, 383-386, 1992

A:Title: A rat brain-derived neurotrophic factor-encoding gene generates multiple tr

A:Reference number: 160275; MUID:93077058; PMID:1446835

A:Accession: 160275

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-249 <RES>

A:Cross-references: GB:D10938; NID:g220996; PIDD:BA01732.1; PID:g286257

R:Timmusk, T.; Palm, K.; Metsis, M.; Reintam, T.; Pealme, V.; Saarma, M.; Persson, H.

Neuron 10, 475-489, 1993

A:Title: Multiple promoters direct tissue-specific expression of the rat BDNF gene.

A:Reference number: 160545; MUID:93213504; PMID:8461137

A:Accession: 160545

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 8-249 <REZ>

A:Cross-references: EMBL:X67108; NID:g55820; PIDD:CAA47481.1; PID:g55821

C:Genetics:

A:Gene: BDNF

C:Superfamily: nerve growth factor beta chain

Query Match 97.3%; Score 622.5; DB 2; Length 249;  
 Best Local Similarity 99.2%; Pred. No. 1,1e-56;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARRGELSYCDISISMTADKTAADKTAADMSGCTVLEKVPVSKGOLKQYFETKCNP 61  
 |||||||  
 DB 131 HSDPARRGELSYCDISISMTADKTAADKTAADMSGCTVLEKVPVSKGOLKQYFETKCNP 190  
 |||||||  
 OY 62 MGYTEGCGIDKRRHNSOCTTOSYVRAALTMDSKRRIGRFRIDTSCV-TLTIKRR 119  
 |||||||  
 DB 191 MGYTEGCGIDKRRHNSOCTTOSYVRAALTMDSKRRIGRFRIDTSCV-TLTIKRR 249

## RESULT 4

A30361 brain-derived neurotrophic factor precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 16-Jul-1999

A:Accession: A30361

R:Leibrock, J.; Lottspesch, F.; Kohn, A.; Hofer, M.; Hengeler, B.; Masiakowski, P.; J

Nature 341, 149-152, 1989

A:Title: Molecular cloning and expression of brain-derived neurotrophic factor.

A:Reference number: A30361; MUID:89384868; PMID:2779655



OY 2 HSDPARBELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 61  
 DB 2 HSDPARBELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 61  
 OY 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV 111  
 DB 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV 111

## RESULT 9

brain-derived neurotrophic factor - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #ext\_change 16-Jul-1999  
 C:Accession: J151599  
 R:Jackson, P.J.; Towne, M.D.; Huntman, M.M.  
 FEBS Lett. 285, 260-264, 1991  
 A:Title: Comparison of mammalian, chicken and Xenopus brain-derived neurotrophic factor  
 A:Reference number: 150606; MUID:91309745; PMID:1306813  
 A:Accession: J151599  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <ISA>  
 A:Cross-references: EMBL:X61477; NID:9288363; PIDN:CAA43705.1; PID:9288364  
 C:Superfamily: nerve growth factor beta chain

Query Match 87.3%; Score 559; DB 2; Length 114;  
 Best Local Similarity 92.7%; Pred. No. 1,7e-50;  
 Matches 102; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 HSDPARBELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 61  
 DB 2 HSDPARBELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 61  
 OY 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV 111  
 DB 62 MGYTEGCGRIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV 111

## RESULT 10

neurotrophin-4 precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #ext\_change 16-Jul-1999  
 C:Accession: JH0400  
 R:Halibosch, F.; Ibanez, C.F.; Persson, H.  
 Neuron 6, 845-858, 1991  
 A:Title: Evolutionary studies of the nerve growth factor family reveal a novel member at

A:Reference number: JH0400; MUID:9122573; PMID:2025430  
 A:Accession: JH0400  
 A:Molecule type: DNA  
 A:Residues: 1-236 <NAL>

A:Cross-references: GB:230090; NID:9455533; PIDN:CAA82906.1; PID:9455534  
 C:Comment: This protein belongs to the nerve growth factor family.  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:119-113/Domain: signal sequence #status predicted <PRO>  
 F:114-236/Product: neurotrophin-4 #status predicted <MAT>  
 F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.7%; Score 375.5; DB 2; Length 236;  
 Best Local Similarity 60.9%; Pred. No. 3.2e-31;  
 Matches 70; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

OY 6 ARGELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 65  
 DB 123 SRGELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 180  
 OY 66 KEGCGIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV-TLIRGR 119  
 DB 181 TRCGGVGDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV-TLIRGR 235

## RESULT 11

neurotrophin-3 precursor - human  
 C:Accession: C40304  
 N:Alternate names: nerve growth factor 2; NCF-2  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Apr-1992 #sequence\_revision 30-Sep-1993 #ext\_change 16-Jul-1999  
 C:Accession: A36208; JH0141; C40304; S10719; C60536  
 R:Jones, K.R.; Reichardt, L.F.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A:Title: Molecular cloning of a human gene that is a member of the nerve growth factor  
 A:Reference number: A36208; MUID:91045337; PMID:2256018

A:Accession: A36208  
 A:Molecule type: DNA  
 A:Residues: 1-257 <JON>  
 A:Cross-references: GB:M37763; NID:9189300; PIDN:AAA59533.1; PID:9189301  
 R:Rosenthal, A.; Gooddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramée, G.R.; Nikol  
 Neuron 4, 767-773, 1990  
 A:Title: Primary structure and biological activity of a novel human neurotrophic fact

A:Reference number: JH0141; MUID:90262727; PMID:2344409  
 A:Accession: JH0141  
 A:Molecule type: DNA  
 A:Residues: 1-257 <ROS>

R:Maisonpierre, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la  
 Genomics 10, 558-568, 1991  
 A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str

A:Reference number: A40304; MUID:91365361; PMID:1889806  
 A:Accession: C40304

A:Molecule type: DNA  
 A:Residues: 1-257 <NAI>

A:Cross-references: GB:M61180; NID:9189302; PIDN:AAA63231.1; PID:9189303  
 R:Kishino, Y.; Yoshimura, K.; Nakahama, K.  
 FEBS Lett. 266, 187-191, 1990

A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.  
 A:Reference number: S10719; MUID:90306351; PMID:2365067

A:Accession: S10719  
 A:Molecule type: mRNA

A:Residues: 1-257 <NAI>  
 A:Cross-references: GB:X53655; NID:9287794; PIDN:CAA37703.1; PID:9287795  
 R:Yancopoulos, G.D.; Maisonpierre, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul  
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990

A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways  
 A:Reference number: A60536; MUID:9211157; PMID:1966766

A:Accession: C60536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA

A:Residues: 1-73, 'Q', '75-77', 'R', '79-108', 'T', '110-257' <YAN>  
 C:Genetics:  
 A:Gene: GDB:NFP3

A:Cross-references: GDB:125917; OMIM:162660  
 A:Map position: 12p13-12p13  
 C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:119-138/Domain: propeptide #status predicted <PRO>  
 F:139-257/Product: neurotrophin-3 #status predicted <MAT>  
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.8%; Score 344.5; DB 2; Length 257;  
 Best Local Similarity 57.4%; Pred. No. 5.5e-28;  
 Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARGELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 65  
 DB 144 SRGELSVCDISEMYTAADKKTAVDMSCGTVLEKVPVSGOLKQYFETKCNP 201

OY 66 KEGCGIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV-TLIRGR 119  
 DB 202 KEGCGIDKRMHNSCCTTOSYVRLTMDSKKRIGMFRIRIDTSCV-TLIRGR 256

## RESULT 12



## 150400

neurotrophin-3 precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C:Accession: 150400; S42227

R:Maizompiere, P.C.; Belluscio, L.; Conover, J.C.; Yancopoulos, G.D.

DNA Seq. 3, 49-54, 1992

A:Title: Gene sequences of chicken BDNF and NT-3.

A:Reference number: 150400; MUID:93091238; PMID:1457809

A:Accession: 150400

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-257 &lt;NAI&gt;

A:Cross-references: GB:M83378; NID:9212464; PIDN:AAA68880.1; PID:9212465

R:Hallboeck, F.; Ibanez, C.F.; Ebendal, T.; Persson, H.

Eur. J. Neurosci. 5, 1-14, 1993

A:Title: Cellular localization of brain-derived neurotrophic factor and neurotrophin-3

A:Reference number: S42227; MUID:94084226; PMID:8074744

A:Accession: S42227

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 32-257 &lt;NAI&gt;

A:Cross-references: EMBL:Z30092; NID:9455531; PIDN:CAA82908.1; PID:927570

A:Gene: NT-3

C:Superfamily: nerve growth factor beta chain

## Query Match

53.8%; Score 344.5; DB 2; Length 257;

Best Local Similarity 57.4%; Pred. No. 5.5e-28;

Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

Oy

6 ARGELSYVCDISSEWYTAADKRTAVDMSGCTVYLVKVPVSKQLQYETKCPMGT 65

DB 144 SHRGESVCDSESLWVT--DKSSAIDIRGHQVYVLEGITGSPVQYETKCEARPV 201

Oy 66 KECRCIDKRHNNSCARTTOSYVALTMDSKRRIGRFRIDTSCV-TLTIRGR 119

DB 202 KNGCRIDDKHNNSCARTTOSYVALTSENKLVGWRMIRIDTSCVCAISRIGR 256

Db

## RESULT 13

S09155

neurotrophin-3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999

C:Accession: S09155; S51179

R:Hohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.

Nature 344, 339-341, 1990

A:Title: Identification and characterization of a novel member of the nerve growth factor

A:Reference number: S09155; MUID:90190865; PMID:2314473

A:Accession: S09155

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-258 &lt;HOH&gt;

A:Cross-references: GB:M53357; NID:953451; PIDN:CAA37348.1; PID:953452

R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.

Eur. J. Biochem. 225, 995-1003, 1994

A:Title: Characterisation of neurotrophin dimers and monomers.

A:Reference number: S51179; MUID:95045576; PMID:7957235

A:Accession: S51179

A:Status: preliminary

A:Molecule type: protein

A:Residues: 140-152 &lt;KOL&gt;

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted &lt;STIG&gt;

F:140-258/Product: neurotrophin-3 #status predicted &lt;NAI&gt;

F:113/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

53.8%; Score 344.5; DB 2; Length 258;

Best Local Similarity 57.4%; Pred. No. 5.5e-28;

Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

Oy

6 ARGELSYVCDISSEWYTAADKRTAVDMSGCTVYLVKVPVSKQLQYETKCPMGT 65

DB 145 SHRGESVCDSESLWVT--DKSSAIDIRGHQVYVLEGITGSPVQYETKCEARPV 202

Oy 66 KECRCIDKRHNNSCARTTOSYVALTMDSKRRIGRFRIDTSCV-TLTIRGR 119

DB 203 KNGCRIDDKHNNSCARTTOSYVALTSENKLVGWRMIRIDTSCVCAISRIGR 257

Db

## RESULT 14

A35781

hippocampus-derived neurotrophic factor precursor - rat

N:Alternate names: neurotrophin-3 precursor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 16-Jul-1999

C:Accession: A35781; A40094

R:Ernfors, P.; Ibanez, C.F.; Ebendal, T.; Olsson, L.; Persson, H.

Proc. Natl. Acad. Sci. U.S.A. 87, 5454-5458, 1990

A:Title: Molecular cloning and neurotrophic activities of a protein with structural a

A:Reference number: A35781; MUID:90319130; PMID:2164684

A:Accession: A35781

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-282 &lt;ERN&gt;

A:Cross-references: GB:M44643

R:Maizompiere, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furch, M.E.; Lindsay, R.M

Science 247, 1446-1451, 1990

A:Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.

A:Reference number: A40094; MUID:90208301; PMID:2221006

A:Accession: A40094

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 25-282 &lt;NAI&gt;

A:Cross-references: GB:M33968; NID:9205771; PIDN:AAA41727.1; PID:9205772

C:Superfamily: nerve growth factor beta chain

Query Match

53.8%; Score 344.5; DB 2; Length 282;

Best Local Similarity 57.4%; Pred. No. 6e-28;

Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

Oy

6 ARGELSYVCDISSEWYTAADKRTAVDMSGCTVYLVKVPVSKQLQYETKCPMGT 65

DB 169 SHRGESVCDSESLWVT--DKSSAIDIRGHQVYVLEGITGSPVQYETKCEARPV 226

Oy 66 KECRCIDKRHNNSCARTTOSYVALTMDSKRRIGRFRIDTSCV-TLTIRGR 119

DB 227 KNGCRIDDKHNNSCARTTOSYVALTSENKLVGWRMIRIDTSCVCAISRIGR 281

Db

## RESULT 15

B42687

neurotrophin-4 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C:Accession: B42687; JH0504; JH0505

R:Rip, N.Y.; Ibanez, C.F.; Wye, S.H.; McGiln, J.; Jones, P.F.; Gies, D.R.; Belluscio,

Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992

A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distri

A:Reference number: B42687; MUID:92212967; PMID:1113578

A:Accession: B42687

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-209 &lt;IPA&gt;

A:Cross-references: GB:M6742; NID:9205775; PIDN:AAA41728.1; PID:9205776

R:Berkeley, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenth

Neuron 7, 857-866, 1991

A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkb.

A:Reference number: JH0503; MUID:92075279; PMID:1742028

A:Accession: JH0504

A:Molecule type: DNA

A:Residues: 1-209 &lt;BER&gt;

A:Accession: JH0505

A:Molecule type: mRNA

A;Residues: 1-176, 'P', 178-209 <BERI>  
A;Cross-references: CB:569323. NTD:0

C:Comment: This protein is a targeted-derived, diffusible neurotrophic factor.  
A:Cross-references: GB:56323; NID:g240025; PIDN:AAB20548.1; PID:g240026

C:Comment: This protein is a targeted-derived, diffusible neurotrophic factor.

C:comment: The neurotrophins stimulate autophosphorylation and transduce signals through C:Superfamily: nerve growth factor beta chain

**C;Keywords:** glycoprotein

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F:1-20/Domain: signal sequence #status predicted <SIG>
F:1-20/Domain: transmembrane #status predicted <PRO>
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F:21-79/Domain: propeptide %status predicted <PRO>  
E:80-209/Product: neurotrophin-5 %status predicted <NEU>

F:75/Binding site: carbohydrate (Asn) (covalent) #status: F:80-109/Product: neurotrophin-5 #status: predicted <NEUR>

**Binding site:** carbonhydrate (asn) (covalent) \*status predicted

Query Match 52.68; Score 336.5; DB 2; Length 209;

Best Local Similarity	54.50;	Pred. No.	2.9e-27;
Matches	31.	Mismatches	2457.
Conservative			

Matches	67;	Conservative	21;	Mismatches	24;	Indels	11;	Gaps	4;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

6 ARGELSYCDISSEWTTADKTAVDMSGCTVTLEKVPVSKGQ-LKQFYETKCNP--- 61

```
Db      88 SRGELAVCDVAVSGWYT--DRTAVDLRGREVEYLGEVPAGGSPLRQYFFETCKAESA 145
```

62 ---MGTYEGCRGIDKRHNSQCRTTOSTYVALTMDSKKRIGWRFRIOTSCV-TLTK 116

```
08      | :|||::|:||| ||: | ||||| ||: |:||||:||||:|| || :  
       746 CCCCCCCCCCCBUBBUU SCK AKOSVUBALMANSOCBVCPWIRPMACVTMLTSR 205
```

117 PGB 119

oy 117 RGR 119

Search completed: December 2, 2002, 15:13:59  
Job time : 10.4865 secs

Job time : 10.4865 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 4.88277 Seconds

(without alignments)  
1010.837 Million cell updates/sec

Title: US-10-072-681-4

Sequence: 1 PHSDPARGELSYVCDISEM.....GMRFRIDTSCVTLTKRGR 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	97.3	247	1	BDNF_HUMAN
2	622.5	97.3	247	1	BDNF_PROLO
3	622.5	97.3	247	1	BDNF_URSMT
4	622.5	97.3	249	1	BDNF_MOUSE
5	622.5	97.3	249	1	BDNF_MOUSE
6	622.5	97.3	252	1	BDNF_PIG
7	621.5	97.1	255	1	BDNF_CAVPO
8	618.5	96.6	247	1	BDNF_FELCA
9	618.5	96.6	247	1	BDNF_URSAR
10	613.5	95.9	248	1	BDNF_BOVIN
11	594	92.8	114	1	BDNF_MACMU
12	592.5	92.6	246	1	BDNF_CHICK
13	570.5	90.5	270	1	BDNF_CITCA
14	570.5	89.1	269	1	BDNF_XIPMA
15	559	87.3	114	1	BDNF_XENLA
16	375.5	58.7	236	1	NT4_XENLA
17	344.5	53.8	257	1	NT3_CHICK
18	344.5	53.8	257	1	NT3_HUMAN
19	344.5	53.8	258	1	NT3_MOUSE
20	344.5	53.8	258	1	NT3_MOUSE
21	347.5	53.0	260	1	NT3_XENLA
22	339.5	53.0	257	1	NT3_FELCA
23	336.5	52.6	209	1	NT5_RAT
24	336.5	52.6	210	1	NT5_HUMAN
25	317	49.5	229	1	NGF_PIG
26	317	49.5	243	1	NGF_CHICK
27	311.5	48.7	241	1	NGF_HUMAN
28	310	48.4	231	1	NGF_BOVIN
29	310	48.4	241	1	NGF_PRANA
30	308.5	48.2	231	1	NGF_XENLA
31	308.5	48.2	241	1	NGF_MOUSE
32	308.5	48.2	241	1	NGF_RAT
33	306.5	47.9	241	1	NGF_CAVPO

34	301.5	47.1	243	1	NGF_BUNMU
35	300.5	47.0	117	1	NGF_DABRR
36	295	46.1	116	1	NGF_NAJNA
37	292.5	45.7	116	1	NGF_NAJAT
38	253.5	39.6	194	1	NGF_XIPMA
39	245	38.3	140	1	NT7_CYPCA
40	245	38.3	233	1	NT7_BRARE
41	222	34.7	186	1	NT66_HUMAN
42	221	34.5	257	1	NT6A_HUMAN
43	215	33.6	257	1	BDNF_HUMAN
44	214	33.4	43	1	BDNF_RAVCL
45	209	32.7	43	1	BDNF_VIPLE

## ALIGNMENTS

RESULT 1  
BDNF\_HUMAN  
ID BDNF\_HUMAN STANDARD: PRT: 247 AA.  
AC P23560; O9QC24; Q9BY7;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Brain-derived neurotrophic factor precursor (BDNF).  
GN BDNF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91045937; PubMed-2236018;  
RT Jones K.R., Reichardt L.F.,  
RT "Molecular cloning of a human gene that is a member of the nerve  
RT growth factor family.",  
RT Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91365361; PubMed-1889806;  
RA Maisonneuve P.C., Le Beau M.M., Espinosa R. III, Ip N.Y.,  
RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,  
RA Yancopoulos G.D.,  
RT Human and rat brain-derived neurotrophic factor and neurotrophin-3:  
RT gene structures, distributions, and chromosomal localizations.",  
RL Genomics 10:558-568(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92118032; PubMed-1339267;  
RA Shitara A., Ono Y., Katsuo Y., Igarashi K.,  
RA "Characterization of the 5'-flanking region of the human  
RA brain-derived neurotrophic factor gene.",  
RL Biochem. Biophys. Res. Commun. 182:325-334(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Cheng Y., Gu J.,  
RA Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX Wu J., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.,  
RA Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 185-227 FROM N.A.  
RX TISSUE-Leukocyte;  
RA MEDLINE-9122573; PubMed-2025430;  
RA Hallboeek F., Ibanez C.F., Persson H.,  
RT "Evolutionary studies of the nerve growth factor family reveal a  
RT novel member abundantly expressed in Xenopus ovary.",  
RL Neuron 6:845-858(1991).  
RN [7]  
RP SEQUENCE OF 129-144.  
RX TISSUE-Serum;  
RA MEDLINE-96136633; PubMed-8527932;

RA Rosenfeld R.D., Zeng L., Hanu M., Talvenhelmo J., Radka S.F.,  
 RA Bennett L., Miller J.A., Welcher A.A.;  
 RT "Purification and identification of brain-derived neurotrophic factor  
 RT from human serum.";  
 RL Protein Expr. Purif. 6:465-471(1995).  
 RN (8)  
 RN SEQUENCE OF 12-197 FROM N.A.  
 RX MEDLINE-21082082; PubMed-11214319;  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 RN (9)  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE-95317877; PubMed-7703225;  
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.;  
 RT "Structure of the brain-derived neurotrophic factor/neurotrophin 3  
 RT heterodimer.";  
 RL Biochemistry 34:4139-4146(1995).  
 RN (10)  
 RN CHARACTERIZATION, AND MUTAGENESIS OF ARG-54.  
 RX MEDLINE-21201090; PubMed-11152678;  
 RA Nowla S.J., Farhadi H.F., Pareek S., Atwal J.K., Morris S.J.,  
 RA Seidah N.G., Murphy R.A.;  
 RT "Biosynthesis and post-translational processing of the precursor to  
 RT brain-derived neurotrophic factor.";  
 RL J. Biol. Chem. 276:12660-12666(2001).  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CC CONNECTED TO IT.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The propeptide is N-glycosylated and glycosylated.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: M37762; AAA51820.1; -  
 DR EMBL: M61176; AAA69805.2; -  
 DR EMBL: X60201; CAA42761.1; -  
 DR EMBL: AF400438; AAK92487.1; -  
 DR EMBL: M61181; AAA6140.1; -  
 DR EMBL: X51251; CAA62632.1; -  
 DR EMBL: AY011481; AAG47514.1; -  
 DR PIR: B36208; B36208.  
 DR PIR: A40304; A40304.  
 DR PDB: 1BND; 04-APR-96.  
 DR PDB: 1B8M; 09-FEB-99.  
 DR GeneW: HGNC:1033; BDNF.  
 DR MIM: 113505; -  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 2.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF-1; 1.  
 DR PROSITE: PS0270; NGF-2; 1.  
 DR PROSITE: PS0270; NGF-2; 1.  
 KW Growth factor; Signal; Glycoprotein; Polymorphism; 3D-structure.  
 KM SIGNAL 1 18  
 FT PROPEP 19 128  
 FT CHAIN 129 247  
 FT DISULFID 141 208  
 FT DISULFID 186 237  
 FT DISULFID 196 239  
 FT CARBOHYD 121 121  
 FT SITE 57 58  
 FT VARIANT 66 66  
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 /FTID-VAR\_004626.

FT VARIANT 75 75 0 -> H (IN DBSNP:1048218).  
 FT VARIANT 125 125 /FTID-VAR\_011797.  
 FT VARIANT 127 127 R -> M (IN DBSNP:1048220).  
 FT VARIANT 127 127 /FTID-VAR\_011798.  
 FT VARIANT 127 127 R -> L (IN DBSNP:1048221).  
 FT VARIANT 127 127 /FTID-VAR\_011799.  
 FT MUTAGEN 54 54 R -> A; ABOLISHES PROCESSING BY SLP.  
 SQ SEQUENCE 247 AA: 27818 MW: 0860488254722A99 CRC64;  
 Query Match 97.3%; Score 622.5; DB 1; Length 247;  
 Best local similarity 99.2%; Pred. No. 1e-58;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 HSDPARGELSDSISEMTAAKRTAVDMSGGVTVLEKVPYPSKOLKQYETKCNP 61  
 DB 129 HSDPARGELSDSISEMTAAKRTAVDMSGGVTVLEKVPYPSKOLKQYETKCNP 188  
 QY 62 MGYTREGCGIDRRHNSCORTTOSYVRLTYDSKRRIGMFRIDISCV-TLTKRGR 119  
 DB 189 MGYTREGCGIDRRHNSCORTTOSYVRLTYDSKRRIGMFRIDISCVCTLTFRGR 247  
 RESULT 2  
 BDNF\_PROTO STANDARD: PRT: 247 AA.  
 ID BDNF\_PROTO 018735;  
 AC 018735;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS Procyon lotor (Raccoon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Procyon.  
 OX MBL TaxID=9634;  
 RX (1)  
 RN RN SEQUENCE FROM N.A.  
 RA Lln F.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CC CONNECTED TO IT (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: AF003188; AAB71654.1; -  
 DR HSSP: P23560; 1B8M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF-1; 1.  
 DR PROSITE: PS0270; NGF-2; 1.  
 DR PROSITE: PS0270; NGF-2; 1.  
 KW Growth factor; Signal.  
 KM SIGNAL 1 18  
 FT PROPEP 19 128  
 FT CHAIN 129 247  
 FT SITE 57 58  
 FT DISULFID 141 208  
 FT DISULFID 186 237  
 FT DISULFID 196 239  
 FT CARBOHYD 121 121  
 SQ SEQUENCE 247 AA: 27834 MW: 5FC377E4FE1F52A0 CRC64;  
 POTENTIAL.  
 BY SIMILARITY.  
 BRAIN-DERIVED NEUROTROPHIC FACTOR.  
 CLEAVAGE (BY SLP) (BY SIMILARITY).  
 BY SIMILARITY.  
 BY SIMILARITY.  
 BY SIMILARITY.  
 N-LINKED (GLCNAc...) (POTENTIAL).  
 CLEAVAGE (BY SLP).  
 V -> M.  
 /FTID-VAR\_004626.

Query Match 97.3%: Score 622.5; DB 1; Length 247;  
Best Local Similarity 99.2%: Pred. No. 1e-58;  
Matches 118: Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 2 HSDPARRGELSYCDISISEMTAAADKTAVDMSGGTIVLEKVPVSKQLQYFETKCNP 61  
129 HSDPARRGELSYCDISISEMTAAADKTAVDMSGGTIVLEKVPVSKQLQYFETKCNP 188  
62 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCV-TLTIRGR 119  
189 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCVTLTIRGR 247

RESULT 3  
ID BDNF\_URSML STANDARD; PRT; 247 AA.  
AC 018753;  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Brain-derived neurotrophic factor precursor (BDNF).  
GN BDNF.  
OS Ursus malayanus (Malayan sun bear) (Heliarctos malayanus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Heliarctos.  
OX NCBI\_TaxID=9634;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lin F.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
CC CONNECTED TO IT (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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CC -----  
DR EMBL: AF002240; AAB71653.1; -  
DR HSSP: P23560; 188M.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF; 1.  
DR PRINTS: PR00268; NGF.  
DR PRODOM: PD002052; NGF; 1.  
DR SMART: SM00140; NGF; 1.  
DR SMART: SM00248; NGF; 1.  
DR PROSITE: PS00248; NGF\_1; 1.  
DR PROSITE: PS50270; NGF\_2; 1.  
DR PROSITE: PS50270; NGF\_2; 1.  
KM Growth factor: Signal.  
FT SIGNAL 1 18  
FT PROPEP 19 128  
FT CHAIN 129 247  
FT SITE 57 58  
FT DISULFID 141 208  
FT DISULFID 186 237  
FT DISULFID 196 239  
FT CARBOHYD 121 121  
FT CARBOHYD 121 121  
SO SEQUENCE 247 AA; 27807 MW; FA1B3DFC4704DB83 CRC64;

Query Match 97.3%: Score 622.5; DB 1; Length 247;  
Best Local Similarity 99.2%: Pred. No. 1e-58;  
Matches 118: Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 2 HSDPARRGELSYCDISISEMTAAADKTAVDMSGGTIVLEKVPVSKQLQYFETKCNP 61  
129 HSDPARRGELSYCDISISEMTAAADKTAVDMSGGTIVLEKVPVSKQLQYFETKCNP 188  
62 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCV-TLTIRGR 119  
189 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCVTLTIRGR 247

Db 189 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCVTLTIRGR 247  
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RESULT 4  
ID BDNF\_MOUSE STANDARD; PRT; 249 AA.  
AC P21237;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Brain-derived neurotrophic factor precursor (BDNF).  
GN BDNF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-90316101; PubMed-2369898;  
RA Hofer M., Pagliusi S.R., Hohn A., LeDrook J., Barde Y.-A.;  
RT "Regional distribution of brain-derived neurotrophic factor mRNA in  
RT the adult mouse brain."  
RL EMBO J. 9:2459-2464(1990).  
CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
CC CONNECTED TO IT.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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CC -----  
DR EMBL: X55373; CAA39159.1; -  
DR PIR: S12555; S12555.  
DR HSSP: P23560; 188M.  
DR MGD: MGI:88145; Bdnf.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF; 1.  
DR PRINTS: PR00268; NGF.  
DR PRODOM: PD002052; NGF; 1.  
DR SMART: SM00140; NGF; 1.  
DR PROSITE: PS00248; NGF; 1.  
DR PROSITE: PS50270; NGF; 2; 1.  
KM Growth factor: Signal.  
FT SIGNAL 1 18  
FT PROPEP 19 130  
FT CHAIN 131 249  
FT SITE 57 58  
FT DISULFID 143 210  
FT DISULFID 188 239  
FT DISULFID 198 241  
FT CARBOHYD 123 123  
SO SEQUENCE 249 AA; 28123 MW; 90CE1F168B235C97 CRC64;

Query Match 97.3%: Score 622.5; DB 1; Length 249;  
Best Local Similarity 99.2%: Pred. No. 1e-58;  
Matches 118: Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 2 HSDPARRGELSYCDISISEMTAAADKTAVDMSGGTIVLEKVPVSKQLQYFETKCNP 61  
131 HSDPARRGELSYCDISISEMTAAADKTAVDMSGGTIVLEKVPVSKQLQYFETKCNP 190  
62 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCV-TLTIRGR 119  
191 MGYTEGCGRIDKRRHNSOCRTTOSYVRALTMDSKRRIGRFRIRDTSCVTLTIRGR 249

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RESULT 5
BNDF_RAT STANDARD: PRT: 249 AA.
AC P23163:
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
GN BDNF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN 11:
RP MEDLINE-91365361; PubMed-1889806;
RX Malsinier P.C., le Beau M.M., Esplinoza R. III, Ip N.Y.,
RX Belluscio L., de la Monte S.M., Squinto S., Furth M.E.,
RX Yancopoulos G.D.;
RA "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
RT gene structures, distributions, and chromosomal localizations.";
RN Genomics 10:558-568(1991).
RL 12:
RP SEQUENCE FROM N.A.
RA Ohara O.;
RN Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
RN 13:
RP SEQUENCE FROM N.A.
RX MEDLINE-9211157; PubMed-1966766;
RX Yancopoulos G.D., Malsinier P.C., Ip N.Y., Aldrich T.H.,
RX Belluscio L., Boulton T.G., Cobb M.H., Squinto S.P., Furth M.E.;
RT "Neurotrophic factors, their receptors, and the signal transduction
RT pathways they activate.";
RN Cold Spring Harb. Symp. Quant. Biol. 55:371-379(1990).
RL 14:
RP SEQUENCE OF 8-249 FROM N.A.
RX MEDLINE-93213504; PubMed-8461137;
RA Timmusk T., Palm K., Metsis M., Reintam T., Palme V., Saarma N.,
RA Persson H.;
RT "Multiple promoters direct tissue-specific expression of the rat BDNF
RT gene.";
RN Neuron 10:475-489(1993).
RL 15:
RP SEQUENCE OF 187-229 FROM N.A.
RX STRAIN-Sprague-Dawley; Tissue-Liver;
RX MEDLINE-9122573; PubMed-2025430;
RA Hallböök F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RN Neuron 6:845-858(1991).
RL 16:
RP FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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DR PRINTS: PR00268; NGF.
DR Prodom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
KM Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 130
FT CHAIN 131 249
FT SITE 57 58
FT DISULFID 143 210
FT DISULFID 188 239
FT DISULFID 198 241
FT CARBOHYD 123 123
SQ SEQUENCE 249 AA; 28109 MW; F9CAA5DEF9A78B7 CRC64;

Query Match 97.3%; Score 62.5; DB 1; Length 249;
Best Local Similarity 99.2%; Pred. No. 1e-58; 0; Indels 1; Gaps 1;
Matches 118; Conservative 0; Mismatches 0;

OY 2 HSDPARGELSYDSEISEWYTAADKRTAVDMSGTVLEVPVSKGOLKOFETKCNP 61
DB 131 HSDPARGELSYDSEISEWYTAADKRTAVDMSGTVLEVPVSKGOLKOFETKCNP 130
OY 62 MGTKKCCRGIDRRHNSCORTTOSYVRLTMDSKRIGRIFRIDSCV-TLTIKGR 119
DB 191 MGTKKCCRGIDRRHNSCORTTOSYVRLTMDSKRIGRIFRIDSCV-TLTIKGR 249

RESULT 6
BNDF_PIG STANDARD: PRT: 252 AA.
AC P14082:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
GN BDNF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OK NCBI_TaxID=9623;
RN 11:
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE-93384868; PubMed-2779653;
RX Leebrock J., Lottspeich F., Hohn A., Hofer M., Hengerer B.,
RX Maslakovski P., Thoenen H., Barde Y.-A.;
RT "Molecular cloning and expression of brain-derived neurotrophic
RT factor.";
RN Nature 341:149-152(1989).
RL 12:
RP FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND CENTRAL NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS00270; NCF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 13 133  
 FT CHAIN 134 252  
 FT SITE 57 58  
 FT DISULFID 146 213  
 FT DISULFID 191 242  
 FT DISULFID 201 244  
 FT CARBOHYD 126 126  
 SO SEQUENCE 253 AA: 28287 MW: 5DAB45E73BE087E CRC64.

POTENTIAL.  
 BRAIN-DERIVED NEUROTROPHIC FACTOR.  
 CLEAVAGE (BY SLP) (BY SIMILARITY).  
 BY SIMILARITY.  
 BY SIMILARITY.  
 N-LINKED (GLCNAC... ) (POTENTIAL).

Query Match 97.3% Score 622.5; DB 1; Length 252;  
 Best Local Similarity 99.2% Pred. No. 1e-58;  
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISEWYTAADKRTAVDMSCGTATLEKVPVSKGOLKQYFETKCNP 61  
 DB 134 HSDPARGELSVCDISEWYTAADKRTAVDMSCGTATLEKVPVSKGOLKQYFETKCNP 193  
 OY 62 MGYTEGCGRIDKRMHNSOCTRTOSYVRLTMDSKRIGRIRIDTSCV-TLTIKGR 119  
 DB 194 MGYTEGCGRIDKRMHNSOCTRTOSYVRLTMDSKRIGRIRIDTSCVTLTIKGR 252

## RESULT 7

ID BDNF\_CAVPO STANDARD: PRT: 255 AA.  
 AC 070183;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Hartley white; TISSUE-Liver;  
 RA Inoue M., Nakayama C., Noguchi H.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBS databases.

-1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY CONNECTED TO IT (BY SIMILARITY).  
 -1- SUBCELLULAR LOCATION: Secreted.

-1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.  
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CC EMBL: AB012097; BAA25116.1; -  
 DR HSSP: P23560; 1B8M.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF; 1.  
 DR PRINTS: PR00268; NCF.  
 DR PRODOM: PD002052; NCF; 1.  
 DR SMART: SM00140; NCF; 1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS00270; NCF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 13 136  
 FT CHAIN 137 255  
 FT SITE 57 58  
 FT DISULFID 149 216

POTENTIAL.  
 BY SIMILARITY.  
 BRAIN-DERIVED NEUROTROPHIC FACTOR.  
 CLEAVAGE (BY SLP) (BY SIMILARITY).  
 BY SIMILARITY.

FT DISULFID 194 245  
 FT DISULFID 204 247  
 FT CARBOHYD 129 129  
 SO SEQUENCE 255 AA: 28308 MW: BA05BA3EBB8BFA04 CRC64.

BY SIMILARITY.  
 BY SIMILARITY.  
 N-LINKED (GLCNAC... ) (POTENTIAL).

Query Match 97.1% Score 621.5; DB 1; Length 255;  
 Best Local Similarity 98.3% Pred. No. 1.3e-58;  
 Matches 117; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 2 HSDPARGELSVCDISEWYTAADKRTAVDMSCGTATLEKVPVSKGOLKQYFETKCNP 61  
 DB 137 HSDPARGELSVCDISEWYTAADKRTAVDMSCGTATLEKVPVSKGOLKQYFETKCNP 196  
 OY 62 MGYTEGCGRIDKRMHNSOCTRTOSYVRLTMDSKRIGRIRIDTSCV-TLTIKGR 119  
 DB 197 MGYTEGCGRIDKRMHNSOCTRTOSYVRLTMDSKRIGRIRIDTSCVTLTIKGR 255

## RESULT 8

ID BDNF\_FELCA STANDARD: PRT: 247 AA.  
 AC 097573;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE-20211727; PubMed-10745216;  
 RA Lein E.S., Hohn A., Shatz C.J.;  
 RT "Dynamic regulation of BDNF and NT-3 expression during visual system development.";  
 RL J. Comp. Neurol. 420:1-18(2000).

-1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY CONNECTED TO IT (BY SIMILARITY).  
 -1- SUBCELLULAR LOCATION: Secreted.

-1- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.  
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CC EMBL: AF192537; AAF03423.1; -

DR HSSP: P23560; 1B8M.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF; 1.  
 DR PRINTS: PR00268; NCF.  
 DR PRODOM: PD002052; NCF; 1.  
 DR SMART: SM00140; NCF; 1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS00270; NCF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 13 128  
 FT CHAIN 129 247  
 FT DISULFID 141 208  
 FT DISULFID 186 237  
 FT DISULFID 196 239  
 FT CARBOHYD 121 121  
 SO SEQUENCE 247 AA: 27802 MW: 864BA1BD26E0A0F3 CRC64.

POTENTIAL.  
 BY SIMILARITY.  
 BRAIN-DERIVED NEUROTROPHIC FACTOR.  
 BY SIMILARITY.  
 BY SIMILARITY.  
 N-LINKED (GLCNAC... ) (POTENTIAL).

Query Match 96.6% Score 618.5; DB 1; Length 247;  
 Best Local Similarity 98.3% Pred. No. 2.7e-58;

Matches 117: Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 HSDPARRELSVCDISSEVTAADKTAADMVSGTIVLEKVPVSKGOLKOFETKCNP 61  
 DB 129 HSDPARRELSVCDISSEVTAADKTAADMVSGTIVLEKVPVSKGOLKOFETKCNP 188  
 OY 62 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGRFRIRIDTSCV-TLTIKGR 119  
 DB 189 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGRFRIRIDTSCVTLTIKGR 247

## RESULT 9

BDNF\_URSAR STANDARD: PRT: 247 AA.

AC 018752:  
 DT 15-JUL-1998 (rel. 36, Created)  
 DT 15-JUL-1998 (rel. 36, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS Ursus arctos (Brown bear) (Grizzly bear).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
 OX NCBI\_TaxID=9644;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lin F.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CONNECTED TO IT (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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CC EMBL: AF002239; AAB71652.1; --  
 DR HSSP: P23560; 188M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRINTS: PR00268; NGF. 1.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 128  
 FT CHAIN 129 247  
 FT SITE 57 58  
 FT DISULFID 141 208  
 FT DISULFID 186 237  
 FT CARBOHYD 121 121  
 SQ SEQUENCE 247 AA: 27837 MW: EFIB3256F70AD883 CMC64;  
 Query Match 96.6%; Score 618.5; DB 1; Length 247;  
 Best Local Similarity 98.3%; Pred. No. 2.7e-58;  
 Matches 117: Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 HSDPARRELSVCDISSEVTAADKTAADMVSGTIVLEKVPVSKGOLKOFETKCNP 61  
 DB 129 HSDPARRELSVCDISSEVTAADKTAADMVSGTIVLEKVPVSKGOLKOFETKCNP 188  
 OY 62 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGRFRIRIDTSCV-TLTIKGR 119  
 DB 189 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGRFRIRIDTSCVTLTIKGR 247

RESULT 10  
 BDNF\_BOVIN STANDARD: PRT: 248 AA.

AC 095106:  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF) (Fragment).  
 GN BDNF.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-97186702; PubMed-9034318;  
 RA Arab S.F., Krohn K., Lachmund A., Unsicker K., Suter-Crazzolara C.,  
 RT "The gene encoding bovine brain-derived neurotrophic factor (BDNF)."  
 RL Gene 185:95-98(1997).  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CONNECTED TO IT (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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CC EMBL: X97914; CA66488.1; --  
 DR HSSP: P23560; 188M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 16  
 FT PROPEP 17 129  
 FT CHAIN 130 248  
 FT SITE 55 56  
 FT DISULFID 142 208  
 FT DISULFID 187 238  
 FT DISULFID 197 240  
 SQ SEQUENCE 248 AA: 27897F233F777C7 CMC64;  
 Query Match 95.9%; Score 613.5; DB 1; Length 248;  
 Best Local Similarity 97.5%; Pred. No. 9.1e-58;  
 Matches 116: Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 2 HSDPARRELSVCDISSEVTAADKTAADMVSGTIVLEKVPVSKGOLKOFETKCNP 61  
 DB 130 HSDPARRELSVCDISSEVTAADKTAADMVSGTIVLEKVPVSKGOLKOFETKCNP 189  
 OY 62 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGRFRIRIDTSCV-TLTIKGR 119  
 DB 190 MGYTEGCGRIDKRMHNSOCTTOSYVRLATMDSKRRIGRFRIRIDTSCVTLTIKGR 248  
 RESULT 11  
 BDNF\_MACMU STANDARD: PRT: 114 AA.  
 ID BDNF\_MACMU  
 AC 006225;  
 DT 01-FEB-1995 (rel. 31, Created)



DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Brain-derived neurotrophic factor (BDNF) (fragment).  
 GN BDNF.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NC NCBI\_TaxID=9544;  
 RN [1]  
 RP MEDLINE-91309745; PubMed-1906813;  
 RA Jackson P.J., Townner M.D., Huntsman M.M.;  
 RT "Comparison of mammalian, chicken and Xenopus brain-derived  
 RT neurotrophic factor coding sequences.";  
 RL FEBS Lett. 285:260-264(1991).  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CC CONNECTED TO IT.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: X61475; CAA43703.1; -;  
 DR HSSP: P23560; 188M.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF\_1.  
 DR ProDom: PD002052; NCF\_1.  
 DR SMART: SM00140; NCF\_1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS50270; NCF\_2; 1.  
 KW Growth factor.  
 FT NON\_TER 1 1  
 FT DISULFID 14 81 BY SIMILARITY.  
 FT DISULFID 59 110 BY SIMILARITY.  
 FT DISULFID 69 112 BY SIMILARITY.  
 FT NON\_TER 114 114  
 SO SEQUENCE 114 AA; 12956 MW; D5F1BEDD8F4B925 CRC64;  
 Query Match 92.8%; Score 594; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-56;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 61  
 DB 2 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 61  
 QY 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV 111  
 DB 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV 111  
 DB 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV 111  
 RESULT 12  
 BDNF\_CHICK STANDARD: PRT: 246 AA.  
 AC P23423;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NC NCBI\_TaxID=9031;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Leghorn; TISSUE=Liver;  
 RX MEDLINE-913091238; PubMed-1457809;  
 RA Maisonneuve P., Belluscio L., Conover J.C., Yancopoulos G.D.;  
 RT "Gene sequences of chicken BDNF and NT-3.";  
 RL DNA Seq. 3:49-54(1992).  
 RN [2]  
 RP SEQUENCE OF 127-240 FROM N.A.  
 RX MEDLINE-91309745; PubMed-1906813;  
 RA Jackson P.J., Townner M.D., Huntsman M.M.;  
 RT "Comparison of mammalian, chicken and Xenopus brain-derived  
 RT neurotrophic factor coding sequences.";  
 RL FEBS Lett. 285:260-264(1991).  
 RN [3]  
 RP SEQUENCE OF 184-226 FROM N.A.  
 RX MEDLINE-91222573; PubMed-2025430;  
 RA Hallboeek F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a novel  
 RT member abundantly expressed in Xenopus ovary.";  
 RL Neuron 6:845-858(1991).  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CC CONNECTED TO IT.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M83377; AAC42220.1; -;  
 DR EMBL: X61476; CAA43704.1; -;  
 DR HSSP: P23560; 188M.  
 DR InterPro: IPR002072; NCF.  
 DR Pfam: PF00243; NCF\_1.  
 DR PRINTS: PR00268; NCF.  
 DR ProDom: PD002052; NCF\_1.  
 DR SMART: SM00140; NCF\_1.  
 DR PROSITE: PS00248; NCF\_1; 1.  
 DR PROSITE: PS50270; NCF\_2; 1.  
 KW Growth factor; Signal.  
 FT NON\_TER 1 18  
 FT PROPEP 19 127  
 FT CHAIN 128 246  
 FT SITE 57 58  
 FT DISULFID 140 207  
 FT DISULFID 185 236  
 FT DISULFID 195 238  
 FT CARBOHYD 120 120  
 SO SEQUENCE 246 AA; 27714 MW; CE1D93BE9FDD3BA0 CRC64;  
 Query Match 92.6%; Score 592.5; DB 1; Length 246;  
 Best Local Similarity 93.3%; Pred. No. 1.5e-55;  
 Matches 111; Conservative 3; Mismatches 4; Indels 1; Gaps 1;  
 QY 2 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 61  
 DB 128 HSDPARRGELSYCDISISEMTAAADKRTAVMSGCTVYLEKVPVSGQLOKQFYETKCNP 187  
 QY 62 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCV-TLTIKGR 119  
 DB 188 MGYTKEGCGIDKRRHNSOCRTOSYVVALTMDSKRRIGRFRIDTSCVTLTIKGR 246  
 RESULT 13  
 BDNF\_CYPCA STANDARD: PRT: 270 AA.  
 AC Q90322;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS *Cyrtinus carpio* (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 RN NCBI\_TaxID=7962;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Liu T.S., Chang G.D., Huang F.L., Lo T.B.;  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE  
 ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CONNECTED TO IT (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: L27171; AAA49204.1; -  
 DR HSP: P23560; 188M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF. 1; 1.  
 DR PROSITE: PS00270; NGF\_2; 1.  
 DR Growth factor; Signal.  
 KM Growth factor; Signal.  
 FT PROPEP 1 18  
 FT CHAIN 152 270  
 FT DISULFID 164 231  
 FT DISULFID 209 260  
 FT DISULFID 219 262  
 FT CARBOHYD 144 144  
 SQ SEQUENCE 270 AA: 29572 MW: 049DEIECE64742EAA CRC64:  
 Query Match 90.5%; Score 579.5; DB 1; Length 270;  
 Best Local Similarity 90.8%; Pred. No. 4e-54;  
 Matches 108; Conservative 7; Mismatches 3; Indels 1; Gaps 1;  
 Oy 2 HSDPARRGELSVCDISISEWYTAADKTAADVMSGVTYVLEKVPVSKGOLKQYFETKCNP 61  
 DB 152 HSDPARRGELSVCDISISEWYTAADKTAADVMSGVTYVLEKVPVNGOLKQYFETKCNP 211  
 Oy 62 MGYTKEGCRGIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCV-TITIKRR 119  
 DB 212 LGYTKGCRGIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCVCTITIKRR 270  
 RESULT 14  
 BDNF\_XIPMA STANDARD: PRT: 269 AA.  
 ID BDNF\_XIPMA  
 AC Q02193;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS *Xiphophorus maculatus* (Southern platyfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.  
 RN NCBI\_TaxID=8083;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92333301; PubMed=1629719;  
 RA Gots R., Raulf F., Scharl M.;  
 RT "Brain-derived neurotrophic factor is more highly conserved in  
 structure and function than nerve growth factor during vertebrate  
 evolution".  
 RL J. Neurochem. 59:432-442(1992).  
 CC -1- FUNCTION: BDNF PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT  
 ARE ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY  
 CONNECTED TO IT.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: X59943; CAA42567.1; -  
 DR HSP: P23560; 188M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF. 1; 1.  
 DR PROSITE: PS00270; NGF\_2; 1.  
 DR Growth factor; Signal.  
 KM Growth factor; Signal.  
 FT PROPEP 1 18  
 FT CHAIN 151 269  
 FT DISULFID 163 230  
 FT DISULFID 208 259  
 FT DISULFID 218 261  
 FT CARBOHYD 143 143  
 SQ SEQUENCE 269 AA: 29709 MW: DA6774B7923E5E52 CRC64:  
 Query Match 89.1%; Score 570.5; DB 1; Length 269;  
 Best Local Similarity 89.1%; Pred. No. 3.5e-53;  
 Matches 106; Conservative 7; Mismatches 5; Indels 1; Gaps 1;  
 Oy 2 HSDPARRGELSVCDISISEWYTAADKTAADVMSGVTYVLEKVPVSKGOLKQYFETKCNP 61  
 DB 151 HSDPARRGELSVCDISISEWYTAADKTAADVMSGVTYVLEKVPVNGOLKQYFETKCNP 210  
 Oy 62 MGYTKEGCRGIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCV-TITIKRR 119  
 DB 211 MGYTKEGCRGIDKRRHNSOCTTOSYVRALTNDSKKRIGRRIRIDTSCVCTITIKRR 269  
 RESULT 15  
 BDNF\_XENLA STANDARD: PRT: 114 AA.  
 ID BDNF\_XENLA  
 AC P23432;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Brain-derived neurotrophic factor (BDNF) (Fragment).  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 RN NCBI\_TaxID=8355;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91309745; PubMed=1906813;  
 RA Isackson P.J., Towne M.D., Huntsman M.M.;

```

RT      *Comparison of mammalian, chicken and Xenopus brain-derived
RT      neurotrophic factor coding sequences.*;
RL      FEBS Lett. 285:260-264(1991).
RN      [2]
RP      SEQUENCE OF 58-100 FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE-91222573: Pubmed-2025430:
RA      Halboeck F., Ibanez C.F., Persson H.;
RT      *Evolutionary studies of the nerve growth factor family reveal a
RT      novel member abundantly expressed in Xenopus ovary.*;
RL      Neuron 6:845-858(1991).
CC      -1- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC      ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC      CONNECTED TO IT.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: X61477; CAA43705.1; -.
DR      HSSP: P23560; 1BND.
DR      InterPro: IPR002072; NGF.
DR      Pfam: PF00243; NGF; 1.
DR      ProDom: PD002052; NGF; 1.
DR      SMART: SM00140; NGF; 1.
DR      PROSITE: PS00248; NGF_1; 1.
DR      PROSITE: PS50270; NGF_2; 1.
KW      Growth factor.
FT      NON_TER 1
FT      DISULFID 14
FT      DISULFID 59
FT      DISULFID 110
FT      DISULFID 112
FT      CONFLICT 69
FT      CONFLICT 73
FT      CONFLICT 96
FT      CONFLICT 96
FT      NON_TER 114
FT      NON_TER 114
SQ      SEQUENCE 114 AA; 13031 MW; 409ACFB5B8EA887 CRC64;

Query Match      87.3% Score 559; DB 1; Length 114;
Best Local Similarity 92.7% Pred. No. 2.3e-52;
Matches 102; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 HSDPARGELSYCDISISKMTAADKKTAVDMSGCTVLEKVPVSKGLKQYFETKCNP 61
QY      |||||
DB      2 HSDPARGELSYCDISISKMTAAANKTAVDMSGATVLEKVPVSKGLKQYFETKCNP 61
DB      |||||
QY      62 MGTKEGCGIKGRHNSOCRTTOSYVALTMDSKKRIGNRFIRIDTSCV 111
QY      |||||
DB      62 MGTMEGCGIEKIRYNSOCRTTOSYVALFTMDSKKRIGNRFIRIDTSCV 111
DB      |||||

```

Search completed: December 2, 2002, 15:12:43  
 Job time : 4.88277 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 : Search time 18.415 seconds  
(without alignments)  
1331.501 Million cell updates/sec

Title: US-10-072-681-4

Perfect score: 640  
Sequence: 1 PHSDPARRGELSYCDISEM.....GNRFRIDTSCVLTIRKGR 119

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_PROTOZOA:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_CHEAP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	97.3	153	11 09CYL3	09CYL3 mus musculus
2	622.5	97.3	247	6 097759	097759 allurus ful
3	622.5	97.3	249	11 08VH4	08VH4 mus musculus
4	592.5	92.6	177	13 091812	091812 poephilla gu
5	578.5	90.4	246	13 080G75	080G75 pharynoceph
6	574.5	89.8	246	13 080G76	080G76 japalura sp
7	572.5	89.5	270	13 09YH42	09YH42 brechydano
8	562.5	87.9	246	13 080G74	080G74 cyclophilops
9	552.5	86.3	247	13 080G77	080G77 tylosotritio
10	544	85.0	101	6 097T22	097T22 macaca fusc
11	448	70.0	85	6 002792	002792 notoryctes
12	445	69.5	85	6 013114	013114 isodon mac
13	445	69.5	85	6 013122	013122 tarsipes ro
14	445	69.5	85	6 002795	002795 ornithorhyn
15	445	69.5	85	6 002798	002798 petaurus br
16	445	69.5	85	6 013104	013104 cercartetus

17	445	69.5	85	6 013105	013105 dasyuroides
18	445	69.5	85	6 002801	002801 tachylosau
19	444	69.4	85	6 002803	002803 trichosaurus
20	437	68.3	85	6 002790	002790 macropus fu
21	369	57.7	184	6 09BFJ5	09BFJ5 capia mmo
22	369	57.7	185	6 09BFK5	09BFK5 talpa alai
23	369	57.7	185	6 09BFK5	09BFK5 condylura c
24	369	57.7	186	6 09BFJ3	09BFJ3 choleopus h
25	369	57.7	186	6 09BFJ2	09BFJ2 choleopus d
26	369	57.7	186	6 09BFK3	09BFK3 tamandua te
27	369	57.7	186	6 09BFK8	09BFK8 myrmecophag
28	369	57.7	186	6 09BFK4	09BFK4 sorax arane
29	369	57.7	186	6 09BFK2	09BFK2 lorodonta a
30	369	57.7	186	6 09BFK1	09BFK1 oxyceropus
31	369	57.7	186	6 09BFJ9	09BFJ9 oxyceropus
32	369	57.7	186	6 09BFJ8	09BFJ8 sylviag
33	369	57.7	186	6 09BFJ7	09BFJ7 ochotona hy
34	369	57.7	186	6 09BFJ4	09BFJ4 lemur catla
35	369	57.7	186	6 09BFJ1	09BFJ1 macaca mula
36	369	57.7	186	6 09BFJ2	09BFJ2 hylobates c
37	369	57.7	186	6 09BFJ9	09BFJ9 artibeus ja
38	369	57.7	186	6 09BFJ8	09BFJ8 pteropus gl
39	369	57.7	186	6 09BFJ7	09BFJ7 rousettus ch
40	369	57.7	186	6 09BFJ6	09BFJ6 nycterus ch
41	369	57.7	186	6 09BFJ5	09BFJ5 lama glama
42	369	57.7	186	6 09BFH8	09BFH8 equus cabal
43	369	57.7	186	6 09BFH7	09BFH7 ceratotheri
44	369	57.7	186	6 09BFH6	09BFH6 caprius ind
45	369	57.7	186	6 09BFH5	09BFH5 felis alive

## ALIGNMENTS

RESULT 1  
09CYL3 PRELIMINARY: PRT: 153 AA.  
ID 09CYL3;  
AC 09CYL3;  
DT 01-JUN-2001 (TRMBLrel. 17, Created)  
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)  
DE Brain derived neurotrophic factor.  
GN BDNF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBryo;  
RX MEDLINE=21085660; Pubmed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia K.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schiml L.H., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boftelli D., Bojunga N., Carlini P., de Bonaldo M.F.,  
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Komdeur P.,  
RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto M.,  
RA Sasaki H., Sato K., Schoedon C., Seta T., Shibata Y., Storch K.F.,  
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitlaker C., Wilmig L.,  
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.,  
\*Functional annotation of a full-length mouse cDNA collection.\*;  
RT Nature 409:685-690(2001).  
DR EMBL: AK017559; BAB30805.1; -.  
HSSP: P23560; 188M.



QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIRGR 119  
Db 119 KGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCVTLTIRGR 177

## RESULT 5

ID 080G75 PRELIMINARY; PRT; 246 AA.  
AC 080G75;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DE Brain derived neurotrophic factor.  
GN BDNF.  
OS Phrynocephalus hongyuanensis.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Agamidae;  
OC Phrynocephalus.  
OX NCBI\_Taxid=171648;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cao M., Yang Y.H., Zhang Y.Z.;  
RT "Molecular cloning of brain derived neurotrophic factor gene from  
RT amphibians and reptiles and its application in the research of  
RT phylogeny and taxonomy."  
RU Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF497714.1; -  
FT CHAIN 128 246 BRAIN DERIVED NEUROTROPHIC FACTOR  
FT PRECURSOR.  
SQ SEQUENCE 246 AA; 27792 MW; 7709D3058B7AFA30 CRC64;

Query Match Best Local Similarity 90.4%; Score 578.5; DB 13; Length 246;  
Matches 109; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVDSISEVWTAADKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 61  
Db 128 HSDPARRGELSYVDSISEVWTAADKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 187  
QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIRGR 119  
Db 188 KGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCVTLTIRGR 246

## RESULT 6

ID 080G76 PRELIMINARY; PRT; 246 AA.  
AC 080G76;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DE Brain derived neurotrophic factor.  
GN BDNF.  
OS Japalura splendida.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconidae;  
OC Japalura.  
OX NCBI\_Taxid=118209;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cao M., Yang Y.H., Zhang Y.Z.;  
RT "Molecular cloning of brain derived neurotrophic factor gene from  
RT amphibians and reptiles and its application in the research of  
RT phylogeny and taxonomy."  
RU Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF497713.1; -  
FT CHAIN 128 246 BRAIN DERIVED NEUROTROPHIC FACTOR  
FT PRECURSOR.  
SQ SEQUENCE 246 AA; 27883 MW; 47B1A03DA88EF78 CRC64;

Query Match Best Local Similarity 89.8%; Score 574.5; DB 13; Length 246;  
Matches 109; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Matches 108; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVDSISEVWTAADKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 61  
Db 128 HSDPARRGELSYVDSISEVWTAADKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 187  
QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIRGR 119  
Db 188 KGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCVTLTIRGR 246

## RESULT 7

ID 09YH42 PRELIMINARY; PRT; 270 AA.  
AC 09YH42;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE Brain-derived neurotrophic factor.  
GN BDNF.  
OS Brachydanio rerio (zebrafish) (zebra danio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_Taxid=9955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hashimoto M., Heinrich G.;  
RU Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U42489; AAD00016.1; -  
DR HSSP: P23560; 188W.  
DR ZFIN: ZDB-GENE-000412-1; bdnf.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF; 1.  
DR PRINTS: PR00268; NGF; 1.  
DR ProDom: PD002052; NGF; 1.  
DR SMART: SM00140; NGF; 1.  
DR PROSITE: PS00248; NGF\_1; 1.  
DR PROSITE: PS00270; NGF\_2; 1.  
SQ SEQUENCE 270 AA; 29482 MW; 6BF136101BAE45C0 CRC64;

Query Match Best Local Similarity 89.5%; Score 572.5; DB 13; Length 270;  
Matches 107; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYVDSISEVWTAADKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 61  
Db 152 HSDPARRGELSYVDSISEVWTAADKTAVDMSGGTVLEKVPVSKQLQYFETKCNP 211  
QY 62 MGYTKEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCV-TLTIRGR 119  
Db 212 LGYTKGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGRFIRIDTSCVTLTIRGR 270

## RESULT 8

ID 080G74 PRELIMINARY; PRT; 246 AA.  
AC 080G74;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DE Brain derived neurotrophic factor.  
GN BDNF.  
OS Cyclophiops major.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;  
OC Colubridae; Colubridae; Cyclophiops.  
OX NCBI\_Taxid=192173;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cao M., Yang Y.H., Zhang Y.Z.;  
RT "Molecular cloning of brain derived neurotrophic factor gene from  
RT amphibians and reptiles and its application in the research of

Query Match Best Local Similarity 89.8%; Score 574.5; DB 13; Length 246;  
Matches 109; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

```

RT phylogeny and taxonomy."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AF497715; AAA18716.1;
FT CHAIN 128 246 BRAIN DERIVED NEUROTROPHIC FACTOR
FT SEQUENCE 246 AA; 27773 MW; BA0178034937856 CRC64;
SQ
Query Match
Best Local Similarity 89.1%; Pred. No. 1.5e-55;
Matches 106; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

OY 2 HSDPARGLSVCDSTSEMTADKKTAVDMSGGTVLEKVPVSKGLKQYFETKCNP 61
DB 128 HSDPARGLSVCDSTSEMTADKKTAVDMSGGTVLEKVPVSKGLKQYFETKCNP 187
OY 62 MGTYKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGMRFIRIDTSCV-TLTIKGR 119
DB 188 KGAKKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGMRFIRIDTSCVCTLTIKGR 246

RESULT 9
OY 080G77 PRELIMINARY; PRT: 247 AA.
AC 080G77;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
OS Tylosorion tallangensis.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC Tylosorion.
OX NCBI_TaxID=129885;
RN 11
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Cloning and sequence analysis of brain derived neurotrophic factor
RT (BDNF) gene from Sichuan Newt (Tylosorion tallangensis).";
RL Ying Yung Yu Huan Ching Sheng Wu Hsueh Pao 8:0-0(2002).
DR EMBL: AF497712; AAA18076.1;
SQ SEQUENCE 247 AA; 27841 MW; FFCB5F28A7620DE0 CRC64;

Query Match
Best Local Similarity 86.3%; Score 552.5; DB 13; Length 247;
Matches 105; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

OY 2 HSDPARGLSVCDSTSEMTADKKTAVDMSGGTVLEKVPVSKGLKQYFETKCNP 61
DB 129 HSDPARGLSVCDSTSEMTADKKTAVDMSGGTVLEKVPVSKGLKQYFETKCNP 188
OY 62 MGTYKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGMRFIRIDTSCV-TLTIKGR 119
DB 189 MGTYKCGRCIGIDKRHMNSOCRTQSYVALTMDSKKRIGMRFIRIDTSCVCTLTIKGR 247

RESULT 10
OY 09TT22 PRELIMINARY; PRT: 101 AA.
AC 09TT22;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
OS Macaca fasciata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN 11
RP SEQUENCE FROM N.A.
RA Hashimoto T., Okuno H., Tokuyama W., Li Y.-X., Miyashita Y.;

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RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
RT their receptor messenger RNAs in monkey rhinal cortex.";
RL Neuroscience 0:0-0(1999).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE=99270338; PubMed=10340513;
RA Okuno H., Tokuyama W., Li Y.-X., Hashimoto T., Miyashita Y.;
RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
RT visual and limbic areas along the occipito-temporo-hippocampal pathway
RT in adult macaque monkeys.";
RL J. Comp. Neurol. 408:378-398(1999).
DR EMBL: AF208982; AAF24762.1;
DR HSSP: P23560; 1BND.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF. 1.
DR PROSITE: PS50270; NGF. 2. 1.
FT NON_TER 1 101
FT SEQUENCE 101 AA; 11476 MW; D6A568D497961740 CRC64;

Query Match
Best Local Similarity 85.0%; Score 544; DB 6; Length 101;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 LSVCDSEMTADKKTAVDMSGGTVLEKVPVSKGLKQYFETKCNPMGYTKGCR 70
DB 1 LSVCDSEMTADKKTAVDMSGGTVLEKVPVSKGLKQYFETKCNPMGYTKGCR 60
OY 71 GIDKRHMNSOCRTQSYVALTMDSKKRIGMRFIRIDTSCV 111
DB 61 GIDKRHMNSOCRTQSYVALTMDSKKRIGMRFIRIDTSCV 101

RESULT 11
OY 002792 PRELIMINARY; PRT: 85 AA.
AC 002792;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
OS Notoryctes typhlops (Marasipal mole).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Notoryctemorphia; Notoryctidae; Notoryctes.
OX NCBI_TaxID=37699;
RN 11
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBSJ databases.
DR EMBL: U93380; AAB5685.1;
DR HSSP: P23560; 1BND.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF. 1.
DR PROSITE: PS50270; NGF. 2. 1.
FT NON_TER 1 85
FT SEQUENCE 85 AA; 9577 MW; 33754EA015314661 CRC64;

Query Match
Best Local Similarity 97.6%; Score 448; DB 6; Length 85;
Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKRRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKRRIG 85

RESULT 12
OY 013114 PRELIMINARY: PRT: 85 AA.
AC 013114:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Isodon macrurus (Short-nosed bandicoot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Peramelomorpha; Peramelidae; Isodon.
OX NCBI_TaxID=37698;
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U93374; AAB58679.1; -.
DR HSSP: P23560; 1BND.
DR InterPro: IPR02072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT MON_TER 1
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 69.5% Score 445; DB 6; Length 85;
Best Local Similarity 96.5% Pred. No. 8.4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKRRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKRRIG 85

RESULT 13
OY 013122 PRELIMINARY: PRT: 85 AA.
AC 013122:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Tarapetes rostratus (honey possum).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Tarsipedidae; Tarsipes.
OX NCBI_TaxID=38632;
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
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RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U93375; AAB58680.1; -.
DR HSSP: P23560; 1BND.
DR InterPro: IPR02072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT MON_TER 1
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 69.5% Score 445; DB 6; Length 85;
Best Local Similarity 96.5% Pred. No. 8.4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKRRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKRRIG 85

RESULT 14
OY 002795 PRELIMINARY: PRT: 85 AA.
AC 002795:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT Monotremes and Marsupials.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U93376; AAB58681.1; -.
DR HSSP: P23560; 1BND.
DR InterPro: IPR02072; NGF.
DR Pfam: PF00243; NGF. 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF. 1.
DR SMART: SM00140; NGF. 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
FT NON_TER 1
FT MON_TER 1
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 69.5% Score 445; DB 6; Length 85;
Best Local Similarity 96.5% Pred. No. 8.4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 16 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 75
DB 1 SISEWTAADKKTAVDMSGGTIVLEKVPVSKGOLKQYFETKCNPMGYTKKCGCRIDKR 60
OY 76 HNSOCCRTTOSYVRALTMDSKRRIG 100
DB 61 HNSOCCRTTOSYVRALTMDSKRRIG 85

RESULT 15
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002798
ID 002798      PRELIMINARY:      PRT:      85 AA.
AC 002798:
DT 01-JUL-1997 (TRENBLREL. 04, Created)
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Brain-derived neurotrophic factor (Fragment).
GN BDNF.
OS Petrusus breviceps (Australian sugar gilder).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Petauridae; Petrusus.
OX NCBJ_TaxID=34899;
RN (1)
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RT "Molecular phylogeny and evolution of the neurotrophins from
RT monotremes and marsupials."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93377; AAB58682.1; -.
DR HSSP; P23560; 1BND.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS0270; NGF_2; 1.
FT NON_TER      1
FT NON_TER      85
SQ SEQUENCE      85 AA; 9604 MW; 33754EA01520B661 CRC64;

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Query Match      59.58; Score 445; DB 6; Length 85;
Best Local Similarity 96.58; Pred. No. 8,4e-43;
Matches 82; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 16 SISENTAADKKTAVDMSCGTVLEKVPVSKGOLKQFYETKCNPMGYTKESCRGIDKR 75
Db 1 SISENTAADKKTAVDMSCGTVLEKVPVSKGOLKQFYETKCNPMGYTKESCRGIDKR 60
OY 76 HNSOCRTOSYVRALTMDSKRRIG 100
Db 61 HNSOCRTOSYVRALTMDSKRRIG 85

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Search completed: December 2, 2002, 15:12:02  
 Job time : 19.415 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 8.23095 Seconds  
(without alignments) 425.386 Million cell updates/sec

Title: US-10-072-681-4

Sequence: 1 PHSDPARRCGLSVCSISEM.....GWRFRIDSCVTLLTKRGR 119

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	100.0	119	4	US-09-675-503-4
2	633	98.9	118	3	US-08-970-865-4
3	633	98.9	118	3	US-08-581-662-3
4	633	98.9	118	4	US-09-363-573-4
5	633	98.9	118	4	US-09-664-295-3
6	622.5	97.3	119	1	US-08-440-048-4
7	622.5	97.3	119	2	US-08-441-513A-4
8	622.5	97.3	119	5	PCT-US95-06918-4
9	622.5	97.3	119	2	US-08-502-348-1
10	622.5	97.3	120	4	US-09-214-214A-8
11	622.5	97.3	120	4	US-08-451-947-3
12	622.5	97.3	247	2	US-08-424-826A-3
13	622.5	97.3	247	2	US-08-595-043A-77
14	622.5	97.3	247	5	US-08-928-694-3
15	622.5	97.3	247	5	PCT-US91-06950-3
16	622.5	97.3	257	4	US-09-636-368-8
17	622.5	97.3	270	4	US-09-636-368-7
18	622.5	97.3	271	4	US-09-636-368-10
19	619.5	96.8	247	5	US-08-466-080B-3
20	619.5	96.8	247	5	PCT-US95-05423-3
21	614.5	96.0	119	1	US-07-979-630-2
22	614.5	96.0	119	1	US-08-340-131-1
23	614.5	96.0	119	5	PCT-US93-11292-2
24	610.5	95.4	120	1	US-08-340-131-2
25	605.5	94.6	274	4	US-09-636-368-9
26	598.5	93.5	120	4	US-09-214-214A-9
27	596.5	93.2	120	4	US-09-214-214A-10

28	346	54.1	120	4	US-09-675-503-5	Sequence 5, Appl1
29	345.5	54.0	119	3	US-08-970-865-5	Sequence 5, Appl1
30	345.5	54.0	119	3	US-08-581-662-2	Sequence 2, Appl1
31	345.5	54.0	119	4	US-09-363-573-5	Sequence 5, Appl1
32	345.5	54.0	119	4	US-09-664-295-2	Sequence 2, Appl1
33	344.5	53.8	119	1	US-07-979-630-3	Sequence 3, Appl1
34	344.5	53.8	119	1	US-08-440-049-2	Sequence 2, Appl1
35	344.5	53.8	119	1	US-08-340-131-3	Sequence 3, Appl1
36	344.5	53.8	119	3	US-08-441-513A-2	Sequence 2, Appl1
37	344.5	53.8	119	3	US-08-910-691-2	Sequence 12, Appl1
38	344.5	53.8	119	4	US-08-845-541B-2	Sequence 2, Appl1
39	344.5	53.8	119	4	US-09-066-065A-2	Sequence 2, Appl1
40	344.5	53.8	119	5	PCT-US93-11292-3	Sequence 2, Appl1
41	344.5	53.8	119	5	PCT-US95-06918-2	Sequence 3, Appl1
42	344.5	53.8	119	5	PCT-US95-06918-5	Sequence 2, Appl1
43	344.5	53.8	120	1	US-08-340-131-4	Sequence 5, Appl1
44	344.5	53.8	120	3	US-08-581-662-32	Sequence 32, Appl1
45	344.5	53.8	120	4	US-09-214-214A-1	Sequence 1, Appl1

## ALIGNMENTS

```

RESULT 1
US-09-675-503-4
; Sequence 4, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmeizer, Charles H.
; APPLICANT: Beck, Joanne T.
; TITLE OF INVENTION: ISOLATION OF NEUTROPHILS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUTROPHIL VARIANTS
; FILE REFERENCE: GENE 037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-675-503-4

Query Match
Best Local Similarity 100.0%; Score 640; DB 4; Length 119;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PHSDPARRCGLSVCSISEMTADKKTAVDMSCGYTVLEKVPKSGOLKQYFETKCN 60
DB 1 PHSDPARRCGLSVCSISEMTADKKTAVDMSCGYTVLEKVPKSGOLKQYFETKCN 60
QY 61 PKGYREGCGIDKGRHNSOCRTTOSYVRALTNDSKKRIGMFRIRIDTSCVTLTKRGR 119
DB 61 PKGYREGCGIDKGRHNSOCRTTOSYVRALTNDSKKRIGMFRIRIDTSCVTLTKRGR 119

RESULT 2
US-08-970-865-4
; Sequence 4, Application US/08970865
; Patent No. 6005081
; GENERAL INFORMATION:
; APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck
; TITLE OF INVENTION: Purification of NGF

```

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipath (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,865  
FILING DATE: 14-NO. 6005081-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030838  
FILING DATE: 11/15/1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1063R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-970-865-4

Query Match 98.9%: Score 633: DB 3: Length 118:  
Best Local Similarity 100.0%: Pred. No. 4.9e-64:  
Matches 118: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 61  
DB 1 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 60

QY 62 MGYTREGCGRIDKRHMNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITKRG 119  
DB 61 MGYTREGCGRIDKRHMNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITKRG 118

RESULT 3  
US-08-581-662-3  
Sequence 3, Application US/08581662  
Patent No. 6121235  
GENERAL INFORMATION:  
APPLICANT: Gao, Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments  
FILE REFERENCE: P0981  
CURRENT APPLICATION NUMBER: US/08/581,662  
CURRENT FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 36  
SEQ ID NO 3  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-581-662-3

Query Match 98.9%: Score 633: DB 3: Length 118:  
Best Local Similarity 100.0%: Pred. No. 4.9e-64:  
Matches 118: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 61  
DB 1 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 60

DB 1 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 60  
QY 62 MGYTREGCGRIDKRHMNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITKRG 119  
DB 61 MGYTREGCGRIDKRHMNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITKRG 118

RESULT 4  
US-09-363-573-4  
Sequence 4, Application US/09363573  
Patent No. 6184360  
GENERAL INFORMATION:  
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck  
TITLE OF INVENTION: Purification of MGF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipath (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,573  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,865  
FILING DATE: 14-NO. 6184360-1997  
APPLICATION NUMBER: 60/030838  
FILING DATE: 11/15/1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1063R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-363-573-4

Query Match 98.9%: Score 633: DB 4: Length 118:  
Best Local Similarity 100.0%: Pred. No. 4.9e-64:  
Matches 118: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 61  
DB 1 HSDPARGELSYCDISISEWYTAADKRTAVDMSCGTVLEKVPVSKQLKQYFETKCNP 60

QY 62 MGYTREGCGRIDKRHMNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITKRG 119  
DB 61 MGYTREGCGRIDKRHMNSCCTTOSYVRLTMDSKKRIGRFIRIDTSCVLTITKRG 118

RESULT 5  
US-09-664-295-3  
Sequence 3, Application US/09664295  
Patent No. 6429196  
GENERAL INFORMATION:  
APPLICANT: Gao, Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments

FILE REFERENCE: GENENT 051C1  
CURRENT APPLICATION NUMBER: US/09/664,295  
CURRENT FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 08/581,662  
PRIOR FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 37  
SEQ ID NO 3  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-664-295-3

Query Match 98.9%; Score 633; DB 4; Length 118;  
Best Local Similarity 100.0%; Pred. No. 4.9e-64;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARGLSVCDISSEMTAADKKTAVDMSGGTVYLEKVPVSKGOLKOFYETKCNP 61  
DB 1 HSDPARGLSVCDISSEMTAADKKTAVDMSGGTVYLEKVPVSKGOLKOFYETKCNP 60  
QY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGMRFIRIDTSCVTLTIKRG 119  
DB 61 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGMRFIRIDTSCVTLTIKRG 118

## RESULT 6

US-08-440-049-4  
Sequence 4, Application US/08440049  
Patent No. 5728803  
GENERAL INFORMATION:  
APPLICANT: Ufer, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winshaw, John W.  
TITLE OF INVENTION: PANTROPIC NEUTROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,049  
FILING DATE: 12-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-440-049-4

Query Match 97.3%; Score 622.5; DB 1; Length 119;  
Best Local Similarity 99.2%; Pred. No. 7.6e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARGLSVCDISSEMTAADKKTAVDMSGGTVYLEKVPVSKGOLKOFYETKCNP 61  
DB 1 HSDPARGLSVCDISSEMTAADKKTAVDMSGGTVYLEKVPVSKGOLKOFYETKCNP 60  
QY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGMRFIRIDTSCVTLTIKRG 119  
DB 61 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGMRFIRIDTSCVTLTIKRG 119

## RESULT 7

US-08-441-513A-4  
Sequence 4, Application US/08441513A  
Patent No. 5981480  
GENERAL INFORMATION:  
APPLICANT: Ufer, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winshaw, John W.  
TITLE OF INVENTION: PANTROPIC NEUTROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,513A  
FILING DATE: 15-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-441-513A-4

Query Match 97.3%; Score 622.5; DB 2; Length 119;  
Best Local Similarity 99.2%; Pred. No. 7.6e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARGLSVCDISSEMTAADKKTAVDMSGGTVYLEKVPVSKGOLKOFYETKCNP 61  
DB 1 HSDPARGLSVCDISSEMTAADKKTAVDMSGGTVYLEKVPVSKGOLKOFYETKCNP 60  
QY 62 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGMRFIRIDTSCVTLTIKRG 119  
DB 61 MGYTEGCGIDKRRHNSOCRTTOSYVRALTMDSKKRIGMRFIRIDTSCVTLTIKRG 119

## RESULT 8

PCT-US95-06918-4  
Sequence 4, Application PC/TUS9506918  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: PANTROPIC NEUTROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06918  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchio, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 505PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US95-06918-4

Query Match 97.3%; Score 622.5; DB 5; Length 119;  
Best Local Similarity 99.2%; Pred. No. 7.6e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVTVLEKVPVSKGLKQYETKCNP 61  
DB 1 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVTVLEKVPVSKGLKQYETKCNP 60  
QY 62 MGYTKESGCRGIDKRHNMSQCRRTOSYVRALTMDSKKRIGMFRIDTSCV-TLTIKGR 119  
DB 61 MGYTKESGCRGIDKRHNMSQCRRTOSYVRALTMDSKKRIGMFRIDTSCVCTLIKGR 119

RESULT 9  
US-08-502-348-1  
Sequence 1, Application US/08502348  
Patent No. 5830857  
GENERAL INFORMATION:  
APPLICANT: Carnahan, Josette F  
APPLICANT: Depaulis, Antoine  
APPLICANT: Faltz, Paul  
APPLICANT: Larnet, Yves  
APPLICANT: Marescaux, Christian  
APPLICANT: Nawa, Hiroyuki  
TITLE OF INVENTION: METHOD OF TREATING EPILEPSY  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: US  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/502,348

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mazza, Richard J.  
REFERENCE/DOCKET NUMBER: A-348  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-502-348-1

Query Match 97.3%; Score 622.5; DB 2; Length 120;  
Best Local Similarity 99.2%; Pred. No. 7.7e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVTVLEKVPVSKGLKQYETKCNP 61  
DB 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVTVLEKVPVSKGLKQYETKCNP 61  
QY 62 MGYTKESGCRGIDKRHNMSQCRRTOSYVRALTMDSKKRIGMFRIDTSCV-TLTIKGR 119  
DB 62 MGYTKESGCRGIDKRHNMSQCRRTOSYVRALTMDSKKRIGMFRIDTSCVCTLIKGR 120

RESULT 10  
US-09-214-214A-8  
Sequence 8, Application US/09214214A  
Patent No. 6211150  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen N.  
APPLICANT: Herdenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411A US Revised 073100  
CURRENT APPLICATION NUMBER: US/09/214,214A  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: PCT/US97/12609  
PRIOR FILING DATE: 1997-07-17  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Human  
US-09-214-214A-8

Query Match 97.3%; Score 622.5; DB 4; Length 120;  
Best Local Similarity 99.2%; Pred. No. 7.7e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVTVLEKVPVSKGLKQYETKCNP 61  
DB 2 HSDPARRGELSVCDISSEMTADKKTAVDMGSGTVTVLEKVPVSKGLKQYETKCNP 61  
QY 62 MGYTKESGCRGIDKRHNMSQCRRTOSYVRALTMDSKKRIGMFRIDTSCV-TLTIKGR 119  
DB 62 MGYTKESGCRGIDKRHNMSQCRRTOSYVRALTMDSKKRIGMFRIDTSCVCTLIKGR 120

RESULT 11  
US-08-451-947-3  
Sequence 3, Application US/08451947  
Patent No. 5702906  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPIC FACTOR

NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,947  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-947-3

Query Match 97.3% Score 622.5; DB 1; Length 247;  
Best Local Similarity 99.2% Pred. No. 1.9e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISSEKVTAAADKRTAVDMSGGTVLEKVPVSKGLKQYETKCNP 61  
|||||  
DB 129 HSDPARRGELSYCDISSEKVTAAADKRTAVDMSGGTVLEKVPVSKGLKQYETKCNP 168  
|||||  
QY 62 MGYTEGCGRGIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCV-TLTIRGR 119  
|||||  
DB 189 MGYTEGCGRGIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCVTLTIRGR 247  
|||||

RESULT 12  
US-08-424-826A-3  
Sequence 3, Application US/08424826A  
Patent No. 5830858  
GENERAL INFORMATION:  
APPLICANT: Rosenthal, Arnon  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,826A  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240387  
FILING DATE: 10-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0666PIC2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-424-826A-3

Query Match 97.3% Score 622.5; DB 2; Length 247;  
Best Local Similarity 99.2% Pred. No. 1.9e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 HSDPARRGELSYCDISSEKVTAAADKRTAVDMSGGTVLEKVPVSKGLKQYETKCNP 61  
|||||  
DB 129 HSDPARRGELSYCDISSEKVTAAADKRTAVDMSGGTVLEKVPVSKGLKQYETKCNP 188  
|||||  
QY 62 MGYTEGCGRGIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCV-TLTIRGR 119  
|||||  
DB 189 MGYTEGCGRGIDKRRHNSCRRTOGYVRLALTMDSKKRIGRFRIRIDTSCVTLTIRGR 247  
|||||

RESULT 13  
US-08-595-043A-77  
Sequence 77, Application US/08595043A  
Patent No. 5935824  
GENERAL INFORMATION:  
APPLICANT: SCARLATO, GREGORY D.  
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/595,043A  
FILING DATE: 31-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: SGAR-00371

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-928-694-77

Query Match 97.3% Score 622.5; DB 2; Length 247;  
Best Local Similarity 99.2% Pred. No. 1.9e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 129 HSDPARRGELSYCDISISEMTVAADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 61  
OY 62 MGYTEGCGRIDKRRHNSCCTTOSYVRLTMDSKRRIGRFRIRIDTSCV-TLTIKRR 119  
DB 189 MGYTEGCGRIDKRRHNSCCTTOSYVRLTMDSKRRIGRFRIRIDTSCVTLTIKRR 247

RESULT 14  
US-08-928-694-3  
Sequence 3, Application US/08928694  
Patent No. 6037320  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPalm (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,694  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/451947  
FILING DATE: 26-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P06662C2D2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids

TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-928-694-3

Query Match 97.3% Score 622.5; DB 3; Length 247;  
Best Local Similarity 99.2% Pred. No. 1.9e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 129 HSDPARRGELSYCDISISEMTVAADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 61  
OY 62 MGYTEGCGRIDKRRHNSCCTTOSYVRLTMDSKRRIGRFRIRIDTSCV-TLTIKRR 119  
DB 189 MGYTEGCGRIDKRRHNSCCTTOSYVRLTMDSKRRIGRFRIRIDTSCVTLTIKRR 247

RESULT 15  
PCT-US91-06950-3  
Sequence 3, Application PC/TUS9106950  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06950  
FILING DATE: 19910924  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
ATTORNEY/AGENT INFORMATION:  
NAME: Hensley, Max D.  
REGISTRATION NUMBER: 27,043  
REFERENCE/DOCKET NUMBER: 666P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US91-06950-3

Query Match 97.3% Score 622.5; DB 5; Length 247;  
Best Local Similarity 99.2% Pred. No. 1.9e-62;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 129 HSDPARRGELSYCDISISEMTVAADKKTAVDMSCGTVTLEKVPVSKGOLKQYFETKCNP 61  
OY 62 MGYTEGCGRIDKRRHNSCCTTOSYVRLTMDSKRRIGRFRIRIDTSCV-TLTIKRR 119  
DB 189 MGYTEGCGRIDKRRHNSCCTTOSYVRLTMDSKRRIGRFRIRIDTSCVTLTIKRR 247

Mon Dec 2 15:36:38 2002

us-10-072-681-4.rai

Page 7

Search completed: December 2, 2002, 15:09:43  
Job time : 8.23095 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 4.18523 Seconds

(Without alignments)  
452.778 Million cell updates/sec

Title: US-10-072-681-4

Perfect score: 640

Sequence: 1 PHSDPARRGELSVCSISBWM.....GWRFRIRDTSCVLTIRKGR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEM\_PUB pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB pep:\*

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13: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	100.0	119	12	US-10-072-681-4
2	622.5	97.3	120	10	US-09-745-600-8
3	622.5	97.3	120	10	US-09-742-600-8
4	622.5	97.3	247	8	US-08-450-842-3
5	598.5	93.5	120	10	US-09-745-032-9
6	598.5	93.5	120	10	US-09-742-600-8
7	596.5	93.2	120	10	US-09-745-032-10
8	586.5	93.2	120	10	US-09-742-600-10
9	589.5	92.1	120	9	US-09-848-664-22
10	385	60.2	72	10	US-10-072-681-5
11	346	54.1	120	12	US-09-745-032-1
12	344.5	53.8	120	10	US-09-742-600-1
13	344.5	53.8	120	10	US-09-742-600-1
14	344.5	53.8	257	8	US-08-450-842-4
15	340.5	53.2	119	10	US-09-745-032-6
16	340.5	53.2	119	10	US-09-742-600-6
17	340.5	53.2	119	10	US-09-742-600-6
18	340.5	53.2	120	10	US-09-745-032-3
19	340.5	53.2	120	10	US-09-745-032-3

20	340.5	53.2	120	10	US-09-742-600-3	Sequence 3, Appl1
21	340.5	53.2	120	10	US-09-872-090-3	Sequence 3, Appl1
22	338.5	52.9	130	8	US-08-450-842-47	Sequence 47, Appl1
23	338.5	52.9	132	8	US-08-450-842-51	Sequence 51, Appl1
24	336	52.5	117	10	US-09-745-032-7	Sequence 7, Appl1
25	336	52.5	117	10	US-09-742-600-7	Sequence 7, Appl1
26	336	52.5	117	10	US-09-872-090-7	Sequence 7, Appl1
27	336	52.5	118	10	US-09-745-032-5	Sequence 5, Appl1
28	336	52.5	118	10	US-09-872-090-5	Sequence 5, Appl1
29	336	52.5	118	10	US-09-872-090-5	Sequence 5, Appl1
30	335.5	52.4	130	8	US-08-450-842-23	Sequence 23, Appl1
31	334	52.2	120	9	US-09-813-398-11	Sequence 11, Appl1
32	332.5	52.0	130	8	US-08-450-842-22	Sequence 22, Appl1
33	332.5	52.0	131	9	US-09-813-398-12	Sequence 12, Appl1
34	332.5	52.0	168	8	US-08-450-842-6	Sequence 6, Appl1
35	332.5	52.0	210	8	US-08-450-842-2	Sequence 2, Appl1
36	330.5	51.6	130	8	US-08-450-842-60	Sequence 60, Appl1
37	329.5	51.5	130	8	US-08-450-842-59	Sequence 59, Appl1
38	329.5	51.5	130	8	US-08-450-842-61	Sequence 61, Appl1
39	328.5	51.3	130	8	US-08-450-842-62	Sequence 62, Appl1
40	328.5	51.3	130	8	US-08-450-842-68	Sequence 68, Appl1
41	327.5	51.2	130	8	US-08-450-842-63	Sequence 63, Appl1
42	327.5	51.2	130	8	US-08-450-842-64	Sequence 64, Appl1
43	327.5	51.2	130	8	US-08-450-842-69	Sequence 69, Appl1
44	326.5	51.0	130	8	US-08-450-842-20	Sequence 20, Appl1
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## ALIGNMENTS

RESULT 1

US-10-072-681-4

Sequence 4, Application US/10072681

Patent No. US20020137893A1

GENERAL INFORMATION:

APPLICANT: Burton, Louis E.

APPLICANT: Schmeiler, Charles H.

APPLICANT: Beck, Joanne T.

TITLE OF INVENTION: PURIFICATION OF NCF

FILE REFERENCE: GENENT. 037C3

CURRENT APPLICATION NUMBER: US/10/072.681

CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: 60/030838

PRIOR FILING DATE: 1996-11-15

PRIOR APPLICATION NUMBER: 60/047855

PRIOR FILING DATE: 1997-05-29

PRIOR APPLICATION NUMBER: 08/970865

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: 09/363573

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/675,503

PRIOR FILING DATE: 2000-09-29

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 119

TYPE: PRT

ORGANISM: Homo sapien

US-10-072-681-4

Query Match 100.0%; Score 640; DB 12; Length 119;

Best Local Similarity 100.0%; Pred. No. 5.7e-65;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 PHSDPARRGELSVCSISBWMTAADKTAAYMSGTYLEKYPVSKGOLKQYFTKRN 60

61 PMGYTREGCGIDKXHNMSOCTRTOSYVFRALTDMSKRIRGFRIRDTSCVLTIRKGR 119

62 PMGYTREGCGIDKXHNMSOCTRTOSYVFRALTDMSKRIRGFRIRDTSCVLTIRKGR 119

RESULT 2  
US-09-745-032-8

Patent No. US20010027119A1  
 GENERAL INFORMATION:  
 APPLICANT: Boone, Thomas C.  
 APPLICANT: Cheung, Ellen N.  
 APPLICANT: Herzhenson, Susan I.  
 APPLICANT: Young, John D.  
 TITLE OF INVENTION: ANALOGS OF CATIONIC P  
 FILE REFERENCE: A-411a US Revsd/073100  
 CURRENT APPLICATION NUMBER: 09/745,032  
 CURRENT FILING DATE: 2000-12-19  
 PRIOR APPLICATION NUMBER: 09/214,214  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 08/684,353  
 PRIOR FILING DATE: 1996-07-19  
 NUMBER OF SEQ ID NOS: 2,1  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 8  
 LENGTH: 120  
 TYPE: PR1  
 ORGANISM: Human  
 US-09-745-032-8

Query Match	97.38;	Score 622.5;	DB 10;	Length 120;
Best Local Similarity	99.28;	Pred. No. 5.3e-63;		
Matches 118; conservative	0;	Mismatches 0;	Indels 1;	Gaps 1

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119	61	120	120

### RESULT 3

US-09-742-600-8  
Sequence 8, Application US/09742600  
Patent No. US2002001035A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen N.  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411a US Revised073100  
CURRENT APPLICATION NUMBER: US/09/742,600  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 09/214,214  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ. ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ. ID NO. 8  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Human  
US-09-742-600-8

Query Match	97.3%	Score 622.5;	DB 10;	Length 120;
Best Local Similarity	99.2%	Pred. No. 5.3e-63;		
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Db 62 MGYTKEGCRGIDKRHNSQCRITQSYVALTMDSKKRIGWRFIRIDTSCVCLILKRGK 120

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US-08-450-842-3

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Query Match	97.34;	Score 622.5;	DB 8;	Length 247;
Best Local Similarity	99.24;	Pred. No. 1.3e-62;		
Matches 118; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1

Oy	2	HSDPARGELSYCDISEMYTADDKTIVADMSGCTVLEKVPVSGDLOQIPEYETKCNP	61
Db	129	HSDPARGELSYCDISEMYTADDKTIVADMSGCTVLEKVPVSGDLOQIPEYETKCNP	186
Oy	62	MGYTKBECKRIDKRRHNSCRRTOSTVYALNDSKKRIGRFRIDTSCV-FLTKRGR	119
Db	189	MGYTKBECKRIDKRRHNSCRRTOSTVYALNDSKKRIGRFRIDTSCVCLTIKKRR	247

RESULT 5  
US-09-745-032-9  
; Sequence 9, Application US/09745032  
; Patent No. US20010027179A1

```

; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/745,032
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-745-032-9

Query Match          93.5%: Score 598.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 2.6e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
```

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; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-9

Query Match          93.5%: Score 598.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 2.6e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-9

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Best Local Similarity 95.8%: Pred. No. 2.6e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-9

Query Match          93.5%: Score 598.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 2.6e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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US-09-745-032-10
; Sequence 10, Application US/09745032
; Patent No. US20010027179A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/745,032
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-745-032-10

Query Match          93.2%: Score 596.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 4.4e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-10

Query Match          93.2%: Score 596.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 4.4e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-10

Query Match          93.2%: Score 596.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 4.4e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
```

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; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenon, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-10

Query Match          93.2%: Score 596.5; DB 10; Length 120;
Best Local Similarity 95.8%: Pred. No. 4.4e-60;
Matches 114; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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## RESULT 9

US-09-813-398-10  
Sequence 10, Application US/09813398  
Patent No. US20020169292A1  
GENERAL INFORMATION:  
APPLICANT: Bruce D. Weintraub  
APPLICANT: Mariusz W. Skudlinski  
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: US/09/813,398  
CURRENT FILING DATE: 2001-03-20  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 120  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-09-813-398-10

Query Match 92.1%; Score 589.5; DB 9; Length 120;  
Best Local Similarity 93.3%; Pred. NO. 2.7e-59;  
Matches 112; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 PHSDPARGELVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 60  
DB 1 PHSDPARGELVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 60  
QY 61 PMGYTEGCGIDKRMNSOCTRTOSYVRALTMDSKRRIGRFRIDTSCV-TLTIRGR 119  
DB 61 PMGYTEGCGIDKRMNSOCTRTOSYVRALTMDSKRRIGRFRIDTSCV-TLTIRGR 120

## RESULT 10

US-09-848-664-22  
Sequence 22, Application US/09848664  
Patent No. US2002014641A1  
GENERAL INFORMATION:  
APPLICANT: Sakiyama-Elbert, Shelly E.  
APPLICANT: Hubbell, Jeffrey A.  
TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth  
FILE REFERENCE: ETH 108  
CURRENT APPLICATION NUMBER: US/09/848,664  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/298,084  
PRIOR FILING DATE: 1999-04-22  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 72  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-848-664-22

Query Match 60.2%; Score 385; DB 10; Length 72;  
Best Local Similarity 100.0%; Pred. NO. 1.3e-36;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSDPARGELVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 61  
DB 1 HSDPARGELVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 60  
QY 62 MGYTEGCGID 73  
DB 61 MGYTEGCGID 72

## RESULT 11

US-10-072-681-5  
Sequence 5, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmelzer, Charles H.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: PURIFICATION OF NCF  
FILE REFERENCE: GENENT. 037C3  
CURRENT APPLICATION NUMBER: US/10/072,681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675,503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-072-681-5

Query Match 54.1%; Score 346; DB 12; Length 120;  
Best Local Similarity 55.4%; Pred. NO. 5.6e-33;  
Matches 67; Conservative 21; Mismatches 29; Indels 4; Gaps 3;

QY 1 PHSD-PARGELVCSISSEMTADKRTAVDMGSGTIVLEKVPVSKGOLKOFYETKCN 59  
DB 1 PYAEKSHRGREYVCSSESLEMT--DKSSAIDIKHOVTALGETKNGSPVKOLFETKCN 58  
QY 60 NPMGYTEGCGIDKRMNSOCTRTOSYVRALTMDSKRRIGRFRIDTSCV-TLTIRGR 118  
DB 59 KEARPVNCGCGIDDKRMNSOCTRTOSYVRALTMDSKRRIGRFRIDTSCV-TLTIRGR 118  
QY 119 R 119  
DB 119 R 119

## RESULT 12

US-09-745-032-1  
Sequence 1, Application US/09745032  
Patent No. US20010027179A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen N.  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411A US RevISED 073100  
CURRENT APPLICATION NUMBER: US/09/745,032  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 09/214,214  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Human  
US-09-745-032-1

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Query Match      53.8%; Score 344.5; DB 10; Length 120;
Best Local Similarity 57.4%; Pred. No. 8.3e-32;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYCDISSEMYTAADKRTAVDMGSGTIVLEKVPVSKGOLKQYFETCKNPMGYT 65
DB 7 SHRGESYCDSESLMT--DKSSAIDIRGHQVTLGEIKTGNSPVKQYFETCKREARPV 64
OY 66 KEGCGRIDKRNHNSOCTRTQSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
DB 65 KNGCGRIDKRNHNSOCTRTQSYVRALTSENNKLVGMWRIRIDTSCVCALSRKIGR 119

RESULT 13
US-09-742-600-1
; Sequence 1, Application US/09742600
; Patent No. US20020010135A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/742,600
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/214,214
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-742-600-1

Query Match      53.8%; Score 344.5; DB 10; Length 120;
Best Local Similarity 57.4%; Pred. No. 8.3e-32;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYCDISSEMYTAADKRTAVDMGSGTIVLEKVPVSKGOLKQYFETCKNPMGYT 65
DB 7 SHRGESYCDSESLMT--DKSSAIDIRGHQVTLGEIKTGNSPVKQYFETCKREARPV 64
OY 66 KEGCGRIDKRNHNSOCTRTQSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
DB 65 KNGCGRIDKRNHNSOCTRTQSYVRALTSENNKLVGMWRIRIDTSCVCALSRKIGR 119

RESULT 14
US-09-872-090-1
; Sequence 1, Application US/09872090
; Patent No. US20020052488A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngol Yin
; APPLICANT: Hershenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: Analogs of Nr-3 (As Amended)
; FILE REFERENCE: A-411B
; CURRENT APPLICATION NUMBER: US/09/872,090
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/255,953
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-872-090-1

Query Match      53.8%; Score 344.5; DB 10; Length 120;
Best Local Similarity 57.4%; Pred. No. 8.3e-32;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYCDISSEMYTAADKRTAVDMGSGTIVLEKVPVSKGOLKQYFETCKNPMGYT 65
DB 7 SHRGESYCDSESLMT--DKSSAIDIRGHQVTLGEIKTGNSPVKQYFETCKREARPV 64
OY 66 KEGCGRIDKRNHNSOCTRTQSYVRALTMDSKKRIGRFIRIDTSCV-TLTIKGR 119
DB 65 KNGCGRIDKRNHNSOCTRTQSYVRALTSENNKLVGMWRIRIDTSCVCALSRKIGR 119

RESULT 15
US-08-450-842-4
; Sequence 4, Application US/08450842
; Patent No. US20020045576A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 666P2C1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-842-4

Query Match      53.8%; Score 344.5; DB 8; Length 257;
Best Local Similarity 57.4%; Pred. No. 2.1e-31;
Matches 66; Conservative 17; Mismatches 29; Indels 3; Gaps 2;

OY 6 ARRGELSYCDISSEMYTAADKRTAVDMGSGTIVLEKVPVSKGOLKQYFETCKNPMGYT 65
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Mon Dec 2 15:36:39 2002

us-10-072-681-4.rabb

Page 6

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Job time : 4.18523 secs

GenCore version 5.1.3  
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# OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:37 : Search time 23 9156 Seconds  
(without alignments)

668,605 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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23: /SIDS2/gcgdata/geneseq-emb1/AA2002.DAT.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	646	98.9	119	AAW48889	Human neurotrophin-3
3	646	98.9	119	AAW48889	Human neurotrophin-3
4	646	98.9	119	AAW48889	Human neurotrophin-3
5	641	98.2	119	AAW48889	Human neurotrophin-3
6	641	98.2	119	AAW48889	Human neurotrophin-3
7	641	98.2	119	AAW48889	Human neurotrophin-3
8	641	98.2	119	AAW48889	Human neurotrophin-3
9	641	98.2	119	AAW48889	Human neurotrophin-3
10	641	98.2	119	AAW48889	Human neurotrophin-3

11	641	98.2	120	18	AAW10014	Human neurotrophin
12	641	98.2	120	21	AAW10455	Human R-methuNT pr
13	641	98.2	120	22	AAW05868	Human recombinant
14	641	98.2	136	12	AAW11306	Nerve Growth Factor
15	641	98.2	240	13	AAW26273	NGF/NT-3 in preB3
16	641	98.2	240	14	AAW49337	Sequence of pro re
17	641	98.2	240	15	AAW54451	Human NGF-2/NT-3 e
18	641	98.2	257	12	AAW10352	Human NGF3. Homo
19	641	98.2	257	13	AAW26272	NGF2/NT-3 in preB3
20	641	98.2	257	16	AAW49336	Sequence of pro re
21	641	98.2	257	20	AAW05078	Human neurotrophin
22	641	98.2	257	22	AAW06594	Human neurotrophin
23	641	98.2	257	22	AAW66927	Neurotrophin-3 (NT
24	641	98.2	257	23	AAW20262	Human NF. Homo sa
25	641	98.2	257	23	AAW05847	Human neurotrophin
26	641	98.2	258	11	AAW06648	Human recombinant
27	641	98.2	258	12	AAW13357	Novel polypeptide
28	641	98.2	258	22	AAW66928	Neurotrophin-3. M
29	641	98.2	258	23	AAW57323	Rat NF. Rattus sp
30	641	98.2	271	11	AAW06649	Mouse ischaemic co
31	638	97.7	271	12	AAW13307	Novel polypeptide
32	634	97.1	136	11	AAW06650	Nerve Growth Factor
33	634	97.1	257	15	AAW63067	Novel polypeptide
34	634	97.1	281	14	AAW37801	Human NGF-2/NT-3 e
35	633	96.9	119	17	AAW90530	Rat NT-3. Rattus
36	629	96.3	119	19	AAW52302	Pancreatic neurotro
37	629	96.3	119	22	AAW05871	Mutant huNT-3 1-11
38	629	96.3	120	22	AAW52300	Human NT-3(1-119)R
39	629	96.3	120	22	AAW05869	Mutant met-huNT-3
40	619	94.8	117	19	AAW52303	Human r-methuNT-3
41	619	94.8	117	22	AAW05872	Mutant huNT-3 1-11
42	619	94.8	118	22	AAW52301	Human NT-3(1-117)R
43	619	94.8	118	22	AAW05870	Mutant met-huNT-3
44	613	93.9	120	21	AAW25142	Human r-methuNT-3
45	602	92.2	119	21	AAW92008	N-terminal of neut

## ALIGNMENTS

RESULT 1	AAW48889	Standard; Protein: 119 AA.
ID	AAW48889	
AC	AAW48889	
XX		
DT	12-OCT-1998	(first entry)
XX		
DE	Human neurotrophin-3.	
XX		
KW	Neurotrophin-3; NT-3; human; purification;	
KW	hydrophobic interaction chromatography.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	57..67
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
FT	Region	108..110
FT		/note="conserved Cys-containing region involved in
FT		Cys knot motif"
XX		
PN	MO9821234-AZ.	
XX		
PD	22-MAY-1998.	
XX		
PF	14-NOV-1997.	97MO-US21068.
XX		
PR	29-MAY-1997.	97US-0047855.
PR	15-NOV-1996.	96US-0030838.
XX		
PA	(GETH ) GENENTECH INC.	

XX Beck JT, Burton LE, Schmelzer CH;  
 XX WPI: 1998-322333/28.  
 DR  
 XX  
 XX Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated  
 PT variant(s) - using hydrophobic interaction chromatography,  
 PT optionally in combination with high performance cation exchange  
 chromatography  
 XX  
 XX  
 PS Disclosure: Page 37-38; 59pp: English.  
 XX  
 CC This polypeptide comprises human neurotrophin-3 (NT-3) mature  
 CC polypeptide. Methods are provided for large-scale purification of  
 CC neurotrophins. Including mature NT-3, suitable for clinical use. A  
 CC claimed method comprises: (1) separating the neurotrophin from the  
 CC other proteins using a hydrophobic interaction chromatography resin  
 CC (HICR); and optionally (2) separating the neurotrophin from a  
 CC chemical variant by high performance cation exchange chromatography  
 CC (HPEC). The processes can also be used for purification of e.g.  
 CC human nerve growth factor (NGF) (see AAM4886), mouse NGF (see  
 CC AAM4887), brain-derived neurotrophic factor (see AAM4888) and  
 CC neurotrophin-4/5 (see AAM4890). The processes allow separation of  
 CC neurotrophins from various undesirable misprocessed, misfolded,  
 CC size, glycosylated or charge forms. They allow selective  
 CC separation from variants and other molecules, and from other  
 CC polypeptides with high pI. The processes are applicable to  
 CC starting materials from various sources, including fermentation  
 CC broths or lysed bacterial or mammalian cells.  
 CC  
 XX  
 SO Sequence 119 AA:  
 Query Match 98.9%; Score 646; DB 19; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-60;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 61  
 Db 1 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 60  
 Oy 62 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 120  
 Db 61 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 119  
 RESULT 2  
 AAB29113  
 ID AAB29113 standard; Protein: 119 AA.  
 XX  
 AC AAB29113;  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX  
 DE Human neurotrophin-3.  
 XX  
 XX Neurotrophin: trkB, trkC; ototoxicity-related balance impairment;  
 KW Meniere's syndrome; myringitis; otitis media;  
 KW acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;  
 KW middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6121235-A.  
 XX  
 PD 19-SEP-2000.  
 XX  
 PF 29-DEC-1995; 95US-0581662.  
 XX  
 PR 29-DEC-1995; 95US-0581662.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Gao W;

XX  
 DR WPI: 2000-618200/59.  
 XX  
 XX Treating ototoxin-induced neuronal-related balance impairment and  
 PT promoting vestibular ganglion neuron survival prior to, upon or after  
 PT exposure to an ototoxin, comprises administering a trkB or trkC agonist  
 PT  
 XX  
 PS Disclosure: Column 47-50; 40pp: English.  
 XX  
 CC The present invention relates to treating ototoxin-induced  
 CC neuronal-related balance impairment in a mammal by administering a  
 CC trkB or trkC agonist, particularly neurotrophin-4/5 (NT-4/5).  
 CC ototoxicity-related balance impairments include Meniere's syndrome,  
 CC myringitis, otitis media, acute vestibular neuronitis, herpes zoster  
 CC oticus, labyrinthitis, middle or labyrinthine tumours, petrositis and  
 CC otosclerosis. NT-4/5 may also be used to treat diseases  
 CC induced by gram positive, gram negative and acid-fast bacteria. The  
 CC present sequence is a protein used in the invention.  
 CC  
 XX  
 SO Sequence 119 AA:  
 Query Match 98.9%; Score 646; DB 21; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-60;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 61  
 Db 1 YAEKSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 60  
 Oy 62 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 120  
 Db 61 RPYKNCGRGIDKHMNSCKTSQTYVRALTSNNKLVGMRRIRIDTSCVSLSRKIGRT 119  
 RESULT 3  
 AAR11359  
 ID AAR11359 standard; Protein: 281 AA.  
 XX  
 AC AAR11359;  
 XX  
 DT 31-MAY-1991 (first entry)  
 XX  
 DE Neurotrophin-3.  
 XX  
 XX NT-3; nerve growth factor; NGF; brain derived neurotrophic factor;  
 KW BDNF; Alzheimers disease; Parkinsonism; central nervous system; CNS;  
 KW neuropathy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 25..281  
 FT /label= prepro NT3  
 FT Protein 163..281  
 FT /label= mature NT3  
 XX  
 XX W09103569-A.  
 XX  
 PD 21-MAR-1991.  
 XX  
 PF 29-AUG-1990; 90MO-0504916.  
 XX  
 PR 20-AUG-1990; 90US-0570189.  
 PR 30-AUG-1989; 89US-0400591.  
 PR 07-MAR-1990; 90US-0490004.  
 XX  
 PA (PLAC ) MAX PLANCK GES WISSENSCH.  
 PA (REGG-) REGENERON PHARM INC.  
 XX  
 XX Hohn A, Leibrock J, Bailey K, Barde YA, Thoenen H;  
 PI Malsenpierre PC, Furchme, Lindsay RW;



DR MPI: 1991-102084/14.  
DR N-PSDB: AA011147.  
XX  
XX New neurotrophin-3, neurotrophic factor - related to nerve  
PT growth- and brain derived neurotrophic-factor, for diagnosis and  
PT treatment of neurological disorders.  
XX  
XX  
PS Clalm 26; Fig 11; 149pp; English.  
XX  
CC NT-3 is a new neurotrophic factor and is a member of the NGF/BDGF  
CC gene family. The sequence was deduced from the DNA sequence of a  
CC clone isolated from a human placental genomic DNA library using  
CC probes prep'd. from sequences of NGF and BDGF. The clone contg. the  
CC longest insert was designated phln3(g1).  
CC See also AAR11357 and R111358.  
XX  
SQ Sequence 281 AA;  
Query Match 98.9%; Score 646; DB 12; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-60;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 YAEHSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61  
DB 163 YAEHSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 222  
OY 62 RPKVNCRCGIDDKHNSCKTSQTYVRAVLTSENKLVGMWRIRIDTSCVSLSRKTGRT 120  
DB 223 RPKVNCRCGIDDKHNSCKTSQTYVRAVLTSENKLVGMWRIRIDTSCVSLSRKTGRT 281  
RESULT 4  
ID AAR37800 standard; Protein: 281 AA.  
XX  
AC AAR37800;  
DT 29-SEP-1993 (first entry)  
XX  
XX Human NT-3.  
DE  
XX Chimeric: human; prepro: NGF; brain-derived neurotrophic factor; rat;  
KW BDNF; chimera; fusion; nerve growth factor; peripheral; precursor;  
KW central; nervous system; dorsal root ganglion neuron; NT-3; homology;  
KW neurotrophin; nodose ganglion.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Region 25..162  
FT /note="Human NT-3 prepro region"  
FT Protein 163..281  
FT /note="Human NT-3 mature protein"  
XX  
XX W09J10150-A.  
PN  
XX 27-MAY-1993.  
PD  
XX 13-NOV-1992; 92MO-US09792.  
PF  
XX 14-NOV-1991; 91US-0792492.  
PR  
XX (AMGE-) AMGEN.  
PA (REGE-) REGENERON PHARM INC.  
PI  
XX Gies D, Hu SS, Ip N, Squinto SP, Yancopoulos GD.  
DR WPI: 1993-182492/22.  
DR N-PSDB: AA042572.  
XX  
XX Eukaryotic expression of neurotrophins - using prepro region of a  
PT different neurotrophin for more efficient post-translational  
PT processing

XX  
XX Disclosure; Fig 5; 80pp; English.  
PS  
XX  
CC The sequences given in AAR37800-01 represent human and rat  
CC neurotrophin-3 (NT-3) respectively. NT-3 has a similar structure to  
CC brain derived neurotrophic factor (BDNF) and nerve growth factor (NGF).  
CC A putative signal sequence of 18 amino acids is followed by a prosequence  
CC of 121 amino acids. The 6 Cys residues present in NGF and BDNF are  
CC conserved in NT-3 and are thought to be involved in the formation of  
CC disulphide bridges. A high degree of homology is noted between rat and  
CC human NT-3 within the region encoding the mature protein. The amino  
CC acid sequences of the mature proteins appear absolutely identical. NT-3  
CC is capable of promoting survival and neurite outgrowth of dissociated  
CC dorsal root ganglion neurons in culture. NT-3 is observed to promote  
CC neurite outgrowth from both nodose ganglion but not sympathetic  
CC ganglion, and NGF promoted outgrowth from sympathetic ganglion but  
CC not nodose explants. Therefore NT-3 appears to have a broader  
CC specificity of action than either BDNF or NGF.  
XX  
SQ Sequence 281 AA;  
Query Match 98.9%; Score 646; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-60;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 YAEHSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 61  
DB 163 YAEHSHRGEYSVCDESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKOYFETRCKEA 222  
OY 62 RPKVNCRCGIDDKHNSCKTSQTYVRAVLTSENKLVGMWRIRIDTSCVSLSRKTGRT 120  
DB 223 RPKVNCRCGIDDKHNSCKTSQTYVRAVLTSENKLVGMWRIRIDTSCVSLSRKTGRT 281  
RESULT 5  
ID AAR29495 standard; Protein: 119 AA.  
XX  
AC AAR29495;  
DT 22-APR-1993 (first entry)  
XX  
XX NT-3, mouse.  
DE  
XX Neurotrophin; NT; nerve growth factor; NGF;  
KW brain-derived neurotrophic factor; BDNF.  
KW  
XX Mus musculus.  
OS  
XX  
XX W09J20365-A.  
PN  
XX 26-NOV-1992.  
PD  
XX 20-MAY-1992; 92MO-US04266.  
PF  
XX 21-MAY-1991; 91US-0703450.  
PR 12-JUL-1991; 91US-0729253.  
PR 23-JUL-1991; 91US-0734422.  
PR 28-AUG-1991; 91US-0751356.  
PR 20-SEP-1991; 91US-0762674.  
PR 14-NOV-1991; 91US-0791924.  
XX  
XX (REGE-) REGENERON PHARM INC.  
PA  
XX Hallbook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD;  
PI  
XX WPI: 1992-415468/50.  
DR  
XX  
XX Use of neurotrophin-4 for promoting growth and survival of nerve  
PT cells - useful in treating neurological, fertility and  
PT immunological disorders and in diagnosis  
XX  
XX Disclosure: Page 106-107 + Fig 4B; 180pp; English.

XX A comparison of the mature NT-4 protein (Xenopus) to the mature  
CC NGF, BDNF, and NT-3 proteins from mouse revealed 51%, 60% and 58%  
CC amino acid identity respectively. See sequences AAR2491 and  
CC AAR29493-95.  
XX  
XX Sequence 119 AA:

Query Match 98.2%; Score 641; DB 13; Length 119;  
Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 60  
QY 62 RPKVNCGRIGIDKHMNSQCKTSQTYVRALTSNNKLVGNMIRIDPSVCSALSRKIGRT 120  
DB 61 RPKVNCGRIGIDKHMNSQCKTSQTYVRALTSNNKLVGNMIRIDPSVCSALSRKIGRT 119

# RESULT 6

AAR54086  
ID AAR54086 standard; protein: 119 AA.

XX AAR54086;

XX 10-NOV-1994 (first entry)

XX Neurotrophin-3.

XX Nerve growth factor; NGF; chimeric neurotrophin; neurotrophic factor;  
XX brain-derived neurotrophic factor; BDNF; neurotrophin-3; NF-3;

XX TrkA; TrkB; TrC; receptor; neurological disorder;

XX Parkinson disease; Alzheimer disease.

XX Rattus sp.

XX W09412539-A.

XX 09-JUN-1994.

XX 19-NOV-1993; 93MO-US11292.

XX 20-NOV-1992; 92US-0979630.

XX (MCIN/) MCINTYRE K R.

XX Ibanez CFM, Persson HB;

XX WPI: 1994-200202/24.

XX New chimeric neurotrophic factors and DNA - used to develop  
XX prods. for use in the treatment and diagnosis of neurological  
XX disorders

XX Disclosure: Page 50; 79pp; English.

XX Sequences are provided for rat nerve growth factor (AAR54084), rat  
XX brain-derived neurotrophic factor (AAR54085) and rat neurotrophin-3  
XX (AAR54086). Chimeric neurotrophins capable of binding TrkA, TrkB and  
XX TrC are obtained by substituting amino acids 3-9, 28-37, 40-49,  
XX 61-66, 81-88, 94-98 or 95-97 of a neurotrophin with corresponding  
XX amino acids from NGF, BDNF or NT-3. Recombinant chimeric  
XX neurotrophins are used to treat e.g. Alzheimer disease and  
XX Parkinson disease.

XX Sequence 119 AA:

Query Match 98.2%; Score 641; DB 13; Length 119;  
Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 60  
QY 62 RPKVNCGRIGIDKHMNSQCKTSQTYVRALTSNNKLVGNMIRIDPSVCSALSRKIGRT 120  
DB 61 RPKVNCGRIGIDKHMNSQCKTSQTYVRALTSNNKLVGNMIRIDPSVCSALSRKIGRT 119

# RESULT 7

AAR81118  
ID AAR81118 standard; protein: 119 AA.

XX AAR81118;

XX 01-MAR-1999 (first entry)

XX Neurotrophin-3 wild type.

XX Nerve growth factor; TrkC; neuron; neural disease; animal feed;  
XX neurotrophin assay; nerve cell culture media; neurotrophic factor; NT-3;

XX TrkA; TrkB.

XX Homo sapiens.

XX W09849308-A1.

XX 05-NOV-1998.

XX 23-APR-1998; 98MO-US08242.

XX 29-APR-1997; 97US-0841045.

XX 25-APR-1997; 97US-0845541.

XX (GETH ) GENENTECH INC.

XX Presta LG, Uffer R, Winslow JW;

XX WPI: 1999-009429/01.

XX New variants of nerve growth factor able to bind TrkC - contain  
XX specified mutations and have multiple neurotrophic activities in a  
XX single molecule, used for treating, e.g. peripheral neuropathy

XX Example 1; Page 33; 53pp; English.

XX Neurotrophin-3 was used in the production of new variants of nerve growth  
XX factor (NGF) with substitutions at amino acid positions: 623 and 884, and  
XX one or both of V18 and V20, so that it acquires the ability to bind TrkC.

XX The variants can be used to promote development, maintenance and  
XX regeneration of neurons in vivo or in vitro, so can be used to treat a  
XX wide range of neural diseases, e.g. Alzheimer's, Parkinson's,

XX Huntington's and Meniere's diseases; stroke; amyotrophic lateral  
XX sclerosis; epilepsy; Down's syndrome; nerve deafness; Bell's palsy, or  
XX specifically, peripheral neuropathy. They are also used as cognitive  
XX enhancers and can also be used for diagnosis: in animal feeds; as

XX standards for neurotrophin assays; as additives for nerve cell culture  
XX media, and for generation of specific antibodies. By introducing TrkC  
XX binding/signaling inducing activity, the variants acquire the activity of

XX neurotrophic factor NT-3 while optionally retaining ability to bind TrkA  
XX and/or B and therefore provide several activities in a single molecule,  
XX with more predictable pharmacokinetic and other properties than a mixture  
XX of agents each with a single activity, and better pan-neurotrophic  
XX activity than known compounds.

XX Sequence 119 AA:

Query Match 98.2%; Score 641; DB 20; Length 119;  
Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEIRKGNSPVKQYFETRCKEA 61  
|||||

DB 1 YAEKSHRGEYSVCDSESLMTWKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60  
QY 62 RPVKNGCRGIDDKHNSQCKTSQTYVRALTSNNKLVGRWIRIDTSCVSAISRKIGRT 120  
DB 61 RPVKNGCRGIDDKHNSQCKTSQTYVRALTSNNKLVGRWIRIDTSCVSAISRKIGRT 119

RESULT 8  
ID AAG64995 standard; protein: 119 AA.  
XX AAG64995;  
AC AAG64995;  
XX 25-SEP-2001 (first entry)  
DT 25-SEP-2001 (first entry)  
XX Nerve growth factor variant related protein SEQ ID NO: 2.  
DE Nerve growth factor variant related protein SEQ ID NO: 2.  
XX Nerve growth factor: NGF; trkC-binding activity; trkA; trkB; neuropathy;  
KM neuronal disorder; neurotrophin; variant; mutant; mulein; Bell's palsy;  
KM amyotrophic lateral sclerosis; paralysis; neurodegenerative disease;  
KM Parkinson's disease; Alzheimer's disease; multiple sclerosis.  
XX Unidentified.  
OS US2001012625-A1.  
XX 09-AUG-2001.  
PD 09-AUG-2001.  
XX 24-APR-1998; 98US-0066065.  
PF 24-APR-1998; 97US-0044918.  
XX 25-APR-1997; 97US-0044918.  
PR (PRES/) PRESTA L G.  
XX (URE/) UREER R.  
PA (WINS/) WINSLOW J W.  
XX Presta LG, Ureer R, Winslow JW;  
PI WPI: 2001-464388/50.  
XX Nerve growth factor variants which have trkC-binding activity and  
PT trkC-signal inducing activity, useful for treating a neural disorder in  
PT a mammal such as peripheral neuropathy (e.g. diabetic peripheral  
PT neuropathy) -  
XX Disclousure: Page 19-20; 34pp; English.  
PS The present invention provides a number of nerve growth factor (NGF)  
XX variants with trkC-binding activity and trkC-signal inducing activity.  
CC They may also be capable of binding to trkA and trkB. The variants are  
CC useful in the treatment of neuronal disorders, including peripheral  
CC neuropathy and motor-neurone disorders, such as amyotrophic lateral  
CC sclerosis, Bell's palsy, and various conditions involving spinal muscular  
CC atrophy, or paralysis. They are also useful for treating other human  
CC neurodegenerative disorders, such as Alzheimer's disease, Parkinson's  
CC disease, epilepsy, multiple sclerosis, Huntington's disease, Down's  
CC Syndrome, nerve deafness, Meniere's disease and other conditions  
CC characterized by necrosis or loss of neurones, whether central,  
CC peripheral, or motor neurones.  
XX Sequence 119 AA;  
SO

Query Match 98.2%; Score 641; DB 22; Length 119;  
Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTWKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTWKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60  
QY 62 RPVKNGCRGIDDKHNSQCKTSQTYVRALTSNNKLVGRWIRIDTSCVSAISRKIGRT 120  
DB 61 RPVKNGCRGIDDKHNSQCKTSQTYVRALTSNNKLVGRWIRIDTSCVSAISRKIGRT 119

RESULT 9  
ID AAB35946 standard; protein: 119 AA.  
XX AAB35946;  
AC AAB35946;  
XX 26-FEB-2001 (first entry)  
DT 26-FEB-2001 (first entry)  
XX NT-3 amino acid sequence.  
DE Heparin binding; vascular graft; matrix; cell adhesion; growth factor;  
KM wound healing; dermal wound; wound healing; NT-3.  
XX Unidentified.  
OS WO200064481-A1.  
XX 02-NOV-2000.  
PD 02-NOV-2000.  
XX 22-APR-1999; 99WO-IB00800.  
PF 22-APR-1999; 99WO-IB00800.  
XX 22-APR-1999; 99WO-IB00800.  
PR (ETHZ-) ETH ZURICH & UNIV ZURICH.  
XX Sakiyama SE, Hubbell JA;  
PI WPI: 2001-024627/03.  
XX Matrix for controlled release of growth factor for wound healing, has  
PT substrate that attaches heparin binding peptide, protein growth factor  
PT that bind heparin with low affinity, and heparin or heparin-like  
PT polymer -  
XX Example 5; Page 21; 48pp; English.  
PS This invention relates to a matrix comprising a substrate capable of  
XX providing attachment of a heparin binding peptide (HBP), a peptide  
CC comprising a binding domain which binds heparin with high affinity,  
CC heparin or heparin-like polymer, and a protein growth factor or peptide  
CC fragment which has a domain that binds heparin with low affinity.  
CC Included in the invention is a vascular graft comprising the matrix,  
CC which is capable of supporting cell adhesion. The matrix is used for  
CC delivering low heparin binding affinity growth factor proteins or  
CC peptides in a controlled manner suitable for wound healing. The matrix  
CC can be used in an article for treating dermal wounds, and in an  
CC implantable sterilized composition capable of supporting cell adhesion.  
CC The present sequence represents a growth factor protein. The protein is  
CC used in an example illustrating that non-heparin-binding growth factors  
CC systems based on their low affinity for heparin.  
XX Sequence 119 AA;  
SO

Query Match 98.2%; Score 641; DB 22; Length 119;  
Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTWKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTWKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60  
QY 62 RPVKNGCRGIDDKHNSQCKTSQTYVRALTSNNKLVGRWIRIDTSCVSAISRKIGRT 120  
DB 61 RPVKNGCRGIDDKHNSQCKTSQTYVRALTSNNKLVGRWIRIDTSCVSAISRKIGRT 119

RESULT 10  
ID AAW29392 standard; protein: 120 AA.  
XX AAW29392

AC AAW29392;  
 XX 20-FEB-1998 (first entry)  
 XX Conjugate of neurotrophin-3 with polyethylene glycol.  
 DE  
 XX Brain derived growth factor conjugate; BDNF; polyethylene glycol;  
 XX water-soluble polymer; neurotrophin-3; NT-3; methoxypolyethylene glycol;  
 XX trophic factor; neurodegenerative disease; Parkinson's disease;  
 XX amyotrophic lateral sclerosis; Huntington's disease;  
 XX retinal degeneration; peripheral neuropathies; Alzheimer's disease.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Misc-difference 1 /note= "optionally absent"  
 XX Modified-site 120 /note= "alpha amino group of Thr modified with  
 XX methoxypolyethylene glycol"  
 XX  
 XX M09615146-A1.  
 XX  
 XX 23-MAY-1996.  
 XX  
 XX 13-NOV-1995; 95MO-US14658.  
 XX  
 XX 14-NOV-1994; 94US-0340131.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Kinstler OF, Yan Q;  
 XX  
 XX WPI: 1996-259779/26.  
 XX  
 XX Conjugates of brain derived growth factor or neurotrophin-3 with  
 XX water soluble polymer - having improved migration through brain  
 XX tissue compared with the free peptide, useful e.g. for promoting  
 XX survival and maintenance of neurons  
 XX  
 XX Claim 2; Pages 36-7; 54pp; English.  
 XX  
 XX This sequence represents a new conjugate of neurotrophin-3 (NT-3)  
 XX and methoxypolyethylene glycol, a water soluble polymer. The modification  
 XX may be at the N-terminal alpha-amino group of NT-3 or on one or several  
 XX of the lysine epsilon-amino acid groups of NT-3. These derivatives, and  
 XX similar derivatives of brain derived growth factor (BDGF) have the  
 XX same uses as the trophic factors BDNF and NT-3. They are useful for  
 XX promoting the survival and maintenance of neurons in vitro and in vivo,  
 XX and for treating neurodegenerative diseases, e.g. Parkinson's disease,  
 XX amyotrophic lateral sclerosis, Huntington's disease, retinal  
 XX degeneration, peripheral neuropathies or Alzheimer's disease. Use of the  
 XX derivatives improves migration of BDNF or NT-3 through brain tissue,  
 XX resulting in easier delivery to targets within the brain.  
 XX  
 XX Sequence 120 AA:  
 SQ  
 Query Match 98.2%; Score 641; DB 17; Length 120;  
 Best Local Similarity 99.2%; Pred. No. 4,36-60;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 YAEKSHRGEYSVCDSESLAVTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
 Db 2 YAEKSHRGEYSVCDSESLAVTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
 Oy 62 RPKVNGCRGIDDKHMSOCKTSQTYVRALTSNNKLVGMRIIRIDTSCVSLSRKIGRT 120  
 Db 62 RPKVNGCRGIDDKHMSOCKTSQTYVRALTSNNKLVGMRIIRIDTSCVSLSRKIGRT 120  
 RESULT 11  
 AAW10014  
 ID AAW10014 standard; protein: 120 AA.

XX AAW10014;  
 AC 15-SEP-1997 (first entry)  
 XX Human neurotrophin-3.  
 DE  
 XX NT-3; neurotrophin 3; active; refolded; differentiation; research;  
 XX expression; protein induction; enzyme expression.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Disulfide-bond 15..80  
 XX Disulfide-bond 58..109  
 XX Disulfide-bond 68..111  
 XX  
 XX JP09121886-A.  
 XX  
 XX 13-MAY-1997.  
 XX  
 XX 22-AUG-1996; 96JP-0220963.  
 XX  
 XX 25-AUG-1995; 95JP-0217032.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX WPI: 1997-314237/29.  
 XX  
 XX Preparation of active correctly folded neurotrophin-3 - which can be  
 XX used in cell differentiation, and protein expression research  
 XX  
 XX Disclosure; Fig 1; 15pp; Japanese.  
 XX  
 XX This sequence is human neurotrophin 3 (NT-3). Active NT-3 is produced by  
 XX the method of the invention, which comprises transforming a prokaryotic  
 XX host cell with an NT-3 gene to express the NT-3, and then NT-3 produced  
 XX is refolded correctly in a redox buffer. The active NT-3 produced by the  
 XX method can be used as a reagent for research on the differentiation of  
 XX cells, genetic expression and induction of protein and enzyme expression.  
 XX  
 XX Sequence 120 AA:  
 SQ  
 Query Match 98.2%; Score 641; DB 18; Length 120;  
 Best Local Similarity 99.2%; Pred. No. 4,36-60;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 YAEKSHRGEYSVCDSESLAVTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
 Db 2 YAEKSHRGEYSVCDSESLAVTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
 Oy 62 RPKVNGCRGIDDKHMSOCKTSQTYVRALTSNNKLVGMRIIRIDTSCVSLSRKIGRT 120  
 Db 62 RPKVNGCRGIDDKHMSOCKTSQTYVRALTSNNKLVGMRIIRIDTSCVSLSRKIGRT 120  
 RESULT 12  
 AAB10455  
 ID AAB10455 standard; protein: 120 AA.  
 AC AAB10455;  
 XX 01-DEC-2000 (first entry)  
 XX Human R-methuM protein.  
 DE  
 XX Human; R-methuM; gastrointestinal hypomotility; constipation; diarrhea;  
 XX trk neurotrophin-3 receptor; surgery; neuropathy; Parkinson's disease;  
 XX multiple sclerosis; irritable bowel syndrome; spinal cord injury;  
 XX paraplegia; quadriplegia; antidiarrheic; laxative.  
 OS Homo sapiens.  
 OS Synthetic.

XX WO200041719-A1.  
 XX 20-JUL-2000.  
 XX 11-JAN-2000; 2000WO-US00682.  
 XX 15-JAN-1999; 99US-0232171.  
 XX (REG-1) REGENERON PHARM INC.  
 XX Cedarbaum JM;  
 XX WPI; 2000-475953/41.  
 XX Treating constipation and diarrhea using agonists and antagonists of  
 XX 5-HT<sub>2</sub> receptor activity -  
 XX Disclosure: Page 16; 63pp; English.

CC This invention describes novel methods (I) and (II) for treating  
 CC disorders associated with gastrointestinal motility (i.e. constipation  
 CC and diarrhea (respectively), comprising administering agonists and  
 CC antagonists of 5-HT<sub>2</sub> receptor activity. (I) is used to  
 CC treat patients in an intensive care or coronary care unit for  
 CC gastrointestinal hypomotility such as acute constipation associated with  
 CC orthopedic, gynecological, thoracic and/or urological surgery.  
 CC Alternatively, the constipation may be chronic and associated with  
 CC enteric neuropathy, Parkinson's disease, multiple sclerosis, chronic use  
 CC of opiate pain killers, irritable bowel syndrome or constipation in  
 CC hospital patients. In particular, the constipation may be associated with  
 CC spinal cord injury, paraplegia or quadriplegia. The products of the  
 CC invention have antidiarrhetic and laxative activity. This sequence  
 CC represents the R-methuNT protein which is used in the method of the  
 CC invention. R-methuNT is produced in *Escherichia coli* into which a plasmid  
 CC containing a coding sequence for human NT-3 has been inserted. R-methuNT  
 CC has an amino acid sequence identical to native human NT-3 with the  
 CC addition of an amino terminal methionine.

XX Sequence 120 AA:  
 XX SQ

Query Match 98.2%; Score 641; DB 21; Length 120;  
 Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
 Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGESVCDSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEA 61  
 DB 2 YAEKSHRGESVCDSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEA 61  
 QY 62 RPKVNCGRGIDDKHNSCKTSQTYVRLTSENKLVGMWIRIDTSCVLSRKIGRT 120  
 DB 62 RPKVNCGRGIDDKHNSCKTSQTYVRLTSENKLVGMWIRIDTSCVLSRKIGRT 120

RESULT 13  
 AAE05868 standard; protein: 120 AA.  
 AAE05868:  
 24-SEP-2001 (first entry)  
 Human recombinant neurotrophic factor-3 (NT-3), r-methuNT-3.  
 Human: Isoelectric point; PI: neurotrophic factor-3; NT-3;  
 pharmacokinetic behaviour; recombinant protein; r-methuNT-3.  
 Homo sapiens.  
 Key Location/Qualifiers  
 Misc-difference 1 /note- "this residue is expressed when the protein is  
 produced recombinantly in *E. coli* bacterial cells;"

FT This protein is expressed without the methionine  
 XX residue when occurring naturally in mammalian cells.  
 XX US6271364-B1.  
 XX 07-AUG-2001.  
 XX 23-FEB-1999; 99US-0255953.  
 XX 23-FEB-1999; 99US-0255953.  
 XX (AMGE-1) AMGEN INC.  
 XX Cheung ENY, Boone TC, Hershenson SI, Young JD;  
 XX WPI; 2001-464215/50.  
 XX Polypeptide analogs of the neurotrophin factor (NT-3) and its  
 XX recombinant production method -  
 XX Disclosure: Fig 1; 24pp; English.

CC The present invention relates to a method for production of a  
 CC polypeptide analogue of a cationic polypeptide selected from 4 fully  
 CC defined polypeptide sequences, where the polypeptide analogue has an  
 CC isoelectric point which is lower and an in vivo circulating life and/or  
 CC absorption which is increased relative to those properties in unmodified  
 CC neurotrophic factor-3 (NT-3). The method is useful for producing certain  
 CC analogues of NT-3 which have a relatively lower PI, yet retain the  
 CC structure and biological activity of the protein in its 'native' state,  
 CC to assess the impact of the PI on the pharmacokinetic behaviour of  
 CC proteins. The present sequence is human recombinant neurotrophic  
 CC factor-3 (NT-3), r-methuNT-3. This sequence is recombinantly produced  
 CC in *E. coli* bacterial cells and thus expressing the methionine residue at  
 CC its N-terminus.

XX Sequence 120 AA:  
 XX SQ

Query Match 98.2%; Score 641; DB 22; Length 120;  
 Best Local Similarity 99.2%; Pred. No. 4.3e-60;  
 Matches 118: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGESVCDSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEA 61  
 DB 2 YAEKSHRGESVCDSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEA 61  
 QY 62 RPKVNCGRGIDDKHNSCKTSQTYVRLTSENKLVGMWIRIDTSCVLSRKIGRT 120  
 DB 62 RPKVNCGRGIDDKHNSCKTSQTYVRLTSENKLVGMWIRIDTSCVLSRKIGRT 120

RESULT 14  
 AAR11306 standard; protein: 136 AA.  
 AAR11306:  
 29-MAY-1991 (first entry)  
 Nerve Growth Factor-like pro-protein from human glioma cells.  
 Nerve growth factor; NGF; cell proliferation; glioma cell.  
 Homo sapiens.  
 Key Location/Qualifiers  
 FT Peptide 1..17  
 FT Peptide /label- propeptide  
 FT Protein 18..136  
 FT Peptide /label- NGF-like polypeptide  
 FT Peptide 18..31  
 FT /note- "12-14 successive amino acids from this

FT Peptide 127..135 peptide are claimed\*  
 FT /label= claimed partial peptide  
 FT /note= "8-9 successive amino acids from this  
 FT peptide are claimed"  
 XX  
 XX EP418590-A.  
 XX  
 XX 27-MAR-1991.  
 XX  
 XX 24-AUG-1990; 90EP-0116234.  
 XX  
 XX 28-AUG-1989; 89JP-0218711.  
 XX 25-MAY-1990; 90JP-0134058.  
 XX  
 XX (TAKE ) TAKEDA CHEMICAL IND KK.  
 XX  
 XX Nakahama K, Fukuda T, Kurokawa T, Kuroshima K;  
 XX WPI: 1991-088264/13.  
 XX N-PSDB: AAQ11097.  
 DR  
 XX  
 XX Antibodies for peptide having sequence similar to nerve growth  
 PT factor - for use in medicine in simple and accurate immunosay  
 PS  
 XX Disclosure: Fig 2; 42pp; English.  
 CC  
 XX A human glioma-derived lambda g11 cDNA library was used to infect E.  
 CC coli 11090 and the colonies transferred to a nylon membrane. The  
 CC filter was screened with labelled DNA coding for human beta-NGF as a  
 CC probe. A positive clone was designated "lambda beta-G1131" and was  
 CC digested with EcoRI. The insert was cloned in EcoRI-digested pUC118  
 CC to give plasmid pUNK5. The cDNA insert was sequenced and the deduced  
 CC amino acid sequence was found to have 60 per cent homology to human  
 CC beta-NGF. The invention relates to an antibody to a peptide  
 CC including at least 8 consecutive amino acids from position 18 to  
 CC position 135 of this sequence.  
 CC See also AAQ11096.  
 CC  
 XX  
 XX Sequence 136 AA:  
 SQ  
 Query Match 98.2%; Score 641; DB 12; Length 136;  
 Best Local Similarity 99.2%; Pred. No. 5.1e-60;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGESYVCSSESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 61  
 DB 18 YAEKSHRGESYVCSSESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 77  
 QY 62 RPYKNGCGRGIDDKHMSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVSAISRKTIGRT 120  
 DB 78 RPYKNGCGRGIDDKHMSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVSAISRKTIGRT 136

RESULT 15  
 AAR26273  
 ID AAR26273 standard; Protein: 240 AA.  
 XX  
 XX AAR26273:  
 AC  
 XX 04-FEB-1993 (first entry)  
 DT  
 XX NGF2/NT-3 in PTB1339.  
 DE  
 XX NGF-2; PTB1344; drug: hippocampus; cerebellum; nodose ganglion.  
 XX  
 XX Synthetic.  
 XX  
 XX key location/Qualifiers  
 FT Peptide 1..18  
 FT /label= signal\_peptide  
 FT Peptide 19..126  
 FT /label= pro-peptide

FT Protein 127..240  
 FT /label= Mature\_NGF2/NT-3  
 XX  
 XX EP499993-A.  
 XX  
 XX 26-AUG-1992.  
 XX  
 XX 15-FEB-1992; 92EP-0102555.  
 XX  
 XX 18-FEB-1991; 91JP-0023579.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Igarashi K, Iwane M, Kaisho Y;  
 XX WPI: 1992-286117/35.  
 XX N-PSDB: AAQ27513.  
 DR  
 XX  
 XX Prodn. of human nerve growth factor-2 - used in research on brain  
 PT and nervous system and as drug for senile dementia  
 PS  
 XX Disclosure: Fig 8; 7pp; English.  
 CC  
 XX The sequences given in AAR26272-73 are the protein encoded by the  
 CC sequences of the human nerve growth factor-2 gene (NGF2/NT-2) within  
 CC the plasmids PTB1339 or PTB1344. (See also AAQ27510-11). NGF2/NT-3 is  
 CC highly expressed in the human hippocampus and cerebellum. It is  
 CC expressed more highly in newborn animals than in adults. It acts on  
 CC nerve cells, such as nodose ganglion derived nerve cells and is thought  
 CC to play a key role in nervous system development. The NGF2/NT-3  
 CC obtained by culturing plasmids PTB1339 or PTB1344 may be used as a  
 CC reagent for research on the brain and nervous system and may be  
 CC expected to serve as a therapeutic drug for senile dementia. The  
 CC plasmid vectors used allow production of NGF2/NT-3 stably and in  
 CC large amounts ie. for industrial large scale production.  
 CC  
 XX  
 XX Sequence 240 AA:  
 SQ  
 Query Match 98.2%; Score 641; DB 13; Length 240;  
 Best Local Similarity 99.2%; Pred. No. 1e-59;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YAEKSHRGESYVCSSESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 61  
 DB 122 YAEKSHRGESYVCSSESLMTDKSSAIDIRGHQVTVLGEIKTNSPVKQFYETRCKEA 181  
 QY 62 RPYKNGCGRGIDDKHMSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVSAISRKTIGRT 120  
 DB 182 RPYKNGCGRGIDDKHMSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVSAISRKTIGRT 240

Search completed: December 2, 2002, 15:08:40  
 Job time : 24.9156 secs

GenCore version 5.1.3  
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# OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:43 ; Search time 9.56624 Seconds  
(without alignments)  
1205.921 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653

Sequence: 1 PYAEKSHRGVSVCSDSL.....RWIRIDSCVSLSRKIGRT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	641	98.2	257	2 C40304	neurotrophin-3 pre
2	641	98.2	258	2 S09155	neurotrophin-3 pre
3	641	98.2	282	2 A35781	hippocampus-derive
4	638	97.7	257	2 I50400	neurotrophin-3 pre
5	392.5	60.1	243	2 A26311	nerve growth facto
6	385	59.0	235	2 S14481	nerve growth facto
7	382.5	58.6	229	2 I46614	nerve growth facto
8	378.5	58.0	245	2 I56570	beta-nerve growth
9	378	57.9	236	2 JH0400	neurotrophin-4 pre
10	375.5	57.2	125	2 A26312	nerve growth facto
11	373.5	57.2	286	1 NGHUBM	nerve growth facto
12	371.5	56.9	241	2 J10097	nerve growth facto
13	370	56.7	303	1 NGPRBA	nerve growth facto
14	368.5	56.4	307	1 NGASMG	nerve growth facto
15	354	54.2	247	2 A40304	brain-derived neur
16	354	54.2	249	2 S12555	brain-derived neur
17	354	54.2	249	2 B40304	brain-derived neur
18	354	54.2	252	2 A30361	brain-derived neur
19	352.5	54.0	243	2 S15193	nerve growth facto
20	352	53.9	209	2 B42687	neurotrophin-4 pre
21	350	53.6	210	2 A42687	neurotrophin-4 pre
22	350	53.6	248	2 JG6183	brain-derived neur
23	349	53.4	117	2 S28161	nerve growth facto
24	349	53.4	269	2 I51708	brain-derived neur
25	345	52.8	114	2 I50606	brain-derived neur
26	343	52.5	114	2 I84765	brain-derived neur
27	326	49.9	114	2 I51599	brain-derived neur
28	323.5	49.5	116	1 NGNXXI	nerve growth facto
29	317.5	48.6	116	2 A58566	nerve growth facto

30	317.5	48.6	246	2 A59218	nerve growth facto
31	295.5	45.3	194	2 I51709	nerve growth facto
32	266	40.7	286	2 S50855	neurotrophin-6 - s
33	78	11.9	1268	2 B88209	protein R02A2.6 (1
34	72	11.0	390	2 JC4023	transforming growt
35	71.5	10.9	145	2 S74292	hypothetical prote
36	71.5	10.9	647	2 C87693	acetyl-CoA synthet
37	71	10.9	326	2 T10166	restriction endonu
38	71	10.9	498	2 B83884	beta-xylosidase /
39	71	10.9	783	2 B91124	probable isomerase
40	71	10.9	783	2 A85369	probable isomerase
41	70.5	10.8	718	2 T05840	subtilisin-like pr
42	70	10.7	759	2 S53922	PMF protein - yea
43	70	10.7	1099	2 T18257	phospholipase C -
44	69.5	10.6	195	2 A13153	hypothetical prote
45	69.5	10.6	230	2 A98134	hypothetical prote

## ALIGNMENTS

### RESULT 1

C40304

neurotrophin-3 precursor - human

M:Alternate names: nerve growth factor 2; NGF-2

C:Species: Homo sapiens (man)

C>Date: 03-Apr-1992 #sequence, revision 30-Sep-1993 #text, change 16-Jul-1999

C:Accession: A36208; JH0141; C40304; S10719; C60536

R:Jones, K.R.; Reichardt, L.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A:Title: Molecular cloning of a human gene that is a member of the nerve growth facto

A:Reference number: A36208; MUID:91045937; PMID:2236018

A:Accession: A36208

A:Molecule type: DNA

A:Residues: 1-257 <JUN>

A:Cross-references: GB:M3763; NID:9189300; PIDN:AA5953.1; PID:9189301

R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nixol

Neuron 4, 767-773, 1990

A:Title: Primary structure and biological activity of a novel human neurotrophic fact

A:Reference number: JH0141; MUID:90265727; PMID:2344409

A:Accession: JH0141

A:Molecule type: DNA

A:Residues: 1-257 <ROS>

R:Naltonperre, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la

Genomics 10, 558-568, 1991

A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene str

A:Reference number: A40304; MUID:91365361; PMID:1889806

A:Accession: C40304

A:Molecule type: DNA

A:Residues: 1-257 <MAI>

A:Cross-references: GB:M61180; NID:9189302; PIDN:AA63231.1; PID:9189303

R:Kaisho, Y.; Yoshimura, K.; Nakahama, K.

FEBS Lett. 266, 187-191, 1990

A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.

A:Reference number: S10719; MUID:90306351; PMID:2365067

A:Accession: S10719

A:Molecule type: mRNA

A:Residues: 1-257 <MAI>

A:Cross-references: GB:M33655; NID:9287794; PIDN:CAA7703.1; PID:9287795

R:Rancopoles, G.D.; Maisomperre, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boul

Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990

A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways

A:Reference number: A60536; MUID:92111157; PMID:1966766

A:Accession: C60536

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-73, 'O', '75-77', 'R', '79-108', 'T', '110-257' <YAN>

C:Genetics:

A:Gene: GDB:MTF3

A:Cross-references: GDB:125917; OMIM:162660

A:Map position: 12p13-12p13

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-18/Domain: propeptide #status predicted <PRO>  
F:139-257/Product: neurotrophin-3 #status predicted <NT>  
F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.2%; Score 641; DB 2; Length 257;  
Best Local Similarity 99.2%; Pred. No. 2.4e-57;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 61  
DB 139 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 198  
OY 62 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 120  
DB 199 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 257

## RESULT 2

S09155  
neurotrophin-3 precursor - mouse  
C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
C:Accession: S09155; S51179  
R:Hohn, A.; Leibrock, J.; Bailey, K.; Barde, Y.A.

Nature 344, 339-341, 1990

A:Title: Identification and characterization of a novel member of the nerve growth factor family  
A:Reference number: S09155; MUID:90190865; PMID:2314473

A:Accession: S09155  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA

A:Residues: 1-258 <NO>  
A:Cross-references: GB:X53257; MUI:953451; PIDN:CAA37348.1; PID:953452

R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.  
Eur. J. Biochem. 225, 995-1003, 1994

A:Title: Characterisation of neurotrophin dimers and monomers.  
A:Reference number: S51179; MUID:95045576; PMID:7957235

A:Accession: S51179  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 140-152 <KOL>

C:Superfamily: nerve growth factor beta chain  
C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>  
F:140-268/Product: neurotrophin-3 #status predicted <NT>  
F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.2%; Score 641; DB 2; Length 258;  
Best Local Similarity 99.2%; Pred. No. 2.5e-57;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 61  
DB 140 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 199  
OY 62 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 120  
DB 200 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 258

## RESULT 3

A35781  
hippocampus-derived neurotrophic factor precursor - rat  
N:Alternate names: neurotrophin-3 precursor

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 16-Jul-1999  
C:Accession: A35781; A40094

R:Ernfors, P.; Ibanez, C.F.; Ebendal, T.; Olson, L.; Persson, H.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5454-5458, 1990

A:Title: Molecular cloning and neurotrophic activities of a protein with structural similarity to nerve growth factor  
A:Reference number: A35781; MUID:90319130; PMID:2164684

A:Accession: A35781  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-282 <ERN>

A:Cross-references: GB:M34643  
R:Malsonpiere, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furch, M.E.; Lindsay, R.M.

Science 247, 1446-1451, 1990

A:Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.  
A:Reference number: A40094; MUID:90208301; PMID:2321006

A:Accession: A40094  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 25-282 <NT>

A:Cross-references: GB:M33968; MUI:9205771; PIDN:AAA11727.1; PID:9205772  
C:Superfamily: nerve growth factor beta chain

Query Match 98.2%; Score 641; DB 2; Length 282;  
Best Local Similarity 99.2%; Pred. No. 2.7e-57;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 61  
DB 164 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 223  
OY 62 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 120  
DB 224 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 282

## RESULT 4

I50400  
neurotrophin-3 precursor - chicken  
C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: I50400; S42227  
R:Malsonpiere, P.C.; Belluscio, L.; Conover, J.C.; Yancopoulos, G.D.

DNA Seq. 3, 49-54, 1992  
A:Title: Gene sequences of chicken BDNF and NT-3.

A:Reference number: I50400; MUID:93091238; PMID:1457809

A:Accession: I50400  
A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA  
A:Residues: 1-257 <NAI>

A:Cross-references: GB:M83378; MUI:9212464; PIDN:AA68880.1; PID:9212465

R:Hallboeck, F.; Ibanez, C.F.; Ebendal, T.; Persson, H.  
Eur. J. Neurosci. 5, 1-14, 1993

A:Title: Cellular localization of brain-derived neurotrophic factor and neurotrophin-3  
A:Reference number: S42227; MUID:94084226; PMID:8074744

A:Accession: S42227  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 32-257 <NAL>  
A:Cross-references: EMBL:Z30092; MUI:9455531; PIDN:CAA82908.1; PID:9927570

C:Genetics:  
A:Gene: NT-3

C:Superfamily: nerve growth factor beta chain

Query Match 97.7%; Score 638; DB 2; Length 257;  
Best Local Similarity 98.3%; Pred. No. 4.9e-57;  
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 61  
DB 139 YAEKSHRGEYSVCDSESLMTDKSSAIDIRGHQVTVLGEITGNSPVKQFYETRCKEA 198  
OY 62 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 120  
DB 199 RPYKNGCRGIDDKHNSOCTSTQTYVRLATSENKLVGWRWIRIDTSCVLSRRKIGRT 257

## RESULT 5

A26311  
nerve growth factor beta chain precursor - chicken (fragment)  
C:Species: Gallus gallus (chicken)

C:Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 21-Jul-2000



```

C:Accession: A26311; A24857; S00127; S12532
R:Edendal, T.; Larnhammar, D.; Persson, H.
EMBO J. 5, 1483-1487, 1986
A>Title: Structure and expression of the chicken beta nerve growth factor gene.
A:Reference number: A26311; MUID:86300646; PMID:3017695
A:Accession: A26311
A:Molecule type: mRNA
A:Residues: 1-243 <EBE>
A:Cross-references: GB:X04003; NID:963697; PIDN:CAA27633.1; PID:g1334740
R:Milom, D.; Perret, C.; Frechin, N.; Keller, A.; Behar, G.; Bricchet, P.; Auffray, C.
FEBS Lett. 203, 82-86, 1986
A>Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in
A:Reference number: A24857; MUID:86248129; PMID:3720959
A:Accession: A24857
A:Molecule type: DNA
A:Residues: 118-243 <MIO>
A:Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:9222840; PIDN:BA00008.1; PID:g
R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
EMBO J. 5, 1489-1493, 1986
A>Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of
A:Reference number: A26311; MUID:86300647; PMID:2427334
A:Accession: S00127
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 121-243 <MEI>
A:Cross-references: GB:M26810; NID:9212446; PIDN:AAA8984.1; PID:9212447
R:Ibanez, C.F.; Hallböök, F.; Edendal, T.; Persson, H.
EMBO J. 9, 1477-1483, 1990
A>Title: Structure-function studies of nerve growth factor: functional importance of hid
A:Reference number: S12532; MUID:90228346; PMID:2328722
A:Accession: S12532
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 126-243 <IBA>
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor
F:1-133/Domain: signal sequence
Fstatus predicted <Sig>
F:136-243/Product: nerve growth factor beta chain
Fstatus predicted <Mat>

Query Match      60.1%   Score 392.5; DB 2; Length 243;
Best Local Similarity 62.5%; Pred. No. 3.2e-37;
Matches 70; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

OY 8 HRGEYSVCSESLMTVDKSSAIDINGHOVTYVAGETIKGNSPFOYETRECKEARPYKXG 67
||||| ||||| -|-||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 132 HRGEFSVCDSVMWVCDKTATTDIKGKEVTYLVGEVININNNFKQYFFETCRDPRPSVG 191
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 68 CRGIDDHNNSSCKTSOTYVRALTSFNKNKLGVNRIRIRIDSVCVALSRKRIG 119
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 192 CRGDIAKHNNSTCTTHTTFVKALIME-GKQAANRFRIIDRTACVCLSKRGR 242
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
S14481
nerve growth factor beta chain precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C:Accession: S14481
R:Carriero, F.; Campton, M.; Cardinali, B.; Pierandrei-Amaldi, P.
Submitted to the EMBL Data Library, October 1990
A:Description: Structure and expression of the nerve growth gene in Xenopus oocyte and e
A:Reference number: S14481
A:Accession: S14481
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-235 <CAR>
A:Cross-references: EMBL:X55716; NID:964914; PIDN:CAA9249.1; PID:g64915
C:Superfamily: nerve growth factor beta chain

Query Match      59.0%   Score 385; DB 2; Length 235;
Best Local Similarity 61.9%; Pred. No. 1.7e-31;
Matches 70; Conservative 18; Mismatches 23; Indels 2; Gaps 2;
```

Oy   8 HRCGYSCDESLMWTDKSSAIDIRGHQVTVLGEIKTGNSPKROYEYERCKREAPRVNG 67  
|::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db   125 HKCEYSVCDSVMWGDKTATDINKEKETVLGEEVININSVFYOFEETCRADPKPVSG 184

Oy   68 CRGIDCKHNNNSOCTSYVRALTSBNKKLVGMNRITIDSVSALSRRKGRT 120  
||||| |||| | ::||::||::||::||::||::||::||  
Db   185 CRGIDAKHHNNSYCCTTHTRTFVKALTME-GKOAAAFRIRIDPACVLSRKAR GRT 235

RESULT 7  
I46614  
nerve growth factor B - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 16-Jul-1999  
R:Lahbib-Ménasria Y.; Mellink, C.; Verle, M.; Cellin, J.  
Cytogetic. Cell Genet. 67: 120-125, 1994  
A>Title: A new marker (NCGB) on pig chromosome 4, isolated by using consensus sequence  
A:Reference number: I46614; MWID:94313891; PMID:8039422  
A:Accession: I46614  
A>Status: preliminary; translated from GB/EMBL/DDBaj  
A:Molecule type: DNA  
A:Residues: 1-229 <LAN>  
A:Cross-references: GB:IJ1898; MID:g476732; PIDN:AAA23301.1; PTD:9533771  
C:Genetics:  
A:Gene: NCGB  
C:Superfamily: nerve growth factor beta chain

Query Match                 58.6%; Score 382.5; DB 2; Length 229;  
Best Local Similarity 60.7%; Pred.No. 3e-31;  
Matches 68; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

Oy   8 HRCGYSCDESLMWTDKSSAIDIRGHQVTVLGEIKTGNSPKROYEYERCKREAPRVNG 67  
|::||::||::||::||::||::||::||::||::||::||::||::||  
Db   117 HRGEFSVCDSVMWDKTTATDINKGETVYLGEVNINNSVFYOFETTCRAPNVDSG 176

Oy   68 CRGIDCKHNNNSOCTSYVRALTSBNKKLVGMNRITIDSVSALSRRKGRT 119  
||||| |||| | ::||::||::||::||::||::||::||  
Db   177 CGRIDSKHNNSCYCTTHTRFVALTMD-GKOAAFRI RIRDPACVLSRKAGR 227

RESULT 8  
I56570  
beta-nerve growth factor - rat (fragment)  
C:Species: Rattus norvegicus (Norway Rat)  
C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
A:Accession: I56570  
R:Whittemore, S.R.; Friedman, P.L.; Larhammer, D.G.; Persson, H.; Gonzalez-Carvajal,  
J. Neurosci. Res. 20, 403-410, 1988  
A>Title: Rat beta-nerve growth factor sequence and site of synthesis In the adult hip  
A:Reference number: I56570; MWID:89037223; PMID:3184206  
A:Accession: I56570  
A>Status: preliminary; translated from GB/EMBL/DDBj  
A:Molecule type: DNA  
A:Residues: 1-245 <RES>  
A:Cross-references: GB:M3589; MID:g205691; PIDN:AAA41697.1; PID:g205692  
C:Superfamily: nerve growth factor beta chain

Query Match                 58.0%; Score 378.5; DB 2; Length 245;  
Best Local Similarity 59.8%; Pred.No. 8.3e-31;  
Matches 67; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

Oy   8 HRGEYSVCDESLLMTVDKSASIIDIRGHQVTVLGELTKGNSPKROYEYERCKREAPRVNG 67  
|::||::||::||::||::||::||::||::||::||::||::||::||  
Db   133 HMGEFSVCDSVMWDKTTATDINKGETVYLGEVNINNSVFYOFETTCRAPNVESG 192

Oy   68 CRGIDCKHNNNSOCTSYVRALTSBNKKLVGMNRITIDSVSALSRRKGRT 119  
||||| |||| | ::||::||::||::||::||::||::||  
Db   193 CCGIDSRKHNSYCCTTHTRTFVKALTMD-DGOAAAFRIRIDPACVLSRKARR 243

RESULT 9  
JHD0400





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A:Molecule type: mRNA
A:Residues: 1-247 <MAX>
A:Cross-references: GB:M61176; MID:g179A04; PIDN:AAA69805.1; PID:g8966463
A:Note: the sequence in GenBank entry H06BDNFb, release 106.0, (PID:g896463) begins tran
R:Yamamoto, H.; Gurney, M.E.
J. Neurosci. 10, 3469-3478, 1990
A>Title: Human platelets contain brain-derived neurotrophic factor.
A:Reference number: A37218; MUID:91038253; PMID:2230938
A:Accession: A37218
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 138-236 <MAX>
R:Kosenthal, A.; Goeddel, D.V.; Nguyen, T.; Martin, E.; Burton, L.E.; Smith, A.; Laramée
Endocrinology 129, 1289-1294, 1991
A>Title: Primary structure and biological activity of human brain-derived neurotrophic f
A:Reference number: A61115; MUID:91339743; PMID:1874171
A:Accession: A61115
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-65, 'M', 67-247 <ROS>
R:ShiLian, A.; Ono, Y.; Katsuo, Y.; Igarashi, K.
Biochem. Biophys. Res. Commun. 182, 325-332, 1992
A>Title: Characterization of the 5'-flanking region of the human brain-derived neurotro
A:Reference number: 138072; MUID:92118032; PMID:1339267
A:Accession: 138072
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247 <SHI>
A:Cross-references: EMBL:X60201; MID:93928269; PIDN:CAA42761.1; PID:g496626
A:Note: the authors do not discuss this mRNA sequence in this reference; attribution is
C:Genetics:
A:Gene: GDNF
A:Cross-references: GDB:125916; OMIM:113505
A:Map position: 11p13-11p13
C:Superfamily: nerve growth factor beta chain
C:Keywords: dimer; glycoprotein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-128/Domain: propeptide #status predicted <PRO>
F:129-247/Product: brain-derived neurotrophic factor #status predicted <MAT>
F:121/Binding site: carbohydrate (asn) (covalent) #status experimental
Query Match 54.2% Score 354; DB 2; Length 247;
Best Local Similarity 57.4% Pred. No. 2,56-28;
Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;
Db 133 ARRGELSYCDISEMYTAAADKTAADMSCGYTLEKPYPSKGLKQYFETKCNPMGYT 192
OY 7 SHREYVYCDSESLAWY--DKSSAIDINGHOVYTGELIKTSNPKVQKPYFETRCKEARPV 64
I :||| ||||| ||| || :||| :| ||||| :|
Db 133 ARRGELSYCDISEMYTAAADKTAADMSCGYTLEKPYPSKGLKQYFETKCNPMGYT 192
OY 65 KNCRGIDDKHNNSOCKTSQTYVRAALTSENNKLVGMWIRIDTSCVALSKRIKGR 119
I :||| ||||| :||| ||||| :| :||| ||||| :| ||
Db 193 KEGCGIDKRNHNSOCTQSYVRAALTMDSKKRIKGMFRIIDTSCVCTLTIKRG 247
Search completed: December 2, 2002, 15:14:00
Job time : 10.5662 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 4.9238 seconds  
(without alignments)  
1010.837 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653  
Sequence: 1 PYAEKSHRGEXVCDSSESL.....RWIRDTSCVSAISRIGRT 120

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	641	98.2	257 1	NT3_HUMAN
2	641	98.2	258 1	NT3_MOUSE
3	641	98.2	258 1	NT3_RAT
4	638	97.7	257 1	NT3_CHICK
5	634	97.1	257 1	NT3_FELCA
6	619	94.8	260 1	NT3_XENLA
7	392.5	60.1	243 1	NGF_XENLA
8	385	59.0	231 1	NGF_CHICK
9	382.5	58.6	229 1	NGF_PIG
10	378.5	58.0	241 1	NGF_RAT
11	378	57.9	236 1	NT4_XENLA
12	373.5	57.2	241 1	NGF_HUMAN
13	372.5	57.0	231 1	NGF_BOVIN
14	371.5	56.9	241 1	NGF_BOVIN
15	370	56.7	241 1	NGF_CAVPO
16	368.5	56.4	241 1	NGF_PANA
17	356	54.5	246 1	BDNF_MOUSE
18	355	54.4	255 1	BDNF_CHICK
19	354	54.2	247 1	BDNF_CAVPO
20	354	54.2	247 1	BDNF_HUMAN
21	354	54.2	247 1	BDNF_PROLO
22	354	54.2	247 1	BDNF_ORSAR
23	354	54.2	249 1	BDNF_ORSML
24	354	54.2	249 1	BDNF_MOUSE
25	354	54.2	252 1	BDNF_PIG
26	352.5	54.0	243 1	NGF_BUNMU
27	352	53.9	209 1	NT5_HUMAN
28	350	53.6	210 1	NT5_RAT
29	350	53.6	247 1	BDNF_FELCA
30	350	53.6	248 1	BDNF_BOVIN
31	350	53.6	270 1	BDNF_CYPCA
32	349	53.4	117 1	NGF_DABRR
33	349	53.4	269 1	BDNF_XIPMA

34	343	52.5	114 1	BDNF_MACMU	006225 macaca mufa
35	326	49.9	116 1	BDNF_XENLA	P25432 xenopus lae
36	320.5	49.1	114 1	NGF_NAJNA	P01140 naja naja (
37	314.5	48.2	116 1	NGF_NAJAT	P21377 naja atra (
38	308	47.2	140 1	NT7_CYPCA	003477 cyprinus ca
39	299	45.8	233 1	NT7_BRARE	071797 brachydonto
40	295.5	45.3	194 1	NGF_XIPMA	P34129 xiphophorus
41	244.5	37.4	257 1	NT6E_HUMAN	P34133 homo sapien
42	241.5	37.0	186 1	NT6G_HUMAN	P34134 homo sapien
43	238.5	36.5	257 1	NT6A_HUMAN	P34132 homo sapien
44	212	32.5	43 1	NT3_RATCL	P25434 raja clavac
45	147	22.5	42 1	NGF_VIPLE	P25428 vipera lebe

## ALIGNMENTS

RESULT 1	NT3_HUMAN	STANDARD:	PRT:	257 AA.
AC	P20783:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (BDNF)			
DE	(Nerve growth factor 2) (NGF-2).			
GN	NT3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606:			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90262727; PubMed=2344409;			
RA	Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,			
RA	Laramee G.R., Nikolic K., Winslow J.W.;			
RT	"Primary structure and biological activity of a novel human			
RT	neurotrophic factor.";			
RL	Neuron 4:767-773(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91045937; PubMed=2236018;			
RA	Jones K.R., Reichardt L.F.;			
RT	"Molecular cloning of a human gene that is a member of the nerve			
RT	growth factor family.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90306351; PubMed=2365067;			
RA	Kaisho Y., Yoshimura K., Nakahama K.;			
RT	"Cloning and expression of a cDNA encoding a novel human neurotrophic			
RT	factor.";			
RL	FEBS Lett. 266:187-191(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91365361; PubMed=1889806;			
RA	Malsompierre P.C., Le Beau M.M., Espinosa R. III, Ip N.Y.,			
RA	Bellusio L., de la Monte S.M., Squitito S., Furch M.E.,			
RT	"Human and rat brain-derived neurotrophic factor and neurotrophin-3:			
RT	gene structures, distributions, and chromosomal localizations.";			
RL	Genomics 10:558-568(1991).			
RN	[5]			
RP	SEQUENCE OF 194-236 FROM N.A.			
RX	TISSUE=leukocyte;			
RA	MEDLINE=91225737; PubMed=2025430;			
RA	Hallboeek F., Ibanez C.F., Persson H.;			
RT	"Evolutionary studies of the nerve growth factor family reveal a			
RT	novel member abundantly expressed in xenopus ovary.";			
RL	Neuron 6:845-858(1991).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).			
RX	MEDLINE=95211877; PubMed=7703225;			



OY 62 RPVKNCGRIDKHNHNSCKTSQTYVRLATSENKLVGMWRIRIDTSCVSLSRKIGRT 120  
 DB 200 RPVKNCGRIDKHNHNSCKTSQTYVRLATSENKLVGMWRIRIDTSCVSLSRKIGRT 258

RESULT 3  
 NT3\_RAT STANDARD: PRT: 258 AA.  
 ID NT3\_RAT  
 AC P16280:  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)  
 DE (Nerve growth factor 2) (NGF-2).  
 GN NTF3 OR NTF-3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90319130; PubMed-2164684;  
 RA Ertfofs P., Ibanez C.F., Ebendal T., Olson L., Persson H.;  
 RT "Molecular cloning and neurotrophic activities of a protein with  
 RT structural similarities to nerve growth factor: developmental and  
 RT topographical expression in the brain";  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:5454-5458(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90208301; PubMed-2321006;  
 RA Maisompierre P.C., Belluscio L., Squinto S., Ip N.Y., Furch M.E.,  
 RA Lindsay R.M., Yancopoulos G.D.;  
 RT "Neurotrophin-3: a neurotrophic factor related to NGF and BDNF";  
 RT Science 247:1446-1451(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91365361; PubMed-1898906;  
 RA Maisompierre P.C., le Beau M.M., Espinosa R. III, Ip N.Y.,  
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,  
 RA Yancopoulos G.D.;  
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:  
 RT gene structures, distributions, and chromosomal localizations";  
 RT Genomics 10:558-568(1991).  
 RN [4]  
 RP SEQUENCE OF 195-237 FROM N.A.  
 RX STRAIN-Sprague-Dawley; TISSUE-liver;  
 RX MEDLINE-9122573; PubMed-2025430;  
 RA Hallboeek F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary";  
 RT Neuron 6:845-858(1991).  
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND  
 CC PROPRIOCEPTIVE SENSOR NEURONS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: M34643; AAA41313.1; -;  
 DR EMBL: M33968; AAA41727.1; -;  
 DR EMBL: M51179; AAA63497.1; -;  
 DR PIR: A35781; A35781;  
 DR PIR: A40094; A40094;  
 DR HSSP: P20783; 188X;  
 DR InterPro: IPR002400; GF\_cysknot.

DR InterPro: IPR002072; NGF.  
 DR Pfam: PR00243; NGF; 1.  
 DR PRINTS: PR00438; GFcysknot.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KR Growth factor; Signal.

FT SIGNAL 1 16  
 FT PROPEP 17 139  
 FT CHAIN 140 258  
 FT DISULFID 153 218  
 FT DISULFID 196 247  
 FT DISULFID 206 249  
 FT CARBOHYD 131 131  
 SO SEQUENCE 258 AA; 29644 MW; 74D537CF8518A1CE CRC64; N-LINKED (GLCNAc...)(POTENTIAL).

Query Match 98.2%; Score 641; DB 1; Length 258;  
 Best Local Similarity 99.2%; Pred. No. 2,2e-59;  
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHREYSCDSSESLMTDSSAIDIRGHOTVYGEIKTGNSPVQYETCKEA 61  
 DB 140 YAEKSHREYSCDSSESLMTDSSAIDIRGHOTVYGEIKTGNSPVQYETCKEA 199  
 OY 62 RPVKNCGRIDKHNHNSCKTSQTYVRLATSENKLVGMWRIRIDTSCVSLSRKIGRT 120  
 DB 200 RPVKNCGRIDKHNHNSCKTSQTYVRLATSENKLVGMWRIRIDTSCVSLSRKIGRT 258

RESULT 4  
 NT3\_CHICK STANDARD: PRT: 257 AA.  
 ID NT3\_CHICK  
 AC P23433;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)  
 DE (Nerve growth factor 2) (NGF-2).  
 GN NTF3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_Taxid=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91091238; PubMed-1457809;  
 RA Maisompierre P., Belluscio L., Conover J.C., Yancopoulos G.D.;  
 RT "Gene sequences of chicken BDNF and NT-3";  
 RT DNA Seq. 3:49-54(1992).  
 RN [2]  
 RP SEQUENCE OF 194-236 FROM N.A.  
 RX MEDLINE-9122573; PubMed-2025430;  
 RA Hallboeek F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary";  
 RT Neuron 6:845-858(1991).  
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND  
 CC PROPRIOCEPTIVE SENSOR NEURONS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M63378; AAA68880.1; -;

DR HSSP: P20783; 188K.  
DR InterPro: IPR002400; GF\_cysknot.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF\_1.  
DR PRINTS: PR00438; GFCSKNOT.  
DR PRINTS: PR00268; NGF.  
DR ProDom: PD02052; NGF\_1.  
DR SMART: SM00140; NGF\_1.  
DR PROSITE: PS00248; NGF\_1; 1.  
DR PROSITE: PS50270; NGF\_2; 1.  
KM Growth factor; Signal.  
FT SIGNAL 1 16 POTENTIAL.  
FT PROPEP 17 138  
FT CHAIN 139 257 NEUROTROPHIN-3.  
FT DISULFID 152 217 BY SIMILARITY.  
FT DISULFID 195 246 BY SIMILARITY.  
FT DISULFID 205 248 BY SIMILARITY.  
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 257 AA; 29701 MW; E8043BA2A005C1E7 CRC64;

Query Match 97.7% Score 638; DB 1; Length 257;  
Best Local Similarity 98.3%; Pred. No. 4; Se-59;  
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDESESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 61  
DB 139 YAEKSHRGEYSVCDESESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 198  
OY 62 RPYKNGCRGIDDKHNSQCKTSQTVYRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 120  
DB 199 RPYKNGCRGIDDKHNSQCKTSQTVYRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 257

RESULT 5  
NT3\_FELCA STANDARD; PRT: 257 AA.  
ID NT3\_FELCA  
AC GPTSTZ;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)  
DE (Nerve growth factor 2) (NGF-2).  
GN NTFS.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Feliidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20211727; PubMed=10745216;  
RA Iain E.S., Hohn A., Shatz C.J.;  
RT "Dynamic regulation of BDNF and NT-3 expression during visual system development."  
RL J. Comp. Neurol. 420:1-18(2000).  
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND  
CC -1- PHOTORECEPTIVE SENSOR NEURONS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC -----  
CC EMBL: AF192538; AAF03424.1; -  
CC HSSP: P20783; 188K.  
CC InterPro: IPR002072; NGF.  
CC Pfam: PF00243; NGF\_1.  
CC PRINTS: PR00268; NGF.  
CC ProDom: PD02052; NGF\_1.

DR SMART: SM00140; NGF\_1.  
DR PROSITE: PS00248; NGF\_1; 1.  
DR PROSITE: PS50270; NGF\_2; 1.  
KM Growth factor; Signal.  
FT SIGNAL 1 16 POTENTIAL.  
FT PROPEP 17 138  
FT CHAIN 139 257 NEUROTROPHIN-3.  
FT DISULFID 152 217 BY SIMILARITY.  
FT DISULFID 195 246 BY SIMILARITY.  
FT DISULFID 205 248 BY SIMILARITY.  
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 257 AA; 29403 MW; E83JF7E59C5113E4 CRC64;

Query Match 97.1% Score 634; DB 1; Length 257;  
Best Local Similarity 97.5%; Pred. No. 1; Se-58;  
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGEYSVCDESESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 61  
DB 139 YAEKSHRGEYSVCDESESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKNQYFETRCKEA 198  
OY 62 RPYKNGCRGIDDKHNSQCKTSQTVYRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 120  
DB 199 RPYKNGCRGIDDKHNSQCKTSQTVYRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 257

RESULT 6  
NT3\_XENLA STANDARD; PRT: 260 AA.  
ID NT3\_XENLA  
AC P23435;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF) (Nerve  
DE growth factor 2) (NGF-2).  
OS Xenopus laevis (African clawed frog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97252639; PubMed=9096131;  
RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;  
RT "Activity-dependent expression of NT-3 in muscle cells in culture:  
RT implications in the development of neuromuscular junctions."  
RL J. Neurosci. 17:2947-2958(1997).  
RN [2]  
RP SEQUENCE OF 197-217 FROM N.A.  
RX TISSUE=Liver.  
RX MEDLINE=9122573; PubMed=2025430;  
RA Hallboeek E., Ibanez C.F., Persson H.;  
RT "Evolutionary studies of the nerve growth factor family reveal a  
RT novel member abundantly expressed in Xenopus ovary."  
RL Neuron 6:845-858(1991).  
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND  
CC -1- PHOTORECEPTIVE SENSOR NEURONS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC -----  
CC EMBL: U27576; AB17723.1; -  
CC HSSP: P20783; 188K.  
CC InterPro: IPR002400; GF\_cysknot.  
CC InterPro: IPR002072; NGF.



DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PRO0268; NGF.  
 DR PRODOM: PRO0268; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 16  
 FT PROPEP 17 141 POTENTIAL.  
 FT CHAIN 142 260 NEUROTROPHIN-3.  
 FT DISULFID 155 220 BY SIMILARITY.  
 FT DISULFID 198 249 BY SIMILARITY.  
 FT DISULFID 208 251 BY SIMILARITY.  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 260 AA; 30022 MW; FEB8507A5EA930C5 CRC64;

Query Match 94.88; Score 619; DB 1; Length 260;  
 Best Local Similarity 94.18; Pred. No. 4, 2e-57;  
 Matches 112; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 YAEKSHRGEXVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTGNSPVQYETRECKEA 61  
 DB 142 FAEHKSHRGEXVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTGNSPVQYETRECKEA 201  
 OY 62 RPKNGCGRIDKHNNSCKTSQTYVRLTSENKLVGWRIRIDTSCVSAISRIGRT 120  
 DB 202 RPKNGCGRIDKHNNSCKTSQTYVRLTSENKLVGWRIRIDTSCVSAISRIGRTS 260

## RESULT 7

NGF\_CHICK  
 ID NGF\_CHICK STANDARD; PRT; 243 AA.

AC 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 13-JUN-2002 (Rel. 41, Last annotation update)  
 DE Beta-nerve growth factor precursor (Beta-NGF).  
 CN NGFB.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RX SEQUENCE FROM N.A.  
 RA MEDLINE=86300646; PubMed=3017695;  
 RA Ebdendahl T., Lachhammer D., Persson H.;  
 RT Structure and expression of the chicken beta nerve growth factor  
 RT gene.\*;  
 RL EMBO J. 5:1483-1487(1986).  
 RN [2]

RP SEQUENCE OF 118-243 FROM N.A.  
 RX MEDLINE=86248129; PubMed=3720959;  
 RA Wilson D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,  
 RA Aulicay C.;  
 RT "Molecular cloning of the avian beta-nerve growth factor gene:  
 RT transcription in brain.\*";  
 RL FEBS Lett. 203:82-86(1986).  
 RN [3]

RP SEQUENCE OF 121-243 FROM N.A.  
 RX MEDLINE=86300647; PubMed=2427334;  
 RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;  
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):  
 RT delineation of conserved and unconserved domains and their  
 RT relationship to the biological activity and antigenicity of NGF.\*";  
 RL EMBO J. 5:1489-1493(1986).  
 RN [4]

RP SEQUENCE OF 181-222 FROM N.A.  
 RX MEDLINE=91225573; PubMed=2035430;  
 RA Hallböök F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary.\*";

RL Neuron 6:845-858(1991).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSOR NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSOR NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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DR EMBL: X04003; CAA27633.1; ALT\_INIT.  
 DR EMBL: X04067; CAA27703.1;  
 DR EMBL: M26810; AAA48984.1;  
 DR PIR: A24857; A24857.  
 DR PIR: A26311; A26311.  
 DR HSSP: P01139; 1BET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PRO0268; NGF.  
 DR PRODOM: PRO02052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS50270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PROPEP 23 125  
 FT CHAIN 126 243 BETA-NERVE GROWTH FACTOR.  
 FT DISULFID 139 204 BY SIMILARITY.  
 FT DISULFID 182 232 BY SIMILARITY.  
 FT DISULFID 192 234 BY SIMILARITY.  
 SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 60.14; Score 392.5; DB 1; Length 243;  
 Best Local Similarity 62.58; Pred. No. 1, 2e-13;  
 Matches 70; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

OY 8 HNGEYVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTGNSPVQYETRECKEARPKNG 67  
 DB 132 HNGEYVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTGNSPVQYETRECKEARPKNG 119  
 OY 68 CRGIDKHNNSCKTSQTYVRLTSENKLVGWRIRIDTSCVSAISRIGRT 119  
 DB 192 CRGIDKHNNSCKTSQTYVRLTSENKLVGWRIRIDTSCVSAISRIGRTS 242

## RESULT 8

NGF\_XENLA  
 ID NGF\_XENLA STANDARD; PRT; 231 AA.

AC P21617;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Nerve growth factor precursor (NGF).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RX SEQUENCE FROM N.A.  
 RP MEDLINE=91362944; PubMed=1888511;  
 RA Carriero F., Campioni M., Cardinelli B., Pierandrei-Amaldi P.;  
 RT "Structure and expression of the nerve growth factor gene in Xenopus  
 RT oocytes and embryos.\*";  
 RL Mol. Reprod. Dev. 29:313-322(1991).  
 RN [2]  
 RP SEQUENCE OF 170-211 FROM N.A.

CC TISSUE-Liver!  
 CC MEDLINE-9122573; PubMed-2025430;  
 CC RA Halboeck F., Ibanez C.F., Persson H.;  
 CC "Evolutionary studies of the nerve growth factor family reveal a  
 CC novel member abundantly expressed in Xenopus ovary."  
 CC RL Neuron 6:845-858(1991).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 CC EMBL: X55716; CAA39249.1; ALT\_INIT.  
 CC DR PIR: S14481; S14481.  
 CC DR HSSP: P01139; 1BET.  
 CC DR InterPro: IPR002072; NGF.  
 CC DR Pfam: PF00243; NGF\_1.  
 CC DR PRINTS: PF00268; NGF\_1.  
 CC DR PRODOM: PD002052; NGF\_1.  
 CC DR SMART: SM00140; NGF\_1.  
 CC DR PROSITE: PS00248; NGF\_1; 1.  
 CC DR PROSITE: PS50270; NGF\_2; 1.  
 CC DR Growth factor; Signal.  
 CC KW SIGNAL 1 18  
 CC FT PROPEP 19 114 POTENTIAL.  
 CC FT CHAIN 115 231 NERVE GROWTH FACTOR.  
 CC FT DISULFID 128 193 BY SIMILARITY.  
 CC FT DISULFID 171 221 BY SIMILARITY.  
 CC FT DISULFID 181 223 BY SIMILARITY.  
 CC FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SO SEQUENCE 231 AA; 26416 MW; 72A04E7D00858C5 CRC64;  
 CC -----  
 CC Query Match 59.0%; Score 385; DB 1; Length 231;  
 CC Best Local Similarity 61.9%; Pred. No. 7e-33;  
 CC Matches 70; Conservative 18; Mismatches 23; Indels 2; Gaps 2;  
 CC -----  
 CC QY 8 HRGEYSVDSLSMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEAPYKNG 67  
 CC DB 121 HKGEYSVDSLSMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEAPYKNG 180  
 CC QY 68 CRGIDDKHNSCKTSQTYVRALTSNNKLVGWRMRIRIDTSCVSLSKRIGT 120  
 CC DB 181 CRGIDDKHNSCKTSQTYVRALTSNNKLVGWRMRIRIDTSCVSLSKRIGT 231  
 CC -----  
 CC RESULT 9  
 CC ID NGF\_PIG STANDARD; PRT; 229 AA.  
 CC AC Q29074;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE Beta-nerve growth factor precursor (beta-NGF) (Fragment).  
 CC GN NGFB.  
 CC OS Sus scrofa (Pig).  
 CC CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 CC NCBI\_TaxID=9823;  
 CC RX NCBI\_TaxID=9823;  
 CC RN SEQUENCE FROM N.A.  
 CC RC STRAIN=large white; Tissue=Blood;  
 CC MEDLINE=94313891; PubMed=8039422;

CC RA Lahbib-Mansais Y., Mellink C., Yerie M., Gallin J.;  
 CC "A new marker (NGFB) on pig chromosome 4, isolated by using a  
 CC consensus sequence conserved among species."  
 CC RT Cytogenet. Cell Genet. 67:120-125(1994).  
 CC CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 CC -----  
 CC EMBL: L31898; AAA21301.1; -  
 CC DR HSSP: P01139; 1BET.  
 CC DR InterPro: IPR002072; NGF.  
 CC DR Pfam: PF00243; NGF\_1.  
 CC DR PRODOM: PD002052; NGF\_1.  
 CC DR SMART: SM00140; NGF\_1.  
 CC DR PROSITE: PS00248; NGF\_1; 1.  
 CC DR PROSITE: PS50270; NGF\_2; 1.  
 CC KW Growth factor; Signal.  
 CC FT NON\_TER 1 1  
 CC FT SIGNAL <1 6  
 CC FT PROPEP 7 109 POTENTIAL.  
 CC FT CHAIN 110 229 BETA-NERVE GROWTH FACTOR.  
 CC FT DISULFID 124 189 BY SIMILARITY.  
 CC FT DISULFID 167 217 BY SIMILARITY.  
 CC FT DISULFID 177 219 BY SIMILARITY.  
 CC FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SO SEQUENCE 229 AA; 25275 MW; FE8890771CBA189 CRC64;  
 CC -----  
 CC Query Match 58.6%; Score 382.5; DB 1; Length 229;  
 CC Best Local Similarity 60.7%; Pred. No. 1.3e-32;  
 CC Matches 68; Conservative 18; Mismatches 25; Indels 1; Gaps 1;  
 CC -----  
 CC QY 8 HRGEYSVDSLSMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEAPYKNG 67  
 CC DB 117 HKGEYSVDSLSMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRECKEAPYKNG 176  
 CC QY 68 CRGIDDKHNSCKTSQTYVRALTSNNKLVGWRMRIRIDTSCVSLSKRIGT 119  
 CC DB 177 CRGIDDKHNSCKTSQTYVRALTSNNKLVGWRMRIRIDTSCVSLSKRIGT 227  
 CC -----  
 CC RESULT 10  
 CC ID NGF\_RAT STANDARD; PRT; 241 AA.  
 CC AC P25427;  
 CC DT 01-MAY-1992 (Rel. 22, Created)  
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE Beta-nerve growth factor precursor (beta-NGF).  
 CC GN NGFB.  
 CC OS Rattus norvegicus (Rat).  
 CC CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 CC RX NCBI\_TaxID=10116;  
 CC RN SEQUENCE FROM N.A.  
 CC RC MEDLINE=89037223; PubMed=3184206;  
 CC RX Whittemore S.R., Friedman P.L., Larhammar D.G., Persson H.,  
 CC Gonzalez-Carvajal M., Holets V.R.;  
 CC "Rat beta-nerve growth factor sequence and site of synthesis in the  
 CC adult hippocampus."

RL J. Neurosci. Res. 20:403-410(1988).

RP [2]

RC SEQUENCE OF 178-219 FROM N.A.

RC STRAIN-Sprague-Dawley; TISSUE-Liver;

RX MEDLINE-91222573; PubMed-2025430;

RA Haliboeck F., Ibanez C.F., Persson H.;

RT "Evolutionary studies of the nerve growth factor family reveal a novel member abundantly expressed in xenopus ovary."

RL Neuron 5:845-858(1991).

CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NEUROUS SYSTEMS. IT STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND EMBRYONIC SENSORY NEURONS.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC EMBL: M36589; AAA41697.1; ALT\_INIT.

DR HSSP: P01139; 1BET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF\_1; 1.

DR PROSITE: PS02070; NGF\_2; 1.

KW Growth factor; Signal.

FT SIGNAL 1

FT PROPEP 19

FT CHAIN 121

FT DISULFID 122

FT DISULFID 136

FT DISULFID 179

FT DISULFID 189

FT CARBOHD 69

FT CARBOHD 114

FT CARBOHD 166

SO SEQUENCE 241 AA; 27009 MW; 665f42371563213D CRC64;

Query Match 58.0%; Score 378.5; DB 1; Length 241;

Best Local Similarity 59.8%; Pred. No. 3.5e-32;

Matches 67; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

OY 8 HNGEVSVDSESLAWTDSKSAIDIRGHQVYLGKIKGNSPVQYFETRCKEARPVKN 67

DB 129 HNGEVSVDSESLAWTDSKSAIDIRGHQVYLGKIKGNSPVQYFETRCKEARPVKN 188

OY 68 CGCIDDKHNSCKTSQTYVALTSNNKLVGRNIRIDTSCVSAISRIGT 119

DB 189 CGCIDSKHNSYCTTHFVAKLTLD-KQAMWRFIRIDTACVLSRKAR 239

RESULT 11

NT4\_XENLA STANDARD: PRT: 236 AA.

AC P24727;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neurotrophin-4 precursor (NT-4).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_Taxid=8355;

RA [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RX MEDLINE-91222573; PubMed-2025430;

RA Haliboeck F., Ibanez C.F., Persson H.;

RT "Evolutionary studies of the nerve growth factor family reveal a novel member abundantly expressed in xenopus ovary."

RL Neuron 5:845-858(1991).

CC -1- FUNCTION: NT-4 COULD PLAY A ROLE IN OOCYTESIS AND/OR EARLY AND ELICITS NEURITE OUTGROWTH FROM EXPLANTED DORSAL ROOT GANGLIA WITH NO AND LOWER ACTIVITY IN SYMPATHETIC AND NODOSE GANGLIA, RESPECTIVELY.

CC -1- TISSUE SPECIFICITY: OVARY.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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CC EMBL: Z30090; CAA82906.1; "

DR PIR: JH0400; JH0400.

DR HSSP: P34130; 1B98.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF\_1; 1.

DR PROSITE: PS02070; NGF\_2; 1.

KW Growth factor; Signal.

FT SIGNAL 1

FT PROPEP 19

FT CHAIN 114

FT DISULFID 114

FT DISULFID 131

FT DISULFID 174

FT DISULFID 184

FT CARBOHD 47

FT CARBOHD 106

SO SEQUENCE 236 AA; 26213 MW; A210F97F2016357D CRC64;

Query Match 57.9%; Score 378; DB 1; Length 236;

Best Local Similarity 59.6%; Pred. No. 3.8e-32;

Matches 68; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

OY 7 SHNGEVSVDSESLAWTDSKSAIDIRGHQVYLGKIKGNSPVQYFETRCKEARPVKN 66

DB 123 SHNGEVSVDSESLAWTDSKSAIDIRGHQVYLGKIKGNSPVQYFETRCKEARPVKN 182

OY 67 GCGSIDDKHNSCKTSQTYVALTSNNKLVGRNIRIDTSCVSAISRIGT 120

DB 183 GCGGVKQKIVISCKAKQSYVALTIDANKLVGRNIRIDTACVLTLSRTGT 236

RESULT 12

NGF\_HUMAN STANDARD: PRT: 241 AA.

AC P01138;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Beta-nerve growth factor precursor (beta-NGF).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9605;

RA [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-83244969; PubMed-6688123;

RA Ullrich A., Gray A., Berman C., Dull T.J.;





Mon Dec 2 15:36:41 2002

us-10-072-681-5.rsp

Page 10

OY 116 KIGR 119  
|  
DB 236 KAPR 239

Search completed: December 2, 2002, 15:12:44  
Job time : 5.9238 secs



FT NON\_TER 241 241  
SEQ SEQUENCE 27803 MW: AB95E457CB07113 CRC64:  
Query Match 89.3%; Score 583; DB 6; Length 241;  
Best Local Similarity 100.0%; Pred. No. 7,5e-58;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YAEHSHRGESVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
DB 136 YAEHSHRGESVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 195  
OY 62 RPKKNCRCGIDKHNNSCKTSQTYVRALTSNNKLVGMWRIRDT 107  
DB 196 RPKKNCRCGIDKHNNSCKTSQTYVRALTSNNKLVGMWRIRDT 241

RESULT 2  
O9P208 PRELIMINARY; PRT; 241 AA.  
AC O9P208; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Beta-nerve growth factor (Fragment).  
GN BETA-NGF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RM (1)  
RP SEQUENCE FROM N.A.  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB037517; BAA90437.1; -  
DR HSSP: P01139; 1BET.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF.1.  
DR PRINTS: PR00268; NGF.  
DR PRODOM: PD002052; NGF.1.  
DR SMART: SM00140; NGF.1.  
DR PROSITE: PS00248; NGF.1; 1.  
DR PROSITE: PS50270; NGF.2; 1.  
FT NON\_TER 241 241  
SQ SEQUENCE 241 AA; 26998 MW; D5531ED825D96C14 CRC64;

Query Match 57.2%; Score 373.5; DB 4; Length 241;  
Best Local Similarity 59.8%; Pred. No. 3,8e-34;  
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRGEYSVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 67  
DB 129 HRGEYSVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 188  
OY 68 CRGIDSKHNSYCTTHTFYKALTM-D-GKQAMRFRIIDTACVLSKRAVR 239  
DB 189 CRGIDSKHNSYCTTHTFYKALTM-D-GKQAMRFRIIDTACVLSKRAVR 239

RESULT 3  
O9UKL8 PRELIMINARY; PRT; 241 AA.  
AC O9UKL8; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Nerve growth factor B.  
GN NGFB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RM (1)

RP SEQUENCE FROM N.A.  
RX MEDLINE=99256269; PubMed=10322959;  
RA Tong Y., Wang H., Chen W.;  
RT "Cloning and sequencing of the gene for premature beta nerve growth  
factor";  
RL Chung Kuo ying yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).  
RM (1)  
RP SEQUENCE FROM N.A.  
RA Tong Y., Wang H.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF150960; AAD55975.1; -  
DR HSSP: P01139; 1BET.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF.1.  
DR PRINTS: PR00268; NGF.1.  
DR PRODOM: PD002052; NGF.1.  
DR SMART: SM00140; NGF.1.  
DR PROSITE: PS00248; NGF.1; 1.  
DR PROSITE: PS50270; NGF.2; 1.  
SQ SEQUENCE 241 AA; 26959 MW; 619DFC65EB3BD671 CRC64;

Query Match 57.2%; Score 373.5; DB 4; Length 241;  
Best Local Similarity 59.8%; Pred. No. 3,8e-34;  
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRGEYSVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 67  
DB 129 HRGEYSVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 188  
OY 68 CRGIDSKHNSYCTTHTFYKALTM-D-GKQAMRFRIIDTACVLSKRAVR 239  
DB 189 CRGIDSKHNSYCTTHTFYKALTM-D-GKQAMRFRIIDTACVLSKRAVR 239

RESULT 4  
O9N2F1 PRELIMINARY; PRT; 241 AA.  
AC O9N2F1; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Beta-nerve growth factor (Fragment).  
GN BETA-NGF.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
OX NCBI\_TaxID=9598;  
RM (1)  
RP SEQUENCE FROM N.A.  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB037518; BAA90438.1; -  
DR HSSP: P01139; 1BET.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF.1.  
DR PRINTS: PR00268; NGF.1.  
DR PRODOM: PD002052; NGF.1.  
DR SMART: SM00140; NGF.1.  
DR PROSITE: PS00248; NGF.1; 1.  
DR PROSITE: PS50270; NGF.2; 1.  
FT NON\_TER 241 241  
SQ SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match 57.2%; Score 373.5; DB 6; Length 241;  
Best Local Similarity 59.8%; Pred. No. 3,8e-34;  
Matches 67; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

OY 8 HRGEYSVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 67  
DB 129 HRGEYSVCSLSMTYDKSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEARPYKNG 188





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RX MEDLINE-20193595; PubMed-10727739;
RA Johnson F., Norstrom E., Soderstrom K.;
RT "Increased expression of endogenous biotin, but not BDNF, in
RL telencephalic song regions during zebra finch vocal learning.";
RL Brain Res. Dev. Brain Res. 120:113-123(2000).
DR EMBL: AF255389; AAF78050.2; -.
DR HSSP: P23560; 1BBM.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF; 1; 1.
DR PROSITE: PS50270; NCF; 2; 1.
FT NON_TER
SQ SEQUENCE 177 AA; 20273 MW; BDB9031515BD369D CRC64;

Query Match 54.5%; Score 356; DB 13; Length 177;
Best Local Similarity 58.3%; Pred. No. 2; Se-32;
Matches 67; Conservative 16; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGESVCDSESLWT--DKSSAIDIRGHQVTVLGEIKTNSPVKQYFETCKEARPV 64
DB 63 ARRGELSVCDSTSEWTALEKKTAVDMGATVLEKVPVKGLKQFETCKCNPKGYT 122
OY 65 KNGCRGIDDKHNSOCKTSQTYVRAVLTSENNKLVGMWRIRIDTSCVSLSRKIGR 119
DB 123 KEGCRGIDDKHNSOCKTSQTYVRAVLTMDNKKRVGMFRIRIDTSCVTLTKRGR 177

RESULT 9
OQ0C76 PRELIMINARY; PRT; 246 AA.
AC OQ0C76;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Japalura splendida.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Actodontia; Agamidae; Dipsosauria;
OC Japalura.
OC NCBI_TaxID=118209;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao M., Yang Y.H., Zhang Y.Z.;
RT "Molecular cloning of brain derived neurotrophic factor gene from
RT amphibians and reptiles and its application in the research of
RT phylogeny and taxonomy.";
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF497713; AAM18714.1; -.
FT CHAIN 128 246
FT PRECURSOR.
SQ SEQUENCE 246 AA; 27883 MW; 47B1A03DA838FD8 CRC64;

Query Match 54.4%; Score 355; DB 13; Length 246;
Best Local Similarity 57.4%; Pred. No. 4; Se-32;
Matches 66; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

OY 7 SHRGESVCDSESLWT--DKSSAIDIRGHQVTVLGEIKTNSPVKQYFETCKEARPV 64
DB 132 ARRGESVCDSTSEWTALEKKTAVDMGATVLEKVPVKGLKQFETCKCNPKGYT 191
OY 65 KNGCRGIDDKHNSOCKTSQTYVRAVLTSENNKLVGMWRIRIDTSCVSLSRKIGR 119
DB 192 KEGCRGIDDKHNSOCKTSQTYVRAVLTMDNKKRVGMFRIRIDTSCVTLTKRGR 246

RESULT 10
OQ0C73 PRELIMINARY; PRT; 153 AA.
AC OQ0C73;

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DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Brain derived neurotrophic factor.
GN BDNF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6J; TISSUE-EMBRYO;
RX MEDLINE-21085650; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasl C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Burt C., Fletcher C., Fujita N., Gariboldi M.,
RA Guelincich S., Hill D., Holman M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata C., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weiss C., Whitaker C., Wilming L.,
RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RN "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK017559; BAB30805.1; -.
DR HSSP: P23560; 1BBM.
DR MGD: MGI:88145; Bdnf.
DR InterPro: IPR002072; NCF.
DR Pfam: PF00243; NCF; 1.
DR PRINTS: PR00268; NCF.
DR PRODOM: PD002052; NCF; 1.
DR SMART: SM00140; NCF; 1.
DR PROSITE: PS00248; NCF; 1; 1.
DR PROSITE: PS50270; NCF; 2; 1.
SQ SEQUENCE 153 AA; 17519 MW; CABEB944CE5B37 CRC64;

Query Match 54.2%; Score 354; DB 11; Length 153;
Best Local Similarity 57.4%; Pred. No. 3; Se-32;
Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGESVCDSESLWT--DKSSAIDIRGHQVTVLGEIKTNSPVKQYFETCKEARPV 64
DB 39 ARRGELSVCDSTSEWTALEKKTAVDMGATVLEKVPVKGLKQFETCKCNPKGYT 98
OY 65 KNGCRGIDDKHNSOCKTSQTYVRAVLTSENNKLVGMWRIRIDTSCVSLSRKIGR 119
DB 99 KEGCRGIDDKHNSOCKTSQTYVRAVLTMDNKKRVGMFRIRIDTSCVTLTKRGR 153

RESULT 11
OQ0W38 PRELIMINARY; PRT; 241 AA.
AC OQ0W38;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative neurotrophic growth factor.
GN NGF.
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxID=8726;
RN [1]

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RP SEQUENCE FROM N.A.  
 RC TISSUE-VENOM GLAND:  
 RA Koshima S., Pereira J.O., Atolift Filho S., Soares A.M.,  
 RA Cinctra A.C.O., Giglio J.R., Franca S.C.;  
 RT "Molecular cloning and cDNA sequence of a nerve growth factor  
 RT precursor from Bothrops jararacussu venomous gland."  
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY007318; AAG12169.1;  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR ProDom: PD002052; NGF.1.  
 DR PROSITE: PS00248; NGF.1;  
 DR PROSITE: PS0270; NGF.2; 1.  
 SO SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CRC64;

Query Match 54.2%; Score 354; DB 13; Length 241;  
 Best Local Similarity 55.3%; Pred. No. 6.2e-32;  
 Matches 63; Conservative 22; Mismatches 27; Indels 2; Gaps 2;

OY 4 EKHSH-NGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEAR 62  
 DB 124 DHPVHNGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEAR 183  
 OY 63 PVKNGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVSLSTR 116  
 DB 184 PVPTGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVSLSTR 236

RESULT 12  
 OY97759 PRELIMINARY; PRT; 247 AA.  
 ID 097759;  
 AC 097759;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE Brain derived neurotrophic factor.  
 GN BDNF.  
 OS Allurus fulgens (lesser panda).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Flapsipedia; Procyonidae; Allurus.  
 OC NCB1\_TaxID=9649;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Feng L.;  
 RT "clant Panda (GP) and Lesser Panda (LP) BDNF gene sequences and their  
 RT deduced amino acid sequences."  
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U56639; AAD10843.1;  
 DR HSSP: P23560; 188M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRINTS: PR00268; NGF.  
 DR ProDom: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF.1;  
 DR PROSITE: PS0270; NGF.2; 1.  
 SO SEQUENCE 247 AA; 27870 MW; FEB6C62CF1A6C03EE CRC64;

Query Match 54.2%; Score 354; DB 6; Length 247;  
 Best Local Similarity 57.4%; Pred. No. 6.4e-35;  
 Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEARPV 64  
 DB 133 ARGEISVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEARPV 192  
 OY 65 KNGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVSLSTR 119  
 DB 193 KEGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVSLSTR 247

RESULT 13  
 OY97H14

ID 08VH14 PRELIMINARY; PRT; 249 AA.  
 AC 08VH14;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Anorexia BDNF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B6C3FE-A/A-ANXA/+A;  
 RA Kim S.J., Kim C.S., Cha Y.J., Song K.Y., Yeo M.G.;  
 RT "Anorexia mouse ORF BDNF."  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF459642; AAL58475.1;  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF.1.  
 DR PRINTS: PR00268; NGF.  
 DR ProDom: PD002052; NGF.1.  
 DR SMART: SM00140; NGF.1.  
 DR PROSITE: PS00248; NGF.1;  
 DR PROSITE: PS0270; NGF.2; 1.  
 SO SEQUENCE 249 AA; 28109 MW; 21CEA6A60A235D97 CRC64;

Query Match 54.2%; Score 354; DB 11; Length 249;  
 Best Local Similarity 57.4%; Pred. No. 6.5e-32;  
 Matches 66; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

OY 7 SHRGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEARPV 64  
 DB 135 ARGEISVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEARPV 194  
 OY 65 KNGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVSLSTR 119  
 DB 195 KEGCRGIDKHMNSOCKTSQTYVRLTSENKLVGNRMIRIDTSCVSLSTR 249

RESULT 14  
 ID 080G74 PRELIMINARY; PRT; 246 AA.  
 AC 080G74;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Brain derived neurotrophic factor.  
 GN BDNF.  
 OS Cyclophiops major.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 OC Colubridae; Colubrinae; Cyclophiops.  
 OC NCB1\_TaxID=192173;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cao M., Yang Y.H., Zhang Y.Z.;  
 RT "Molecular cloning of brain derived neurotrophic factor gene from  
 RT amphibians and reptiles and its application in the research of  
 RT phylogeny and taxonomy."  
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF497715; AAM18716.1;  
 DR CHAIN 128  
 FT PRECURSOR  
 SO SEQUENCE 246 AA; 27773 MW; BA01780349F37856 CRC64;

Query Match 53.9%; Score 357; DB 13; Length 246;  
 Best Local Similarity 57.4%; Pred. No. 1.1e-31;  
 Matches 66; Conservative 18; Mismatches 29; Indels 2; Gaps 1;

OY 7 SHRGEYSVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEARPV 64  
 DB 132 ARGEISVCDSESLMT--DKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRECKEARPV 191



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 8.30012 seconds  
(without alignments)  
425.366 Million cell updates/sec

Title: US-10-072-681-5

Perfect score: 653  
Sequence: 1 PRAEHSRGEYSVCDSESL.....RWIRIDTSCVSLSRKIGRT 120

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/pcdata/1/laa/5A.COMB.pep:\*  
2: /cgn2\_6/pcdata/1/laa/5B.COMB.pep:\*  
3: /cgn2\_6/pcdata/1/laa/6A.COMB.pep:\*  
4: /cgn2\_6/pcdata/1/laa/6B.COMB.pep:\*  
5: /cgn2\_6/pcdata/1/laa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/pcdata/1/laa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	120	4	US-09-675-503-5
2	646	98.9	119	3	US-08-970-865-5
3	646	98.9	119	3	US-08-581-662-2
4	646	98.9	119	4	US-09-363-573-5
5	646	98.9	119	4	US-09-664-295-2
6	641	98.2	119	1	US-07-979-630-3
7	641	98.2	119	1	US-08-440-049-2
8	641	98.2	119	1	US-08-340-131-3
9	641	98.2	119	2	US-08-441-513A-2
10	641	98.2	119	3	US-08-910-691-12
11	641	98.2	119	4	US-08-845-541B-2
12	641	98.2	119	4	US-09-066-065A-2
13	641	98.2	119	5	PCR-US93-11292-3
14	641	98.2	119	5	PCR-US95-06918-2
15	641	98.2	119	5	PCR-US95-06918-5
16	641	98.2	120	1	US-08-340-131-4
17	641	98.2	120	4	US-09-214-214A-1
18	641	98.2	120	4	US-09-255-953-1
19	641	98.2	120	4	US-09-872-090-1
20	641	98.2	240	3	US-08-910-691-11
21	641	98.2	257	1	US-08-451-947-4
22	641	98.2	257	2	US-08-424-826A-4
23	641	98.2	257	3	US-08-910-691-7
24	641	98.2	257	3	US-08-928-694-4
25	641	98.2	257	5	PCR-US91-06950-4
26	629	96.3	119	4	US-09-214-214A-6
27	629	96.3	119	4	US-09-235-953-6

28	629	96.3	119	4	US-09-872-090-6	Sequence 6, Appl 1
29	629	96.3	120	4	US-09-214-214A-3	Sequence 3, Appl 1
30	629	96.3	120	4	US-09-255-953-3	Sequence 3, Appl 1
31	629	96.3	120	4	US-09-872-090-3	Sequence 3, Appl 1
32	619	94.8	117	4	US-09-214-214A-7	Sequence 7, Appl 1
33	619	94.8	117	4	US-09-255-953-7	Sequence 7, Appl 1
34	619	94.8	117	4	US-09-872-090-7	Sequence 7, Appl 1
35	619	94.8	118	4	US-09-214-214A-5	Sequence 5, Appl 1
36	619	94.8	118	4	US-09-255-953-5	Sequence 5, Appl 1
37	619	94.8	118	4	US-09-872-090-5	Sequence 5, Appl 1
38	613	93.9	120	3	US-08-581-662-32	Sequence 32, Appl 1
39	613	93.9	120	4	US-09-664-295-32	Sequence 32, Appl 1
40	416.5	63.8	120	4	US-08-845-541B-9	Sequence 9, Appl 1
41	416.5	63.8	120	4	US-09-066-065A-9	Sequence 9, Appl 1
42	411.5	63.0	120	4	US-08-845-541B-7	Sequence 7, Appl 1
43	411.5	63.0	120	4	US-09-066-065A-7	Sequence 7, Appl 1
44	408.5	62.6	120	4	US-08-845-541B-8	Sequence 8, Appl 1
45	408.5	62.6	120	4	US-09-066-065A-8	Sequence 8, Appl 1

#### ALIGNMENTS

```

RESULT 1
US-09-675-503-5
; Sequence 5, Application US/09675503
; Patent No. 6423831
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; APPLICANT: Beck, Joanne T.
; TITLE OF INVENTION: ISOLATION OF NEUTROPHILS FROM A
; TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUTROPHIL VARIANTS
; FILE REFERENCE: GENENT-037C2
; CURRENT APPLICATION NUMBER: US/09/675,503
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-675-503-5

Query Match 100.0%; Score 653; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRAEHSRGEYSVCDSESLVITKSSAIDIRGHOVYVGEITGNSPKVOFYETRCKE 60
DB 1 PRAEHSRGEYSVCDSESLVITKSSAIDIRGHOVYVGEITGNSPKVOFYETRCKE 60
OY 61 ARPVNGRGIDDKMNSOCTSTQYVRAVLTSENNKLVGNRIIDTSCVSLSRKIGRT 120
DB 61 ARPVNGRGIDDKMNSOCTSTQYVRAVLTSENNKLVGNRIIDTSCVSLSRKIGRT 120

RESULT 2
US-08-970-865-5
; Sequence 5, Application US/08970865
; Patent No. 6005081
; GENERAL INFORMATION:
; APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
; TITLE OF INVENTION: Purification of NGF

```

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,865  
FILING DATE: 14-NO. 6005081-1997  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030838  
FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1063R2  
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-970-865-5

Query Match 98.9%: Score 646; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2,3e-69;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
DB 1 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60  
QY 62 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 120  
DB 61 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 119

RESULT 3  
US-08-581-662-2

Sequence 2, Application US/08581662

Patent No. 6121235

GENERAL INFORMATION:

APPLICANT: Gao, Wei-Qiang

TITLE OF INVENTION: Treatment of Balance Impairments

FILE REFERENCE: P0981

CURRENT APPLICATION NUMBER: US/08/581,662

CURRENT FILING DATE: 1995-12-29

NUMBER OF SEQ ID NOS: 36

SEQ ID NO 2

LENGTH: 119

TYPE: PRT

ORGANISM: Homo sapiens

US-08-581-662-2

Query Match 98.9%: Score 646; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2,3e-69;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
DB 1 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60

DB 1 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60  
QY 62 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 120  
DB 61 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 119

RESULT 4  
US-09-363-573-5

Sequence 5, Application US/09363573

Patent No. 6184360

GENERAL INFORMATION:

APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck

TITLE OF INVENTION: Purification of NGF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,573

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/970,865

FILING DATE: 14-NO. 6184360-1997

APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/047855

FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1063R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-363-573-5

Query Match 98.9%: Score 646; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2,3e-69;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 61  
DB 1 YAEHKSRRGEYSVCDSESLWYTDKSSAIDIRGHQVTVLGEIKTGNSPVKQFYETRCKEA 60  
QY 62 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 120  
DB 61 RPKVNCRCGIDDKHNNCKTSQTYVRALTSNNKLVGMWRIRIDTSCVLSRKIGRT 119

RESULT 5  
US-09-664-295-2

Sequence 2, Application US/09664295

Patent No. 6429196

GENERAL INFORMATION:

APPLICANT: Gao, Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments

FILE REFERENCE: GENENT.051C1  
CURRENT APPLICATION NUMBER: US/09/664.295  
CURRENT FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 08/581.662  
PRIOR FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 37  
SEQ ID NO 2  
LENGTH: 119  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-09-664-295-2

Query Match 98.9%; Score 646; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 2, 3e-69;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLMTYDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGESVCDSESLMTYDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 60  
OY 62 RPYKNCRCGIDDKHMSOCTKSTQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120  
DB 61 RPYKNCRCGIDDKHMSOCTKSTQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 119

## RESULT 6

US-07-979-630-3  
Sequence 3, Application US/07979630  
Patent No. 5488099

GENERAL INFORMATION:  
APPLICANT: Persson, et al.  
TITLE OF INVENTION: Multifunctional Neurotrophic Factors  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/979.630  
FILING DATE: 20-NOV-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,369  
FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Kempner Ph.D., Gail M.  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 41  
TELEPHONE: 914-347-7000  
TELEFAX: 914-347-2113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-07-979-630-3

Query Match 98.2%; Score 641; DB 1; Length 119;  
Best Local Similarity 99.2%; Pred. No. 8, 9e-69;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLMTYDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGESVCDSESLMTYDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 60  
OY 62 RPYKNCRCGIDDKHMSOCTKSTQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120  
DB 61 RPYKNCRCGIDDKHMSOCTKSTQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 119

## RESULT 7

US-08-440-049-2  
Sequence 2, Application US/08440049  
Patent No. 5728803

GENERAL INFORMATION:  
APPLICANT: Ufer, Roman  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: PANROTIC NEUROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,049  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0905C2  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-440-049-2

Query Match 98.2%; Score 641; DB 1; Length 119;  
Best Local Similarity 99.2%; Pred. No. 8, 9e-69;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLMTYDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGESVCDSESLMTYDKSSAIDIRGHQVTVLGEITGNSPVKQYFETRCKEA 60  
OY 62 RPYKNCRCGIDDKHMSOCTKSTQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120  
DB 61 RPYKNCRCGIDDKHMSOCTKSTQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 119

## RESULT 8

US-08-340-131-3  
Sequence 3, Application US/08340131  
Patent No. 5770577

GENERAL INFORMATION:  
APPLICANT: Kinsler, Olaf B  
APPLICANT: Yan, Qiao

;; TITLE OF INVENTION: DERIVATIVES OF BDNF AND NT-3  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Amgen Inc.  
;; STREET: 1840 Dehavenland Drive  
;; CITY: Thousand Oaks  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 91320-1789  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/340,131  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mazza, Richard J.  
;; REFERENCE/DOCKET NUMBER: A-298  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-340-131-3

Query Match 98.2%; Score 641; DB 1; Length 119;  
Best Local Similarity 99.2%; Pred. No. 8.9e-69;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YAEHSHRGEYSCVDSSESLWYDKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRCKEA 61  
Db 1 YAEHSHRGEYSCVDSSESLWYDKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRCKEA 60  
Oy 62 RPYKNCRCRIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120  
Db 61 RPYKNCRCRIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 119

RESULT 9  
US-08-441-513A-2  
Sequence 2, Application US/08441513A  
Patent No. 5981480  
GENERAL INFORMATION:  
APPLICANT: Ufer, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John W.  
TITLE OF INVENTION: Pantropic Neurotrophic Factors  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WINPACin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,513A  
FILING DATE: 15-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:

;; NAME: Torchia, Ph.D., Timothy E.  
;; REGISTRATION NUMBER: 36,700  
;; REFERENCE/DOCKET NUMBER: P0905C3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-8674  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: linear  
;; US-08-441-513A-2

Query Match 98.2%; Score 641; DB 2; Length 119;  
Best Local Similarity 99.2%; Pred. No. 8.9e-69;  
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YAEHSHRGEYSCVDSSESLWYDKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRCKEA 61  
Db 1 YAEHSHRGEYSCVDSSESLWYDKSSAIDIRGHQVTVLGEIKTGNSPVQYFETRCKEA 60  
Oy 62 RPYKNCRCRIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120  
Db 61 RPYKNCRCRIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 119

RESULT 10  
US-08-910-691-12  
Sequence 12, Application US/08910691  
Patent No. 6015552  
GENERAL INFORMATION:  
APPLICANT: WATANABE, Tatsuya  
APPLICANT: YOSHITOMI, Sumie  
APPLICANT: SASADA, Reiko  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,691  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,969  
FILING DATE: 19910604  
ATTORNEY/AGENT INFORMATION:  
NAME: NEUNER, George W.  
REGISTRATION NUMBER: 26964  
REFERENCE/DOCKET NUMBER: 12345  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-910-691-12

Query Match 98.2%; Score 641; DB 3; Length 119;





DB 1 YAEKSHRGESVCDSESLWTDKSSAIDIRGHQVTLGEIKTGNSPVKQYFETRCKEA 60  
OY 62 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGRWIRIDTSCVSALSRIKRT 120  
DB 61 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGRWIRIDTSCVSALSRIKRT 119

## RESULT 14

PCT-US95-06918-2

Sequence 2, Application PC/TUS9506918

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: PANITROPIC NEUROTROPIC FACTORS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06918

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 905PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US95-06918-2

Query Match 98.2%; Score 641; DB 5; Length 119;

Best Local Similarity 99.2%; Pred. No. 8.9e-69;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWTDKSSAIDIRGHQVTLGEIKTGNSPVKQYFETRCKEA 61

DB 1 YAEKSHRGESVCDSESLWTDKSSAIDIRGHQVTLGEIKTGNSPVKQYFETRCKEA 60

OY 62 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGRWIRIDTSCVSALSRIKRT 120

DB 61 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGRWIRIDTSCVSALSRIKRT 119

## RESULT 15

PCT-US95-06918-5

Sequence 5, Application PC/TUS9506918

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: PANITROPIC NEUROTROPIC FACTORS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06918

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 905PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US95-06918-5

Query Match 98.2%; Score 641; DB 5; Length 119;

Best Local Similarity 99.2%; Pred. No. 8.9e-69;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YAEKSHRGESVCDSESLWTDKSSAIDIRGHQVTLGEIKTGNSPVKQYFETRCKEA 61

DB 1 YAEKSHRGESVCDSESLWTDKSSAIDIRGHQVTLGEIKTGNSPVKQYFETRCKEA 60

OY 62 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGRWIRIDTSCVSALSRIKRT 120

DB 61 RPYKNGCRGIDDKHMSOCTSTQTYVRALTSNNKLVGRWIRIDTSCVSALSRIKRT 119

Search completed: December 2, 2002, 15:09:44

Job time : 9.30012 secs



RESULT 2  
US-09-745-032-1

Sequence 1, Application US/09745032  
Patent No. US2001002719A1

GENERAL INFORMATION:

APPLICANT: Boone, Thomas C.

APPLICANT: Cheung, Ellen N.

APPLICANT: Herhenson, Susan I.

APPLICANT: Young, John D.

TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS

FILE REFERENCE: A-411A US Revised023100

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US/09/745,032

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 08/684,353

PRIOR FILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 120

TYPE: PRT

ORGANISM: Human

US-09-745-032-1

Query Match

Best Local Similarity 98.2%; Score 641; DB 10; Length 120;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

DB 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

Y 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

RESULT 3

US-09-742-600-1

Sequence 1, Application US/09742600

Patent No. US20020010135A1

GENERAL INFORMATION:

APPLICANT: Boone, Thomas C.

APPLICANT: Cheung, Ellen N.

APPLICANT: Herhenson, Susan I.

APPLICANT: Young, John D.

TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS

FILE REFERENCE: A-411A US Revised073100

CURRENT APPLICATION NUMBER: US/09/742,600

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 09/214,214

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 08/684,353

PRIOR FILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 120

TYPE: PRT

ORGANISM: Human

US-09-742-600-1

Query Match

Best Local Similarity 98.2%; Score 641; DB 10; Length 120;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

DB 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

Y 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

RESULT 4  
US-09-872-090-1

Sequence 1, Application US/09872090

Patent No. US20020052488A1

GENERAL INFORMATION:

APPLICANT: Boone, Thomas C.

APPLICANT: Cheung, Ellen Ngol Yin

APPLICANT: Herhenson, Susan I.

APPLICANT: Young, John D.

TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)

FILE REFERENCE: A-411B

CURRENT APPLICATION NUMBER: US/09/872,090

CURRENT FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: 09/255,953

PRIOR FILING DATE: 1999-02-23

PRIOR APPLICATION NUMBER: 08/684,353

PRIOR FILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 120

TYPE: PRT

ORGANISM: Homo sapiens

US-09-872-090-1

Query Match

Best Local Similarity 98.2%; Score 641; DB 10; Length 120;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

DB 2 YAEKSHRGEYSVCSSESLMTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

Y 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

DB 62 RPVKNCGRGIDDKHNSCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIGRT 120

RESULT 5

US-08-450-842-4

Sequence 4, Application US/08450842

Patent No. US20020045576A1

GENERAL INFORMATION:

APPLICANT: ROSENTHAL, ARNON

APPLICANT: GENENTECH, INC.

TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 KB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,842

FILING DATE: 514

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993



Dy  
62 RPKKNCRGIDDKHNSCKTSQTVLRALTEENKKLVGMRIIRLDTSCVSAISRKGRT 120  
|||  
Dd  
61 APYDNCGRGIDDKHNSCKTSQTVLRALTEENKKLVGMRIIRLDTSCVSAISRKGRT 119

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1      RESULT 9
2      US-09-745-032-3
3      : Sequence 3, Application US/09745032
4      : Patent No. US20010027179A1
5      : GENERAL INFORMATION:
6      : APPLICANT: Boone, Thomas C.
7      : APPLICANT: Cheung, Ellen N.
8      : APPLICANT: Hershenson, Susan I.
9      : APPLICANT: Young, John D.
10     : TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
11     : FILE REFERENCE: A-411a US Revised07/31/00
12     : CURRENT APPLICATION NUMBER: US/09/745.032
13     : CURRENT FILING DATE: 2000-12-19
14     : PRIOR APPLICATION NUMBER: 09/214, 214
15     : PRIOR FILING DATE: 1998-12-23
16     : PRIOR APPLICATION NUMBER: US 08/684,353
17     : PRIOR FILING DATE: 1996-07-19
18     : NUMBER OF SEQ ID NOS: 12
19     : SOFTWARE: PatentIn ver. 2.1
20     : SEQ ID NO 3
21     : LENGTH: 120
22     : TYPE: prt
23     : ORGANISM: Human
24     : US-09-745-032-3

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10 RESULT 10
11 US-09-742-600-3
12 ; Sequence 3, Application US/09742600
13 ; Patent No. US20020010135A1
14 ; GENERAL INFORMATION:
15 ; APPLICANT: Boone, Thomas C.
16 ; APPLICANT: Cheung, Ellen N.
17 ; APPLICANT: Herschenson, Susan I.
18 ; APPLICANT: Young, John D.
19 ; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
20 ; FILE REFERENCE: A-414 US Revise#073100
21 ; CURRENT APPLICATION NUMBER: US/09/742,600
22 ; PRIOR FILING DATE: 2000-12-19
23 ; PRIOR APPLICATION NUMBER: 09/214,214
24 ; PRIOR FILING DATE: 1998-12-23
25 ; PRIOR APPLICATION NUMBER: US 08/684,353
26 ; PRIOR FILING DATE: 1996-07-19
27 ; NUMBER OF SEQ ID NOS: 12
28 ; SOFTWARE: PatentIn Ver. 2.1
29 ; SEQ ID NO 3
30 ; LENGTH: 120
31 ; TYPE: PRT
32 ; ORGANISM: Human
33 ; US-09-742-600-3

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Db 2 YAEKHSKRGCTSYCDESLATYDKSALDIRHQVTYGEIKTNSPVKQYFETRCKEA 61

Oy 62 RPVENKRCRGIDDKHMSQCKTSQTYVRALTSNNKLVGMMRIRLIDTESVSAALSRLRG 120

Db 62 APVDNCRGIDDKHMSQCKTSQTYVRALTSNNKLVGMMRIRLIDTESVSAALSRLRG 120

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RESULT 12  
 US-09-745-032-7  
 \* Sequence 7, Application US/09745032  
 \* Patent NO. US20010027179A1  
 \* GENERAL INFORMATION:  
 \* APPLICANT: Boone, Thomas C.  
 \* APPLICANT: Cheung, Ellen N.  
 \* APPLICANT: Hereshenson, Susan I.  
 \* APPLICANT: Young, John D.  
 \* TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
 \* FILE REFERENCE: A-411a US Revised073100  
 \* CURRENT APPLICATION NUMBER: US/09/745,032  
 \* CURRENT FILING DATE: 2000-12-19  
 \* PRIOR APPLICATION NUMBER: 09/214, 214  
 \* PRIOR FILING DATE: 1998-12-23  
 \* PRIOR APPLICATION NUMBER: US 08/684, 353  
 \* PRIOR FILING DATE: 1996-07-19  
 \* NUMBER OF SEQ ID NOS: 12  
 \* SOFTWARE: PatentIn Ver. 2.1  
 \* SEQ ID NO 7  
 \* LENGTH: 117  
 \* TYPE: PRT  
 \* ORGANISM: Human  
 \* US-09-745-032-7

Query Match 94.8% Score 619; DB 10; Length 117;  
Best Local Similarity 97.4% Pred. No. 3.2e-61;  
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60

QY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 118  
DB 61 APVDNCGRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 117

RESULT 13  
US-09-742-600-7  
Sequence 7, Application US/09742600  
Patent No. US20020010135A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen M.  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411A US Revised073100  
CURRENT APPLICATION NUMBER: US/09/742,600  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 09/214,214  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Human  
US-09-742-600-7

Query Match 94.8% Score 619; DB 10; Length 117;  
Best Local Similarity 97.4% Pred. No. 3.2e-61;  
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60

QY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 118  
DB 61 APVDNCGRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 117

RESULT 14  
US-09-872-090-7  
Sequence 7, Application US/09872090  
Patent No. US20020052488A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen Ngai Yin  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: Analogs of NT-3 (as Amended)  
FILE REFERENCE: A-411B  
CURRENT APPLICATION NUMBER: US/09/872,090  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/255,953  
PRIOR FILING DATE: 1999-02-23  
PRIOR APPLICATION NUMBER: 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 117

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Analog of  
OTHER INFORMATION: human NT-3.  
US-09-872-090-7

Query Match 94.8% Score 619; DB 10; Length 117;  
Best Local Similarity 97.4% Pred. No. 3.2e-61;  
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61  
DB 1 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 60

QY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 118  
DB 61 APVDNCGRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 117

RESULT 15  
US-09-745-032-5  
Sequence 5, Application US/09745032  
Patent No. US20010027179A1  
GENERAL INFORMATION:  
APPLICANT: Boone, Thomas C.  
APPLICANT: Cheung, Ellen M.  
APPLICANT: Hershenson, Susan I.  
APPLICANT: Young, John D.  
TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS  
FILE REFERENCE: A-411A US Revised073100  
CURRENT APPLICATION NUMBER: US/09/745,032  
CURRENT FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 09/214,214  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 08/684,353  
PRIOR FILING DATE: 1996-07-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Human  
US-09-745-032-5

Query Match 94.8% Score 619; DB 10; Length 118;  
Best Local Similarity 97.4% Pred. No. 3.3e-61;  
Matches 114: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61  
DB 2 YAEKSHRGEYSVCDSESLMTYDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFETRCKEA 61

QY 62 RPYKNCRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 118  
DB 62 APVDNCGRCGIDDKHNNKSOCKTSQTYVRALTSNNKLVGMWIRIDTSCVLSRKIG 118

Search completed: December 2, 2002, 15:14:35  
Job time : 5.2204 secs

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:37 : Search time 25.9086 Seconds  
(without alignments)  
668.605 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698

Sequence: 1 GVSETPAPSRGELAVCDAY.....RWIRDPACVCTILSRGTA 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

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1: /SID52/gcgdata/geneseq/emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/emb1/AA1981.DAT.*
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23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698	100.0	130	AA048890	Human neurotrophin-4
2	698	100.0	130	AA048890	Human neurotrophin-4
3	698	100.0	130	AA048890	Human neurotrophin-4
4	694	99.4	210	AA048890	Human neurotrophin-4
5	689	98.7	130	AA048890	Human neurotrophin-4
6	689	98.7	215	AA048890	Human neurotrophin-4
7	689	98.7	215	AA048890	Human neurotrophin-4
8	684	98.0	130	AA048890	Human neurotrophin-4
9	684	98.0	130	AA048890	Human neurotrophin-4
10	683	97.9	130	AA048890	Human neurotrophin-4

11	683	97.9	130	13	AA048890	Human neurotrophin-4
12	683	97.9	130	13	AA048890	Human neurotrophin-4
13	682	97.7	130	13	AA048890	Human neurotrophin-4
14	680	97.4	130	13	AA048890	Human neurotrophin-4
15	678	97.1	130	13	AA048890	Human neurotrophin-4
16	676	96.8	130	13	AA048890	Human neurotrophin-4
17	650	93.1	126	13	AA048890	Human neurotrophin-4
18	642	92.0	124	13	AA048890	Human neurotrophin-4
19	586	84.0	118	22	AA048890	Human neurotrophin-4
20	565	80.9	118	22	AA048890	Human neurotrophin-4
21	540	77.4	142	13	AA048890	Human neurotrophin-4
22	535.5	76.7	107	13	AA048890	Human neurotrophin-4
23	499.5	71.6	186	13	AA048890	Human neurotrophin-4
24	494.5	70.8	216	13	AA048890	Human neurotrophin-4
25	475.5	68.1	257	13	AA048890	Human neurotrophin-4
26	415	59.5	236	15	AA048890	Human neurotrophin-4
27	415	59.5	237	15	AA048890	Human neurotrophin-4
28	415	59.5	239	15	AA048890	Human neurotrophin-4
29	367	52.6	132	13	AA048890	Human neurotrophin-4
30	364	52.1	123	13	AA048890	Human neurotrophin-4
31	361	51.7	123	13	AA048890	Human neurotrophin-4
32	360	51.6	119	22	AA048890	Human neurotrophin-4
33	360	51.6	119	22	AA048890	Human neurotrophin-4
34	360	51.6	120	22	AA048890	Human neurotrophin-4
35	360	51.6	120	22	AA048890	Human neurotrophin-4
36	358	51.3	119	15	AA048890	Human neurotrophin-4
37	358	51.3	119	15	AA048890	Human neurotrophin-4
38	358	51.3	119	20	AA048890	Human neurotrophin-4
39	358	51.3	119	22	AA048890	Human neurotrophin-4
40	358	51.3	119	22	AA048890	Human neurotrophin-4
41	358	51.3	120	17	AA048890	Human neurotrophin-4
42	358	51.3	120	18	AA048890	Human neurotrophin-4
43	358	51.3	120	21	AA048890	Human neurotrophin-4
44	358	51.3	120	22	AA048890	Human neurotrophin-4
45	358	51.3	136	12	AA048890	Human neurotrophin-4

## ALIGNMENTS

RESULT 1	AA048890	standard: Protein: 130 AA.
ID	AA048890	
XX	AA048890	
AC	AA048890	
XX	AA048890	
DT	12-OCT-1998	(first entry)
XX	Human neurotrophin-4/5.	
DE	Human neurotrophin-4/5.	
XX	Neurotrophin-4/5; NT-4/5; human; purification;	
KW	hydrophobic interaction chromatography.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Region	61..78
FT		/note="conserved Cys-containing region involved in
FT	Region	119..121
FT		/note="conserved Cys knot motif"
XX		Cys knot motif"
PN	MO9821234-A2.	
XX		
PD	22-MAY-1998.	
XX		
PE	14-NOV-1997.	97MO-US21068.
XX		
PR	29-MAY-1997.	97US-0047855.
PR	15-NOV-1996.	96US-0030838.
XX		
PA	(GETH ) GENENTECH INC.	



XX	PI	Beck JT, Burton LE, Schmelzer CH;
XX	DR	WPI: 1998-322333/28.
XX	PT	Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated
XX	PT	variant(s) - using hydrophobic interaction chromatography,
XX	PT	optionally in combination with high performance cation exchange
XX	PT	chromatography
XX	PS	Disclosures: Page 38: 59pp: English.
XX	XX	This polypeptide comprises human neurotrophin-4/5 (NT-4/5) mature
XX	XX	polypeptide. Methods are provided for large-scale purification of
XX	XX	neurotrophins, including NT-4/5, suitable for clinical use. A
XX	XX	claimed method comprises: (1) separating the neurotrophin from the
XX	XX	other proteins using a hydrophobic interaction chromatography resin
XX	XX	(HICR); and optionally (2) separating the neurotrophin from a
XX	XX	chemical variant by high performance cation exchange chromatography
XX	XX	(HCEC). The processes can also be used for purification of e.g.
XX	XX	human nerve growth factor (NGF) (see AAM48886), mouse NGF (see
XX	XX	AAM48887), brain-derived neurotrophic factor (see AAM48888) and
XX	XX	neurotrophin-3 (see AAM48893). The processes allow separation of
XX	XX	neurotrophins from various undesirable misprocessed, misfolded,
XX	XX	site, glycosylated or charge forms. They allow selective
XX	XX	separation from variants and other molecules, and from other
XX	XX	polypeptides with high pI. The processes are applicable to
XX	XX	sterilizing materials from various sources, including fermentation
XX	XX	broths or lysed bacterial or mammalian cells.
XX	SO	Sequence 130 AA:
XX	XX	Query Match 100.0%; Score 698; DB 19; Length 130;
XX	XX	Best Local Similarity 100.0%; Pred. No. 1,7e-71;
XX	XX	Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps
XX	XX	0;
XX	QY	1 GVSETAPASRSGELAVCDVSGWVTRRRAVDLRREVEVGEVPAAGSPLRQFFETR 60
XX	DB	1 GVSETAPASRSGELAVCDVSGWVTRRRAVDLRREVEVGEVPAAGSPLRQFFETR 60
XX	QY	61 CAAADAEEGCGAGCGGCGRGVDRRHVYSECKAKOSYVRLTAHQGRVGMIRIDTACV 120
XX	DB	61 CAAADAEEGCGAGCGGCGRGVDRRHVYSECKAKOSYVRLTAHQGRVGMIRIDTACV 120
XX	QY	121 CPTLSRTGRA 130
XX	DB	121 CPTLSRTGRA 130
XX	XX	RESULT 2
XX	ID	AAB29112
XX	XX	AAB29112 standard; Protein: 130 AA.
XX	AC	AAB29112;
XX	XX	02-FEB-2001 (first entry)
XX	DE	Human neurotrophin-4/5.
XX	KM	Neutrophin; trkB; trkC; ototoxicity-related balance impairment;
XX	KM	Meniere's syndrome; myringitis; otitis media;
XX	KM	acute vestibular neuronitis; herpes zoster oticus; labyrinthitis;
XX	KM	middle; labyrinthine tumour; petrositis; otosclerosis; bacteria.
XX	OS	Homo sapiens.
XX	PN	US6121235-A.
XX	PD	19-SEP-2000.
XX	PF	29-DEC-1995; 95US-0581662.
XX	PR	29-DEC-1995; 95US-0581662.

XX	(GETH ) GENENTECH INC.
PA	Gao W:
PI	MPI: 2000-618200/59.
DR	Treating ototoxin-induced neuronal-related balance impairment and
XX	Pt promoting vestibular ganglion neuron survival prior to, upon or after
PT	exposure to an ototoxin, comprises administering a trkB or trkB agonist
PR	-
PS	Disclosure; Column 47-48; 40pp; English.
XX	
CC	The present invention relates to treating ototoxin-induced
CC	neuronal-related balance impairment in a mammal by administering a
CC	trkB or trkB agonist, particularly neurotrophin-4/5 (NT-4/5).
CC	Otorotoxicity-related balance impairments include Meniere's syndrome,
CC	myringitis, otitis media, acute vestibular neuritis, herpes zoster
CC	otitus, labyrinthitis, middle or labyrinthine tumours, petrositis and
CC	otosclerosis. NT-4/5 may also be used to treat diseases
CC	induced by gram positive, gram negative and acid-fast bacteria. The
CC	present sequence is a protein used in the invention.
XX	
SQ	Sequence 130 AA:
Query Match	100.0%; Score 698; DB 21; Length 130;
Best Local Similarity	100.0%; Pred. No. 1,7e-71;
Matches 130; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GVSETAPASRRGELAVCDVSGWVTDRRTAVIDLRCHEVEVLGEVPAGSPLRPFETR 60
DB	1 GVSETAPASRRGELAVCDVSGWVTDRRTAVIDLRGREVEVLGEVPAGSPLRPFETR 60
OY	61 CAAADAEEGGGAGGGCGVDRHHVSECKAKOSVRLATLAAGRGVMNIRIDTACY 120
DB	61 CAAADAEEGGGAGGGCGVDRHHVSECKAKOSVRLATLAAGRGVMNIRIDTACY 120
OY	121 CTLISRTGRA 130
DB	121 CTLISRTGRA 130
RESULT 3	
AAR22465	
ID AAR22465	standard; Protein: 210 AA.
XX AC	AAR22465;
XX DT	22-SEP-1992 (first entry)
XX DE	Neurotrophic factor 4.
XX KM	Huntington's chorea; ALS; NT-4; NGF; BDNF; NT-3; neuron.
XX OS	Homø sapiens.
XX PN	WO9205254-A.
XX PD	02-APR-1992.
XX PF	24-SEP-1991; 91MO-US06950.
XX PR	25-SEP-1990; 90US-0587707.
XX PR	31-JAN-1991; 91US-0648482.
XX PA	(GETH ) GENENTECH INC.
XX PI	Rosenthal A;
XX DR	MPI: 1992-132123/16.
XX DR	N-PADB; AAQ23663.
XX	

PT Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 XX  
 PS Disclosure; Fig 1: 84pp: English.

CC The sequence shows the entire amino acid sequence for the mature  
 CC human neurotrophic factor-4 (NT-4) gene, (nucleotide sequence  
 CC AA023653). This protein can be useful in treating damaged nerve cells  
 CC or neurodegenerative diseases eg. Huntington's chorea, Alzheimer's  
 CC disease, ALS and Parkinson's disease.  
 CC NT-4 is a novel trophic factor with a broad tissue distribution.  
 CC It complements NGF, BDNF, and NT-3, which are trophic factors for  
 CC some peripheral neurons. This factor can act alone or with other  
 CC trophic factors, or defined subsets of neurons to achieve the  
 CC correct neuronal connections both in the peripheral and central  
 CC nervous system.

XX Sequence 210 AA:

Query Match 100.0%; Score 698; DB 13; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 3,1e-71;  
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 60  
 DB 81 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 140  
 OY 61 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRGVGRWIRIDTACV 120  
 DB 141 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRGVGRWIRIDTACV 200  
 OY 121 CTLLSRTGRA 130  
 DB 201 CTLLSRTGRA 210

#### RESULT 4

AA022482  
 ID AAR22482 standard; Protein: 210 AA.

AC AAR22482;

DT 22-SEP-1992 (first entry)

DE Neurotrophic factor 4 activity variants.

KW NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.

OS Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 70..70 /note- "Any amino acid except Glu, Gly, Asp or Pro"

FT MISC-difference 71..71 /note- "Any amino acid except Ala, Pro or Met"

FT MISC-difference 83..83 /note- "Any amino acid except Arg, Asp, Ser or Lys"

FT MO9205254-A.

PD 02-APR-1992.

PF 24-SEP-1991; 91MO-US06950.

PR 25-SEP-1990; 90US-0587707.

PR 31-JAN-1991; 91US-0648482.

PA (GETH ) GENENTECH INC.

PI Rosenthal A.

DR WPI; 1992-132123/16.

XX Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 XX  
 PS Disclosure; Page 9: 84pp: English.

CC The sequence shows a portion of the amino acid sequence of human  
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22482). Positions  
 CC 70, 71 and 83 are positions of various amino acid substitutions.  
 CC Substitutions at these positions can cause a marked differentiation  
 CC in the activity of the trophic element.  
 CC The sites of greatest interest for substitutional mutagenesis include  
 CC sites where the amino acids found in BDNF, NGF, NT-3, and NT-4 are  
 CC substantially different in terms of side chain bulk, charge, or  
 CC hydrophobicity, but where there is also a high degree of homology at  
 CC the selected site within various animal analogues of NGF, NT-3 and  
 CC BDNF.

XX Sequence 210 AA:

Query Match 99.4%; Score 694; DB 13; Length 210;  
 Best Local Similarity 99.2%; Pred. No. 8,9e-71;  
 Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 60  
 DB 81 GYSETAPASRRGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKQYFEETR 140  
 OY 61 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRGVGRWIRIDTACV 120  
 DB 141 CKADNAEEGPGAGGCGRGVDRRHVSECKAKOSYRALTAAAGRGVGRWIRIDTACV 200  
 OY 121 CTLLSRTGRA 130  
 DB 201 CTLLSRTGRA 210

#### RESULT 5

AA092009  
 ID AAY92009 standard; Protein: 130 AA.

AC AAY92009;

DT 19-JUL-2000 (first entry)

DE Human neurotrophin-4 monomer.

KW human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;

XX human neurotrophin-3 monomer; CKGF; mutant; cysteine knot growth factor;



PM W09325684-A.  
 XX 23-DEC-1993.  
 PD  
 XX 11-JUN-1993; 93MO-US05672.  
 PF  
 XX 12-JUN-1992; 92US-0898194.  
 PR  
 XX (REGC-) REGENERON PHARM INC.  
 PA Altar CA, Distefano P, Ip N, Ventimiglia R, Wiegand S;  
 PI Wong V, Yancopoulos GD;  
 XX MPI: 1994-007541/01.  
 DR N-PSDB: AA054715.  
 XX

Neurotrophin-4 proteins which support survival, growth and differentiation of motor neurons - used to treat motor neuron disorders e.g. dopaminergic and cholinergic neuron diseases  
 Disclousure: Page 145; 181pp; English.

The sequences given in AAR47095-104 represent neurotrophin-4 (NT-4), fragments and derivatives of NT-4, and were derived from viper, xenopus, rat and human. NT-4 is a member of the brain-derived neurotrophin factor (BDNF)/nerve growth factor (NGF)/NT-3 gene family. NT-4 proteins can promote the survival, growth and differentiation of neurons, such as basal forebrain cholinergic neurons. NT-4 proteins can be used to treat dopaminergic or cholinergic neuron diseases and disorders. NT-4 related proteins may be used to treat peripheral neuropathy and diseases of the hippocampus and striatum. Disorders which may be treated in this way, include acute neuropathia, neuromuscular atonies, diabetic neuropathy, amyotrophic lateral sclerosis or compression, a tumour, abscess, trauma, Alzheimer's disease, Parkinson's disease or a disorder of the retina, especially involving retinal ganglion cell degeneration. Anti-NT-4 antibodies may be used for diagnostic or therapeutic purposes, eg. to monitor the progression of diseases associated with alterations in the pattern of NT-4 expression.

SO Sequence 215 AA;

Query Match 98.7%: Score 689; DB 15; Length 215;  
Best Local Similarity 99.2%: Pred. No. 3,4e-70;

Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRSGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
 DB 86 GVSETAPASRSGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 145  
 QY 61 CKADNAEEGGPGAGGCGRGVDRRHVSECKAKOSYVALTAHAQGRVGMIRIDTACY 120  
 DB 146 CKADNAEEGGPGAGGCGRGVDRRHVSECKAKOSYVALTAHAQGRVGMIRIDTACY 205  
 QY 121 CTLLSRTGRA 130  
 DB 206 CTLLSRTGRA 215

RESULT 8

AAR22477 standard; Protein: 130 AA.

AC AAR22477;  
 XX 22-SEP-1992 (first entry)  
 DT  
 XX Neurotrophic factor 4 activity variants.  
 DE NT-4; NGF; NT-3; BDNF; variant; deletion; tertiary structure;  
 KW homology; activity.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Misc-difference 53..53  
 FT /Label- HIS  
 XX

PM W09205254-A.  
 XX 02-APR-1992.  
 PD  
 XX 24-SEP-1991; 91MO-US06950.  
 PF  
 XX 25-SEP-1990; 90US-0587707.  
 PR 31-JAN-1991; 91US-0648482.  
 XX  
 PA (GETH) GENENTECH INC.  
 PI Rosenthal A;  
 XX MPI: 1992-132123/16.  
 DR  
 XX  
 XX

Neurotrophic factor-4 - useful for treating neurodegenerative diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells damaged by e.g. diabetes  
 Disclousure: Seq 59; 84pp; English.

The sequence shows an NT-4 variant protein, in which the Arg residue at position 133 of NT-4 (sequence given in AAR22465), is replaced by a His residue. This substitution renders the NT-4 resistant to proteolysis, thereby creating a variant of NT-4 that is more stable. The sites of greatest interest for substitutional mutagenesis include sites where the amino acids found in BDNF, NGF, NT-3, and NT-4 are substantially different in terms of side chain bulk, charge or hydrophobicity, but where there is also a high degree of homology at the selected site within various animal analogues of BDNF, NGF and NT-3.

SO Sequence 130 AA;

Query Match 98.0%: Score 684; DB 13; Length 130;  
Best Local Similarity 98.5%: Pred. No. 6,8e-70;

Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRSGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
 DB 1 GVSETAPASRSGELAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
 QY 61 CKADNAEEGGPGAGGCGRGVDRRHVSECKAKOSYVALTAHAQGRVGMIRIDTACY 120  
 DB 61 CKADNAEEGGPGAGGCGRGVDRRHVSECKAKOSYVALTAHAQGRVGMIRIDTACY 120  
 QY 121 CTLLSRTGRA 130  
 DB 121 CTLLSRTGRA 130

RESULT 9

AAR22479 standard; Protein: 130 AA.

AC AAR22479;  
 XX 22-SEP-1992 (first entry)  
 DT  
 XX Neurotrophic factor 4 activity variants.  
 DE NT-4; NGF; NT-3; BDNF; variant; deletion; tertiary structure;  
 KW homology; activity.  
 OS Synthetic.  
 XX Key Location/Qualifiers

FT MISC-difference 108..108  
 XX /label= PHE  
 PN WO9205254-A.  
 XX  
 PD 02-APR-1992.  
 XX  
 XX 24-SEP-1991; 91MO-US06950.  
 XX  
 XX 25-SEP-1990; 90US-0587707.  
 PR 31-JAN-1991; 91US-0648482.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Rosenthal A;  
 PI  
 XX WPI: 1992-132123/16.  
 DR  
 XX Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 PS  
 XX Disclosure: Seq 61; 84pp: English.  
 CC The sequence shows an NT-4 variant protein, in which the phe  
 CC residue at position 108 of NT-4 (sequence given in AAR22465), is  
 CC replaced by a His residue. This corresponds to position 108 of the  
 CC mature NT-4 protein. The sites of greatest interest for  
 CC substitutional mutagenesis include sites where the amino acids found  
 CC in BDNF, NGF, NT-3, and NT-4 are substantially different in terms of  
 CC side chain bulk, charge or hydrophobicity, but where there is also a  
 CC high degree of homology at the selected site within various animal  
 CC analogues of BDNF, NGF and NT-3.  
 SO Sequence 130 AA:  
 Query Match 98.0%; Score 684; DB 13; Length 130;  
 Best Local Similarity 98.5%; Pred. No. 6.8e-70;  
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFEETR 60  
 Db 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFEETR 60  
 Oy 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120  
 Db 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120  
 Oy 121 CTLLSRTGRA 130  
 Db 121 CTLLSRTGRA 130  
 RESULT 10  
 AAR22471  
 ID AAR22471 standard; Protein: 130 AA.  
 XX  
 XX AAR22471:  
 XX  
 XX 22-SEP-1992 (first entry)  
 XX  
 XX Neurotrophic factor 4 variants (B67).  
 DE  
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution; non-conservative.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH MISC-difference 67..67  
 FT /label= SER, THR  
 XX  
 XX WO9205254-A.  
 XX

PD 02-APR-1992.  
 XX  
 XX 24-SEP-1991; 91MO-US06950.  
 XX  
 XX 25-SEP-1990; 90US-0587707.  
 PR 31-JAN-1991; 91US-0648482.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Rosenthal A;  
 PI  
 XX WPI: 1992-132123/16.  
 DR  
 XX Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 PS  
 XX Disclosure: Page 45-46; 84pp: English.  
 CC The sequence shows a portion of the amino acid sequence of human  
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 67  
 CC is a point of a non-conservative substitution which can cause a  
 CC marked differentiation in the activity of the trophic element.  
 CC Either Ser or Thr may be included at this point. This substitution  
 CC changes an acidic amino acid for a hydrophilicly neutral one. The  
 CC sites of greatest interest for substitutional mutagenesis include  
 CC sites where the amino acids found in BDNF, NGF, NT-3, and NT-4 are  
 CC substantially different in terms of side chain bulk, charge, or  
 CC hydrophobicity, but where there is also a high degree of homology at  
 CC the selected site within various animal analogues of NGF, NT-3 and  
 CC BDNF.  
 SO Sequence 130 AA:  
 Query Match 97.9%; Score 683; DB 13; Length 130;  
 Best Local Similarity 98.5%; Pred. No. 8.9e-70;  
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFEETR 60  
 Db 1 GVSETAPASRGELAVCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFEETR 60  
 Oy 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120  
 Db 61 CKADNAEEGPGAGGGCGVDRRHVSECKAKOSYVRLTAHOGRGVGRMIRIDTACV 120  
 Oy 121 CTLLSRTGRA 130  
 Db 121 CTLLSRTGRA 130  
 RESULT 11  
 AAR22480  
 ID AAR22480 standard; Protein: 130 AA.  
 XX  
 XX AAR22480:  
 XX  
 XX 22-SEP-1992 (first entry)  
 XX  
 XX Neurotrophic factor 4 activity variants.  
 DE  
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH MISC-difference 84..84  
 FT /label= GLN, HIS, ASN, THR, TYR, TRP  
 XX  
 XX WO9205254-A.  
 XX  
 XX 02-APR-1992.  
 XX

PF 24-SEP-1991; 91WO-US06950.  
 XX  
 PR 25-SEP-1990; 90US-0587707.  
 PR 31-JAN-1991; 91US-0648482.  
 XX  
 PA (CETH ) GENENTECH INC.  
 XX  
 PI Rosenthal A;  
 XX MPI; 1992-132123/16.  
 XX  
 PT Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 XX  
 PS Disclosure; Seq 62-67; 84pp; English.  
 XX  
 XX The sequence shows a portion of the amino acid sequence of human  
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 84  
 CC is a point at which substitution mutation causes a marked  
 CC differentiation in the activity of the trophic element. Either Gln,  
 CC His, Asp, Thr, Tyr or Trp may be included at this point. The sites  
 CC of greatest interest for substitutional mutagenesis include sites  
 CC where the amino acids found in BDNF, NGF, NT-3, and NT-4 are  
 CC substantially different in terms of side chain bulk, charge, or  
 CC hydrophobicity, but where there is also a high degree of homology at  
 CC the selected site within various animal analogues of NGF, NT-3 and  
 CC BDNF.  
 XX  
 XX Sequence 130 AA:  
 SQ  
 Query Match 97.9%; Score 683; DB 13; Length 130;  
 Best Local Similarity 98.5%; Pred. No. 8.9e-70;  
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 GVSETAPASRSGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 60  
 DB 1 GVSSETAPASRSGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 60  
 OY 61 CKADNAEEGGPGAGGCGRGVDNRHMYSECKAKOSYVRLATAHAGRGWRIRIDTACY 120  
 DB 61 CKADNAEEGGPGAGGCGRGVDNRHMYSECKAKOSYVRLATAHAGRGWRIRIDTACY 120  
 OY 121 CTLSRTGRA 130  
 DB 121 CTLSRTGRA 130  
 RESULT 12  
 AAR29735  
 ID AAR29735 standard; Protein: 215 AA.  
 XX  
 XX AAR29735;  
 XX  
 DT 22-APR-1993 (first entry)  
 XX  
 DE Human NT-4, encoded by clone 7-2.  
 XX  
 XX Neurotrophin; NT; nerve growth factor; NGF;  
 KW brain-derived neurotrophic factor; BDNF; probe; primer.  
 OS  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH MISC-difference 2 /note- "conserved residue in presequence"  
 FT MISC-difference 6 /note- "conserved residue in presequence"  
 FT MISC-difference 9 /note- "conserved residue in presequence"  
 FT MISC-difference 48..51 /note- "conserved residues in presequence"  
 FT MISC-difference 54 /note- "conserved residues in presequence"

FT MISC-difference 62 /note- "conserved residue in presequence"  
 FT Modified-site 81..83 /note- "conserved residue in presequence"  
 FT Cleavage-site 84..85 /label- N-glycosylation\_site  
 XX  
 XX WO9220365-A.  
 XX  
 XX 26-NOV-1992.  
 XX  
 XX 20-MAY-1992; 92WO-US04266.  
 XX  
 XX 21-MAY-1991; 91US-0703450.  
 PR 12-JUL-1991; 91US-0729253.  
 PR 23-JUL-1991; 91US-0734422.  
 PR 28-AUG-1991; 91US-0751356.  
 PR 20-SEP-1991; 91US-0762674.  
 PR 14-NOV-1991; 91US-0791924.  
 XX  
 XX (REG- ) REGENERON PHARM INC.  
 XX  
 XX Hallbook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD;  
 DR MPI; 1992-415468/50.  
 DR N-PSDB; AAO32230.  
 XX  
 XX Use of neurotrophin-4 for promoting growth and survival of nerve  
 PT cells - useful in treating neurological, fertility and  
 PT immunological disorders and in diagnosis  
 XX  
 XX Disclosure; Page 117-119 + fig 18; 180pp; English.  
 XX  
 PS  
 CC Oligonucleotide probes and primers were synthesised based on the NT  
 CC family including NGF, BDNF and NT-3. These were used to isolate DNA  
 CC encoding NT-4 from nucleic acid from xenopus ovaries. This DNA was  
 CC then used to isolate other mammalian DNA encoding NT-4, including  
 CC human NT-4 DNA.  
 XX  
 XX Sequence 215 AA:  
 SQ  
 Query Match 97.9%; Score 683; DB 13; Length 215;  
 Best Local Similarity 98.5%; Pred. No. 1.6e-69;  
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 GVSETAPASRSGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 60  
 DB 86 GVSETAPASRSGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLROYFFETR 145  
 OY 61 CKADNAEEGGPGAGGCGRGVDNRHMYSECKAKOSYVRLATAHAGRGWRIRIDTACY 120  
 DB 146 CKADNAEEGGPGAGGCGRGVDNRHMYSECKAKOSYVRLATAHAGRGWRIRIDTACY 205  
 OY 121 CTLSRTGRA 130  
 DB 206 CTLSRTGRA 215  
 RESULT 13  
 AAR22481  
 ID AAR22481 standard; Protein: 130 AA.  
 XX  
 XX AAR22481;  
 XX  
 DT 22-SEP-1992 (first entry)  
 XX  
 DE Neurotrophic factor 4 activity variants.  
 XX  
 XX NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.  
 OS  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH

FT Misc-difference 116..116  
 FT /note- "GLU, ASN, GLN, TYR, SER, THR"  
 XX  
 XX  
 PM WO9205254-A.  
 XX  
 PD 02-APR-1992.  
 XX  
 PF 24-SEP-1991; 91WO-US06950.  
 XX  
 PR 25-SEP-1990; 90US-0587707.  
 PR 31-JAN-1991; 91US-0648482.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Rosenthal A;  
 XX WPI: 1992-132123/16.  
 DR  
 XX Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 PS  
 XX Disclosure; Seq 68-73; 84pp; English.  
 CC The sequence shows a portion of the amino acid sequence of human  
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 116  
 CC is a point at which substitution mutation causes a marked  
 CC differentiation in the activity of the trophic element. Either Glu,  
 CC Asn, Gln, Tyr, Ser or Thr may be included at this point. The sites  
 CC of greatest interest for substitutional mutagenesis include sites  
 CC where the amino acids found in BDNF, NGF, NT-3, and NT-4 are  
 CC substantially different in terms of side chain bulk, charge, or  
 CC hydrophobicity, but where there is also a high degree of homology at  
 CC the selected site within various animal analogues of NGF, NT-3 and  
 CC BDNF.  
 XX  
 SQ Sequence 130 AA:  
 Query Match 97.7%; Score 682; DB 13; Length 130;  
 Best Local Similarity 98.5%; Pred. No. 1,2e-69;  
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GVSETAPASRREGELAVCDVSGWVTDRTTAVDLRGREVEVLGEVPAAGSPFLRQYFEETR 60  
 DB 1 GVSETAPASRREGELAVCDVSGWVTDRTTAVDLRGREVEVLGEVPAAGSPFLRQYFEETR 60  
 QY 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120  
 DB 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120  
 QY 121 CTLLSRTGRA 130  
 DB 121 CTLLSRTGRA 130  
 RESULT 14  
 AAR22470  
 ID AAR22470 standard; Protein: 130 AA.  
 XX  
 AC AAR22470;  
 XX  
 DT 22-SEP-1992 (first entry)  
 XX  
 DE Neurotrophic factor 4 variants (R85).  
 XX  
 KW NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 85..85  
 FT /Label= GLU, PHE, PRO, TYR, TRP  
 XX

PN WO9205254-A.  
 XX  
 PD 02-APR-1992.  
 XX  
 PF 24-SEP-1991; 91WO-US06950.  
 XX  
 PR 25-SEP-1990; 90US-0587707.  
 PR 31-JAN-1991; 91US-0648482.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Rosenthal A;  
 XX WPI: 1992-132123/16.  
 DR  
 XX Neurotrophic factor-4 - useful for treating neurodegenerative  
 PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells  
 PT damaged by e.g. diabetes  
 PS  
 XX Disclosure; Page 43; 84pp; English.  
 CC The sequence shows a portion of the amino acid sequence of human  
 CC neurotrophic factor-4 (NT-4), (full sequence AAR22465). Position 85  
 CC is a point at which substitution mutation causes a marked  
 CC differentiation in the activity of the trophic element. Either Glu,  
 CC Phe, Pro, Tyr or Trp may be included at this point. The sites of  
 CC greatest interest for substitutional mutagenesis include sites where  
 CC the amino acids found in BDNF, NGF, NT-3, and NT-4 are substantially  
 CC different in terms of side chain bulk, charge, or hydrophobicity, but  
 CC where there is also a high degree of homology at the selected site  
 CC within various animal analogues of NGF, NT-3 and BDNF.  
 XX  
 SQ Sequence 130 AA:  
 Query Match 97.4%; Score 680; DB 13; Length 130;  
 Best Local Similarity 98.5%; Pred. No. 2e-69;  
 Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GVSETAPASRREGELAVCDVSGWVTDRTTAVDLRGREVEVLGEVPAAGSPFLRQYFEETR 60  
 DB 1 GVSETAPASRREGELAVCDVSGWVTDRTTAVDLRGREVEVLGEVPAAGSPFLRQYFEETR 60  
 QY 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120  
 DB 61 CKADNAEEGGPGAGGGCGVDRRHVSECKAKOSYVRLTAHAGRGVGMIRIDTACY 120  
 QY 121 CTLLSRTGRA 130  
 DB 121 CTLLSRTGRA 130  
 RESULT 15  
 AAR22469  
 ID AAR22469 standard; Protein: 130 AA.  
 XX  
 AC AAR22469;  
 XX  
 DT 22-SEP-1992 (first entry)  
 XX  
 DE Neurotrophic factor 4 variants (G78).  
 XX  
 KW NT-4; NT-3; BDNF; NGF; mutagenesis; substitution.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 78..78  
 FT /Label= LYS, HIS, GLN, ARG  
 XX  
 PN WO9205254-A.  
 XX  
 PD 02-APR-1992.  
 XX

```

PF 24-SEP-1991; 91WO-US06950.
XX
PR 25-SEP-1990; 90US-0587707.
PR 31-JAN-1991; 91US-0648482.
XX
PA (GETH ) GENEWTECH INC.
XX
PI Rosenthal A;
XX
DR WPI: 1992-132123/16.
XX
XX Neurotrophic factor-4 - useful for treating neurodegenerative
PT diseases e.g. Alzheimer's and Parkinson's diseases, nerve cells
PT damaged by e.g. diabetes
XX
XX Disclosure; page 40-41; 84pp; English.
XX
XX The sequence shows a portion of the amino acid sequence of human
CC neurotrophic factor-4 (NT-4), (full sequence AAK22465). Position 78
CC is a point at which substitution mutation causes a marked
CC differentiation in the activity of the trophic element. Either Lys,
CC His, Gln, or Arg may be included at this point. The sites of greatest
CC interest for substitutional mutagenesis include sites where the amino
CC acids found in BDNF, NGF, NT-3, and NT-4 are substantially different
CC in terms of side chain bulk, charge, or hydrophobicity, but where
CC there is also a high degree of homology at the selected site within
CC various animal analogues of NGF, NT-3 and BDNF.
XX
SO Sequence 130 AA;

Query Match 97.1%; Score 678; DB 13; Length 130;
Best Local Similarity 98.5%; Pred. No. 3,3e-69;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYSETPAPASRRGELAVCDANSGWYTDRTTAVDLRGREVEYLGEVPAGGSPLRQYFFETR 60
   |||||||
DB 1 GYSETPAPASRRGELAVCDANSGWYTDRTTAVDLRGREVEYLGEVPAGGSPLRQYFFETR 60
OY 61 CKADNAEKGPGAGGCGRCVDRRHVYSECKAKOSYVRLTAHAGRGVGNRWIRIDTACY 120
   |||||||
DB 61 CKADNAEKGPGAGGCGRCVDRRHVYSECKAKOSYVRLTAHAGRGVGNRWIRIDTACY 120
OY 121 CTLISRTGRA 130
   |||||||
DB 121 CTLISRTGRA 130

```

Search completed: December 2, 2002, 15:08:40  
 Job time : 25.9086 secs



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## OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 ; Search time 10.3634 Seconds  
(without alignments)  
1205.921 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698

Sequence: 1 GVSETAPASRGEVLAVCDV.....RWIRIDPACVCTLSRTGRA 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:\*\*  
2: PIR:\*\*  
3: PIR:\*\*  
4: PIR:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689	98.7	210	2 A42687	neurotrophin-4 pre
2	663	95.0	209	2 B42687	neurotrophin-4 pre
3	415	59.5	236	2 JH0400	neurotrophin-3 pre
4	358	51.3	257	2 C40304	neurotrophin-3 pre
5	358	51.3	257	2 T50400	neurotrophin-3 pre
6	358	51.3	258	2 S09155	neurotrophin-3 pre
7	358	51.3	258	2 A35781	hippocampus-derive
8	345	49.4	247	2 A40304	brain-derived neur
9	345	49.4	249	2 S12555	brain-derived neur
10	345	49.4	249	2 B40304	brain-derived neur
11	345	49.4	252	2 A30361	brain-derived neur
12	342	49.0	248	2 JG5183	brain-derived neur
13	340	48.7	259	2 T51708	brain-derived neur
14	336	48.1	114	2 I84765	brain-derived neur
15	327	46.8	114	2 I50606	brain-derived neur
16	315	45.1	114	2 I51599	brain-derived neur
17	308.5	44.2	245	2 I56570	beta-nerve growth
18	307.5	44.1	125	2 A26312	nerve growth facto
19	307.5	44.1	329	2 I46614	nerve growth facto
20	305.5	43.8	303	1 NGRTBA	nerve growth facto
21	305.5	43.8	307	1 NGMSMG	nerve growth facto
22	302.5	43.3	243	2 A26311	nerve growth facto
23	297.5	42.6	286	1 NGHUBM	nerve growth facto
24	295.5	42.3	241	2 JI4097	nerve growth facto
25	290	41.5	235	2 S14481	nerve growth facto
26	269.5	38.6	243	2 I51193	nerve growth facto
27	265	38.0	116	1 NGKJXI	nerve growth facto
28	264.5	37.9	117	2 S28161	nerve growth facto
29	255	36.5	116	2 A58566	nerve growth facto

30	255	36.5	246	2 A59218	nerve growth facto
31	241.5	34.6	194	2 I51709	nerve growth facto
32	228.5	32.7	286	2 S50855	neurotrophin-6 - s
33	90	12.9	992	2 T08772	hypothetical prote
34	83	11.9	949	2 JC7802	urp protein - mous
35	80.5	11.5	1070	2 T31332	nuclease - Aeronon
36	80.5	11.5	1507	2 A40228	neurexin I-alpha p
37	80	11.5	622	2 JG5425	transcription init
38	79.5	11.4	372	2 H70595	probable entc prot
39	76.5	11.0	860	1 EAMS	elastin precursor
40	76.5	11.0	1530	2 I45944	neurexin I-alpha -
41	74.5	10.7	577	2 B87010	probable isochoris
42	73.5	10.5	6260	2 T30228	polyketide synthas
43	72.5	10.4	625	2 S13919	potassium channel
44	72.5	10.4	940	2 T01854	hypothetical prote
45	72	10.3	894	2 C85756	prophage p12 prote

## ALIGNMENTS

## Result 1

A42687

neurotrophin-4 precursor - human

M:Alternate names: neurotrophin-5

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C:Accession: A42687; JH0503

R:ID, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Giles, D.R.; Belluscio, P.; Natl. Acad. Sci. U.S.A., 89, 3060-3064, 1992

A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distri

A:Reference number: A42687; MUID:92212967; PMID:1133578

A:Accession: A42687

A:Molecule type: DNA

A:Residues: 1-210 <IRP>

A:Cross-references: GB:M86528; NID:G190264; PIDN:AAA60154.1; PID:G190265

A:Note: sequence extracted from NCBI backbone (NCBI:G3810, NCBI:P.93811)

R:Berthelme, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenth

Neuron 7, 857-866, 1991

A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.

A:Reference number: JH0503; MUID:92075279; PMID:1742028

A:Accession: JH0503

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-210 <BER>

C:Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro

C:Genetics:

A:Gene: GDB:NTF5

A:Cross-references: GDB:134723; OMIM:162662

A:Map position: 19pter-19qter

C:Superfamily: nerve growth factor beta chain

C:Keywords: glycoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-80/Domain: propeptide #status predicted <PRO>

F:81-210/Product: neurotrophin-4 #status predicted <NEU>

F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.7% Score 689; DB 2; Length 210;

Best Local Similarity 99.2% Pred. No. 1e-59; 1: Indels 0; Gaps 0;

Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GVSETAPASRGEVLAVCDVSGMVTDRRTAVDLKRCREVEVLGEVPAAGSPRLQRYFEETR	60
DB	81	GVSETAPASRGEVLAVCDVSGMVTDRRTAVDLKRCREVEVLGEVPAAGSPRLQRYFEETR	140
QY	61	CKADNBEGRGAGGCGRVRBRHMSVCAKOSVYALTAHOGVGRHRTITQACV	120
DB	141	CKADNBEGRGAGGCGRVRBRHMSVCAKOSVYALTAHOGVGRHRTITQACV	200
QY	121	CTLSRTGRA 130	
DB	201	CTLSRTGRA 210	

## RESULT 2

842687 neurotrophin-4 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text\_change 16-Jul-1999  
 C:Accession: 842687; JH0504; JH0505  
 R:Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992  
 R:Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992  
 A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribution  
 A:Reference number: A42687; MUID:92212967; PMID:1313578  
 A:Accession: 842687  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-209 <TRAP>  
 A:Cross-references: GB:M8742; NID:9205775; PIDN:AAA1728.1; PID:9205776  
 R:Berkemeier, L.R.; Winslow, J.M.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenthal, Neuron 7, 857-866, 1991  
 A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.  
 A:Reference number: JH0503; MUID:92075279; PMID:1742028  
 A:Accession: JH0504  
 A:Molecule type: DNA  
 A:Residues: 1-209 <BER>  
 A:Accession: JH0505  
 A:Molecule type: mRNA  
 A:Residues: 1-176, 'P', 178-209 <BER1>  
 A:Cross-references: GB:S69323; NID:9240025; PIDN:AAB20548.1; PID:9240026  
 C:Comment: This protein is a targeted-derived, diffusible neurotrophic factor.  
 C:Superfamily: The neurotrophin stimulate autophosphorylation and transduce signals through C/Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-79/Domain: propeptide #status predicted <PRO>  
 F:80-209/Product: neurotrophin-5 #status predicted <PRO>  
 F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.0% Score 663; DB 2; Length 209;  
 Best Local Similarity 94.6% Pred. No. 3 5e-57;  
 Matches 123; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GVSTAPASRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 60  
 |||||  
 DB 80 GVSTAPASRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 139  
 |||||  
 QY 61 CKADNAEGGPGAGCGGCGVDRHRHVSCKAKOSYVALTPAHOGRRVGRIRIDTACV 120  
 |||||  
 DB 140 CKASAGEGPGVGGCGKGVDRHRHVSCKAKOSYVALTPADSGRGRIRIDTACV 199  
 |||||  
 QY 121 CTLLSRTGRA 130  
 |||||  
 DB 200 CTLLSRTGRA 209  
 |||||

RESULT 3  
 JH0400 neurotrophin-4 precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Dec-1991 #sequence, revision 31-Dec-1991 #text\_change 16-Jul-1999  
 C:Accession: JH0400  
 R:Hallboeck, F.; Idenez, C.F.; Persson, H.  
 Neuron 6, 845-858, 1991  
 A:Title: Evolutionary studies of the nerve growth factor family reveal a novel member at  
 A:Reference number: JH0400; MUID:91222573; PMID:2022430  
 A:Accession: JH0400  
 A:Molecule type: DNA  
 A:Residues: 1-236 <HAL>  
 A:Cross-references: GB:Z30090; NID:9455533; PIDN:CAA82906.1; PID:9455534  
 C:Comment: This protein belongs to the nerve growth factor family.  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-113/Domain: propeptide #status predicted <PRO>  
 F:114-236/Product: neurotrophin-4 #status predicted <PRO>

F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.5% Score 415; DB 2; Length 236;  
 Best Local Similarity 63.0% Pred. No. 5 1e-33;  
 Matches 80; Conservative 15; Mismatches 24; Indels 8; Gaps 2;

QY 3 SEFAPASRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 62  
 |||||  
 DB 117 SDSVLSRRCGLAVCAVSGWTDRTAVDLRGREVEVLGEVPAAGSPKRYFFETR 175  
 |||||  
 QY 63 ADNAEGGPGAGCGGCGVDRHRHVSCKAKOSYVALTPAHOGRRVGRIRIDTACV 122  
 |||||  
 DB 176 PS-----GSTRRCGCGVDRHRHVSCKAKOSYVALTPADSGRGRIRIDTACV 228  
 |||||  
 QY 123 LLSRTGR 129  
 |||||  
 DB 229 LLSRTGR 235  
 |||||

## RESULT 4

C40304 neurotrophin-3 precursor - human  
 N:Alternate names: nerve growth factor 2; NGF-2  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Apr-1992 #sequence, revision 30-Sep-1993 #text\_change 16-Jul-1999  
 C:Accession: A36208; JH0141; C40304; S10729; C60536  
 R:Jones, K.R.; Reichardt, L.F.; Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990  
 A:Title: Molecular cloning of a human gene that is a member of the nerve growth factor  
 A:Reference number: A36208; MUID:91045937; PMID:2236018  
 A:Accession: A36208  
 A:Molecule type: DNA  
 A:Residues: 1-257 <ROS>  
 A:Cross-references: GB:M37763; NID:9189300; PIDN:AAA59953.1; PID:9189301  
 R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Lammee, G.R.; Nikolic, Neuron 4, 767-773, 1990  
 A:Title: Primary structure and biological activity of a novel human neurotrophic factor  
 A:Reference number: JH0141; MUID:90262727; PMID:2344409  
 A:Accession: JH0141  
 A:Molecule type: DNA  
 A:Residues: 1-257 <ROS>  
 R:Maloson, P.C.; Le Beau, M.M.; Esplinoza III, R.; Ip, N.Y.; Belluscio, L.; de la Genomica 10, 558-568, 1991  
 A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene structure  
 A:Reference number: A40304; MUID:91365361; PMID:1885806  
 A:Accession: C40304  
 A:Molecule type: DNA  
 A:Residues: 1-257 <NAI>  
 A:Cross-references: GB:M61180; NID:9189302; PIDN:AAA63231.1; PID:9189303  
 R:Kato, Y.; Yoshimura, K.; Nakahama, K.  
 FEBS Lett. 266, 187-191, 1990  
 A:Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.  
 A:Reference number: S10719; MUID:90306351; PMID:2365067  
 A:Accession: S10719  
 A:Molecule type: DNA  
 A:Residues: 1-257 <NAI>  
 A:Cross-references: GB:X53655; NID:9287794; PIDN:CAA37703.1; PID:9287795  
 R:Kato, Y.; Yoshimura, K.; Nakahama, K.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton, Cold Spring Harbor Symp. Quant. Biol. 55, 371-379, 1990  
 A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways  
 A:Reference number: A60536; MUID:92111157; PMID:1966766  
 A:Accession: C60536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-73, 'Q', 75-77, 'R', 79-108, 'T', 110-257 <YAN>  
 C:Genetics:  
 A:Gene: GDNF:NTF3  
 A:Cross-references: GDB:125917; OMIM:162660  
 A:Map position: 12p13-12p13  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-138/Domain: propeptide #status predicted <PRO>



OY 69 GCGAGGCGGCGVDRHNVSECKAKQSYVALTAHAGRGVGMWIRIDPACVCTLLSR 128  
 DB 223 ARPVR--NCGRIIDOKHNSCKRTSYVALTSNNKLVGMIRIDPSCVCLSRKIG 280  
 OY 129 R 129  
 DB 281 R 281

RESULT 8  
 A:Accession: B36208  
 A:Molecule type: DNA  
 A:Residues: 1-247 <CON>  
 A:Cross-references: GB:M37762; NID:9179402; PIDN:AAA51820.1; PID:9179403  
 R:Yancopoulos, G.D.; Masonpierre, P.C.; IP, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton  
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990  
 A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways the  
 A:Reference number: A60536; MUID:9211157; PMID:1966766  
 A:Accession: A60536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-65, 'W', 67-247 <YAN>  
 R:Masonpierre, P.C.; Le Beau, M.M.; Espinosa III, R.; IP, N.Y.; Belluscio, L.; de la MC  
 Genomics 10, 558-568, 1991  
 A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struct  
 A:Reference number: A40304; MUID:91365361; PMID:1889806  
 A:Accession: A40304  
 A:Molecule type: mRNA  
 A:Residues: 1-247 <KMT>  
 A:Cross-references: GB:M61176; NID:9179404; PIDN:AAA69805.1; PID:9896463  
 A:Note: the sequence in Genbank entry M61176, release 106.0, (PID:9896463) begins tran  
 R:Yamanoto, H.; Gurney, M.E.  
 J. Neurosci. 10, 3469-3478, 1990  
 A:Title: Human platelets contain brain-derived neurotrophic factor.  
 A:Reference number: A37218; MUID:91038253; PMID:2230938  
 A:Accession: A37218  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 138-236 <YAN>  
 R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Martin, E.; Burton, L.E.; Shih, A.; Laramee,  
 Endocrinology 129, 1289-1294, 1991  
 A:Title: Primary structure and biological activity of human brain-derived neurotrophic f  
 A:Reference number: A61115; MUID:91339743; PMID:1874171  
 A:Accession: A61115  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-65, 'W', 67-247 <ROS>  
 R:Shintani, A.; Ono, Y.; Katsuno, Y.; Igarashi, K.  
 Biochem. Biophys. Res. Commun. 182, 325-332, 1992  
 A:Title: Characterization of the 5'-flanking region of the human brain-derived neurotro  
 A:Reference number: I38072; MUID:92118032; PMID:1339267  
 A:Accession: I38072  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-247 <SHI>  
 A:Cross-references: EMBL:X60201; NID:93928269; PIDN:CAA42761.1; PID:9496626  
 A:Note: the authors do not discuss this mRNA sequence in this reference; attribution is  
 C:Genetics:  
 A:Gene: GDB:BONF  
 A:Cross-references: GDB:125916; OMIM:113505  
 A:Map position: 11p13-11p13  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: dimer; glycoprotein  
 F:1-16/Domain: signal sequence  
 Status predicted <SIG>

F:17-128/Domain: propeptide  
 F:129-247/Product: brain-derived neurotrophic factor  
 F:121/Binding site: carbohydrate (asn) (covalent)  
 Status predicted <MAT>  
 Query Match 49.4%; Score 345; DB 2; Length 247;  
 Best Local Similarity 53.7%; Pred. No. 3,4e-26;  
 Matches 66; Conservative 22; Mismatches 25; Indels 10; Gaps 3;

OY 9 SRGELAVCDVAVSGWTT--DRRTAVDLRGREVEVLGEVPAAGSGPLROYFEETCKADNA 66  
 DB 133 ARRGELVCDISISEWYTAADKTAADMGGCTVLEKVPVSKGO-LKQYFEETKCNP--- 188  
 OY 67 EEGGPGAGGCGGCVDRHNVSECKAKQSYVALTAHAGRGVGMWIRIDPACVCTLLSR 126  
 DB 189 ----MGYTRKCGGIDGRHNSCKRTTOSYVALTMDSKKRIGMIRIDPSCVCTLLIR 244  
 OY 127 TGR 129  
 DB 245 RGR 247

RESULT 9  
 A:Accession: S12555  
 A:Molecule type: protein  
 A:Residues: 1-249 <HOF>  
 A:Cross-references: GB:X55573; NID:9287898; PIDN:CAA39159.1; PID:9287899  
 R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.  
 Eur. J. Biochem. 225, 995-1003, 1994  
 A:Title: Characterization of neurotrophin dimers and monomers.  
 A:Reference number: S51179; MUID:95045576; PMID:7957235  
 A:Accession: S51180  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 131-135 <KOL>  
 A:Accession: S51181  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 117-121 <KOR>  
 C:Superfamily: nerve growth factor beta chain

Query Match 49.4%; Score 345; DB 2; Length 249;  
 Best Local Similarity 53.7%; Pred. No. 3,4e-26;  
 Matches 66; Conservative 22; Mismatches 25; Indels 10; Gaps 3;  
 OY 9 SRGELAVCDVAVSGWTT--DRRTAVDLRGREVEVLGEVPAAGSGPLROYFEETCKADNA 66  
 DB 133 ARRGELVCDISISEWYTAADKTAADMGGCTVLEKVPVSKGO-LKQYFEETKCNP--- 190  
 OY 67 EEGGPGAGGCGGCVDRHNVSECKAKQSYVALTAHAGRGVGMWIRIDPACVCTLLSR 126  
 DB 191 ----MGYTRKCGGIDGRHNSCKRTTOSYVALTMDSKKRIGMIRIDPSCVCTLLIR 246

RESULT 10  
 A:Accession: B40304  
 A:Molecule type: protein  
 A:Residues: 1-247 <CON>  
 A:Cross-references: GB:M37762; NID:9179402; PIDN:AAA51820.1; PID:9179403  
 R:Yancopoulos, G.D.; Masonpierre, P.C.; IP, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton  
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990  
 A:Title: Neurotrophic factors, their receptors, and the signal transduction pathways the  
 A:Reference number: A60536; MUID:9211157; PMID:1966766  
 A:Accession: A60536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-65, 'W', 67-247 <YAN>  
 R:Masonpierre, P.C.; Le Beau, M.M.; Espinosa III, R.; IP, N.Y.; Belluscio, L.; de la MC  
 Genomics 10, 558-568, 1991  
 A:Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struct  
 A:Reference number: A40304; MUID:91365361; PMID:1889806  
 A:Accession: A40304  
 A:Molecule type: mRNA  
 A:Residues: 1-247 <KMT>  
 A:Cross-references: GB:M61176; NID:9179404; PIDN:AAA69805.1; PID:9896463  
 A:Note: the sequence in Genbank entry M61176, release 106.0, (PID:9896463) begins tran  
 R:Yamanoto, H.; Gurney, M.E.  
 J. Neurosci. 10, 3469-3478, 1990  
 A:Title: Human platelets contain brain-derived neurotrophic factor.  
 A:Reference number: A37218; MUID:91038253; PMID:2230938  
 A:Accession: A37218  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 138-236 <YAN>  
 R:Rosenthal, A.; Goeddel, D.V.; Nguyen, T.; Martin, E.; Burton, L.E.; Shih, A.; Laramee,  
 Endocrinology 129, 1289-1294, 1991  
 A:Title: Primary structure and biological activity of human brain-derived neurotrophic f  
 A:Reference number: A61115; MUID:91339743; PMID:1874171  
 A:Accession: A61115  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-65, 'W', 67-247 <ROS>  
 R:Shintani, A.; Ono, Y.; Katsuno, Y.; Igarashi, K.  
 Biochem. Biophys. Res. Commun. 182, 325-332, 1992  
 A:Title: Characterization of the 5'-flanking region of the human brain-derived neurotro  
 A:Reference number: I38072; MUID:92118032; PMID:1339267  
 A:Accession: I38072  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-247 <SHI>  
 A:Cross-references: EMBL:X60201; NID:93928269; PIDN:CAA42761.1; PID:9496626  
 A:Note: the authors do not discuss this mRNA sequence in this reference; attribution is  
 C:Genetics:  
 A:Gene: GDB:BONF  
 A:Cross-references: GDB:125916; OMIM:113505  
 A:Map position: 11p13-11p13  
 C:Superfamily: nerve growth factor beta chain  
 C:Keywords: dimer; glycoprotein  
 F:1-16/Domain: signal sequence  
 Status predicted <SIG>





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:43 : Search time 5.33411 Seconds  
(without alignments)  
1010.837 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698  
Sequence: 1 GVSETAPASRNGELAVCDAY.....RWIRIDTACVCTILSTRGNA 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database : SwissProt\_40.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	689	98.7	210 1	NT5_HUMAN P34130 homo sapien
2	663	95.0	209 1	NT5_RAT P34131 rattus norv
3	501.5	71.8	186 1	NT6G_HUMAN P34134 homo sapien
4	494.5	70.8	257 1	NT6A_HUMAN P34132 homo sapien
5	478.5	68.6	257 1	NT6B_HUMAN P34133 homo sapien
6	415	59.5	236 1	NT4_XENLA P24727 xenopus lae
7	358	51.3	257 1	NT3_CHICK P25433 gallus gall
8	358	51.3	257 1	NT3_HUMAN P20783 homo sapien
9	358	51.3	258 1	NT3_MOUSE P20181 mus musculu
10	358	51.3	258 1	NT3_RAT P18280 rattus norv
11	356	51.0	257 1	NT3_FELCA O95432 felis silve
12	355	50.9	260 1	NT3_XENLA P25435 xenopus lae
13	346	49.6	255 1	BDNF_CAVPO O70183 cavia porce
14	345	49.4	247 1	BDNF_HUMAN P23560 homo sapien
15	345	49.4	247 1	BDNF_PROLO O18755 procyon lot
16	345	49.4	247 1	BDNF_URSAR O18752 ursus arcto
17	345	49.4	247 1	BDNF_URSML O18753 ursus malay
18	345	49.4	249 1	BDNF_MOUSE P21337 rattus norv
19	345	49.4	249 1	BDNF_MOUSE P23363 rattus norv
20	345	49.4	252 1	BDNF_RAT P14082 sus scrofa
21	344	49.3	247 1	BDNF_FELCA O95433 felis silve
22	342	49.0	248 1	BDNF_BOVIN O95106 bos taurus
23	340	48.7	269 1	BDNF_XIPMU O06225 macaca mula
24	336	48.1	114 1	BDNF_XIPMA P25429 gallus gall
25	336	48.1	270 1	BDNF_CHICK O90322 cyprinus ca
26	335	48.0	270 1	BDNF_CYPICA O90322 cyprinus ca
27	315	45.1	114 1	BDNF_XENLA P13600 bos taurus
28	314.5	45.1	231 1	NGF_BOVIN P25427 rattus norv
29	308.5	44.2	241 1	NGF_RAT O29074 sus scrofa
30	307.5	44.1	229 1	NGF_PIG P01139 sus musculu
31	305.5	43.8	241 1	NGF_MOUSE P20675 pronomys nat
32	305.5	43.8	241 1	NGF_PRANA P05200 gallus gall
33	302.5	43.3	243 1	NGF_CHICK P05200 gallus gall

ALIGNMENTS

RESULT 1	ID	NT5_HUMAN	STANDARD:	PRT:	210 AA.
AC	P34130:				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Neurotrophin-5 precursor (NT-5) (Neurotrophin-4)				
DE	(NT-4) (Neurotrophic factor 4).				
GN	NTF5 OR NTF4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Prostate;				
RX	MEDLINE=92212967; PubMed=1313578;				
RA	IP N.Y., Ibanez C.F., Nye S.H., McGlavin J., Jones P.F., Gies D.R.,				
RA	Belluscio L., le Beau M.M., Esplanosa R. II, Squitino S.P., Persson H.,				
RA	Yancopoulos G.D.;				
RT	Mammalian neurotrophin-4: structure, chromosomal localization,				
RT	tissue distribution, and receptor specificity.;				
RT	Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92075279; PubMed=1742028;				
RA	Berkmeier L.R., Winslow J.W., Kaplan D.R., Nikolic K., Goeddel D.V.,				
RA	Rosenthal A.;				
RT	Neurotrophin-5: a novel neurotrophic factor that activates trk and				
RT	trkB.;				
RL	Neuron 7:857-866(1991).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).				
RX	MEDLINE=20095835; PubMed=10631974;				
RA	Robinson R.C., Radzilewski C., Spraggon G., Greenwald J.,				
RA	Kostura M.R., Butnick L.D., Stuart D.I., Choe S., Jones E.Y.;				
RT	The structure of the neurotrophin 4 homodimer and the brain-derived				
RT	neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-				
RT	binding site.;				
RL	Protein Sci. 8:2589-2597(1999).				
CC	-1- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY				
CC	SYMPATHETIC NEURONS.				
CC	-1- TISSUE SPECIFICITY: HIGHEST LEVELS IN PROSTATE, LOWER LEVELS				
CC	IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC				
CC	AND ADULT TISSUES.				
CC	-1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.				
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				

## ALIGNMENTS

34	297.5	42.6	241 1	NGF_HUMAN	P01138 homo sapien
35	295.5	42.3	241 1	NGF_CAVPO	P19093 cavia porce
36	290	41.5	231 1	NGF_XENLA	P21617 xenopus lae
37	269.5	38.6	243 1	NGF_BUMU	P34128 bungarus mu
38	264.5	37.9	117 1	NGF_DABRA	P10894 dabola russ
39	262	37.5	116 1	NGF_NAJA	P01140 najja najja (
40	252	36.1	116 1	NGF_NAJAT	P21377 najja atra (
41	241.5	34.6	194 1	NGF_XIPMA	P34129 xiphophorus
42	235	33.7	140 1	NT7_CYPICA	O93474 cyprinus ca
43	228	32.7	233 1	NT7_BRARE	O73797 brachydanio
44	153	21.9	43 1	NT4_VIPLE	P25436 vipera lebe
45	119	17.0	43 1	BDNF_RATCL	P25430 raja clavac

DR EMBL: M86528; AAA60154.1; -  
 DR PIR: JH0503; JH0503.  
 DR PIR: A42687; A42687.  
 DR PDB: 1B8M; 03-FEB-99.  
 DR PDB: 1B8M; 26-FEB-99.  
 DR Genew: HGNC:8024; MTF5.  
 DR MIM: 162662; -  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF\_1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF\_1.  
 DR SMART: SM00140; NGF\_1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 DR Growth factor; Signal; 3D-structure.  
 DR SIGNAL: 1 24 POTENTIAL.  
 FT PROPEP 25 80  
 FT CHAIN 81 210 NEUROTROPHIN-5.  
 FT DISULFID 97 170  
 FT DISULFID 141 199  
 FT DISULFID 158 201  
 FT CARBOHYD 76 76  
 SO SEQUENCE 210 AA; 22426 MW; DBC6A30195E139AD CRC64; (POTENTIAL).

Query Match 98.7%; Score 689; DB 1; Length 210;  
 Best Local Similarity 99.2%; Pred. No. 5.5e-60;  
 Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSETAPASRRCGLAVCAVSGVTDRTAVDLRGREVEVLGEVPAAGSPRLRGYFEETR 60  
 DB 81 GVSETAPASRRCGLAVCAVSGVTDRTAVDLRGREVEVLGEVPAAGSPRLRGYFEETR 140  
 OY 61 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLTAAGRGWRIRIDTACV 120  
 DB 141 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLTAAGRGWRIRIDTACV 200  
 OY 121 CTLLSRGTA 130  
 DB 201 CTLLSRGTA 210

## RESULT 2

ID NT5\_RAT STANDARD: PRT: 209 AA.  
 AC P34131;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Neurotrophin-5 precursor (NT-5) (Neurotrophic factor 5) (Neurotrophin-4)  
 DE (NT-4) (Neurotrophic factor 4).  
 OS NT5 OR NT4 OR NT4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID:10116;  
 OX (1)  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-92212967; Pubmed-1313578;  
 RA IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Giles D.R.,  
 RA Belluscio L., le Beau M.N., Espinosa R. III, Squinto S.P., Persson H.,  
 RA Vancopoulos G.D.;  
 RA "Mammalian neurotrophin-4: structure, chromosomal localization,  
 RT tissue distribution, and receptor specificity";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).  
 RN (2)  
 RP MEDLINE-92075279; Pubmed-1742028;  
 RA Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolic K., Goeddel D.V.,  
 RA Rosenthal A.;  
 RA "Neurotrophin-5: a novel neurotrophic factor that activates trk and  
 RT trkB";  
 RT Neuron 7:857-866(1991).  
 RL -1- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR

CC SENSOR AND SYMPATHETIC NEURONS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN,  
 CC HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRIO AND ADULT  
 CC TISSUES.

-1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

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DR EMBL: M86742; AAA11728.1; -  
 DR PIR: S59323; AAB20548.1; -  
 DR PIR: JH0504; JH0504.  
 DR PIR: B42687; B42687.  
 DR HSSP: P34130; 1B8M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF\_1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF\_1.  
 DR SMART: SM00140; NGF\_1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 DR Growth factor; Signal.  
 DR SIGNAL: 1 21 POTENTIAL.  
 FT PROPEP 22 79  
 FT CHAIN 80 209 NEUROTROPHIN-5.  
 FT DISULFID 96 169 BY SIMILARITY.  
 FT DISULFID 140 198 BY SIMILARITY.  
 FT DISULFID 157 200 BY SIMILARITY.  
 FT CARBOHYD 75 75  
 FT CONFLICT 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 209 AA; 22332 MW; DF5112C0C5D5B85 CRC64;

Query Match 95.0%; Score 663; DB 1; Length 209;  
 Best Local Similarity 94.6%; Pred. No. 1.8e-57;  
 Matches 123; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 GVSETAPASRRCGLAVCAVSGVTDRTAVDLRGREVEVLGEVPAAGSPRLRGYFEETR 60  
 DB 80 GVSETAPASRRCGLAVCAVSGVTDRTAVDLRGREVEVLGEVPAAGSPRLRGYFEETR 139  
 OY 61 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLTAAGRGWRIRIDTACV 120  
 DB 140 CKADNAEEGCGAGCGGCGVDRRHVSECKAKOSYVALTLTAAGRGWRIRIDTACV 199  
 OY 121 CTLLSRGTA 130  
 DB 200 CTLLSRGTA 209

## RESULT 3

ID NT6G\_HUMAN STANDARD: PRT: 186 AA.  
 AC P34134;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-OCT-2002 (Rel. 41, Last annotation update)  
 DE Neurotrophin-6 gamma (NT-6 gamma) (Fragment).  
 DE NT6G.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID:9606;  
 OX (1)  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-Fetal;  
 RC MEDLINE-92358359; Pubmed-1496419;  
 RA Berkemeier L.R., Oezcelik T., Francke U., Rosenthal A.;  
 RA "Human chromosome 19 contains the neurotrophin-5 gene locus and three



```

RT related genes that may encode novel acidic neurotrophins.*;
RL Somet. Cell Mol. Genet. 18:233-245(1992).
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL: S41541; AAB22781.1; -.
DR HSSP: P34130; 1B98.
DR Genew: HGNC:8027; NTF6G.
DR MIM: 604023; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; PARTIAL.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; 1.
DR NON_TER 1
FT DISULFID 72 146 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 186 AA; 19553 MW; B584396F5A4981C CRC64;

Query Match 71.8%; Score 501.5; DB 1; Length 186;
Best Local Similarity 77.1%; Pred. No. 7.5e-42;
Matches 101; Conservative 6; Mismatches 23; Indels 1; Gaps 1;

OY 1 GVSETAPASRRGELAVCDVAGVWTDRTTRAVDLRGREVEVLGEVPAAGSPURGYFFETR 60
DB 56 GVSTSPASRHOGEELAVCDVAGVWTDRTTRAVDLVLEVEVLGEVPAAGSSILROHFFVTC 115
OY 61 CKADNAEEGPGAGGCGRGV-DRRHVSECKAKOSYVRLTAHAGRGVNRIRIDTAC 119
DB 116 FKADNSEEGRGVGGAGAAAGVMTGCHVSECKAKOSYVRLTAHAGRGVNRIRIDTAC 175
OY 120 VCTLSRTGRA 130
DB 176 VCTLSRTGRA 186

RESULT 4
NT6A_HUMAN STANDARD: PRT; 257 AA.
ID NT6A_HUMAN
AC P34132;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-6 alpha (NT-6 alpha) (Fragment).
GN NTF6A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92358359; PubMed=1496419;
RA Berlemeter L.R., Oerzcelik T., Francke U., Rosenthal A.;
RT "Human chromosome 19 contains the neurotrophin-5 gene locus and three
RT related genes that may encode novel acidic neurotrophins.*";
RL Somet. Cell Mol. Genet. 18:233-245(1992).
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: S41522; AAB22779.1; -.
DR HSSP: P34130; 1B98.
DR Genew: HGNC:8025; NTF6A.
DR MIM: 604021; -.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; PARTIAL.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Polymorphism.
DR NON_TER 1
FT DISULFID 143 217 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARIANT 186 186 R -> H.
FT VARIANT 186 186 /FTID-VAR_004627.
FT VARIANT 242 242 I -> T.
SQ SEQUENCE 257 AA; 27246 MW; 74AB5C038D78A3BB CRC64;

Query Match 70.8%; Score 494.5; DB 1; Length 257;
Best Local Similarity 76.3%; Pred. No. 5e-41; 23; Indels 1; Gaps 1;
Matches 100; Conservative 7; Mismatches 23; Indels 1; Gaps 1;

OY 1 GVSETAPASRRGELAVCDVAGVWTDRTTRAVDLRGREVEVLGEVPAAGSPURGYFFETR 60
DB 127 GVSTSPASRHOGEELAVCDVAGVWTDRTTRAVDLVLEVEVLGEVPAAGSSILROHFFVTC 186
OY 61 CKADNAEEGPGAGGCGRGV-DRRHVSECKAKOSYVRLTAHAGRGVNRIRIDTAC 119
DB 187 FKADNSEEGRGVGGAGAAAGVMTGCHVSECKAKOSYVRLTAHAGRGVNRIRIDTAC 246
OY 120 VCTLSRTGRA 130
DB 247 VCTLSRTGRA 257

RESULT 5
NT6B_HUMAN STANDARD: PRT; 257 AA.
ID NT6B_HUMAN
AC P34133;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-6 beta (NT-6 beta) (Fragment).
GN NTF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92358359; PubMed=1496419;
RA Berlemeter L.R., Oerzcelik T., Francke U., Rosenthal A.;
RT "Human chromosome 19 contains the neurotrophin-5 gene locus and three
RT related genes that may encode novel acidic neurotrophins.*";
RL Somet. Cell Mol. Genet. 18:233-245(1992).
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC	EMBL	S41540	AA822780.1	-
DR	HSSP	P34130	1B98	
DR	Genew	HGNC:8026	MTF6B	
DR	MIM	604022	-	
DR	Interpro	IPR002072	NSC	
DR	Pfam	PF00243	NSC	1
DR	ProDom	PD002052	NSC	1
DR	SMART	SM00140	NSC	1
DR	ProSITE	PS00248	NSC_1	PARTIAL
DR	ProSITE	PS00270	NSC_2	1
KM	Growth factor			
FT	NON TER	1	1	
FT	DISULFID	143	217	
FT	CARBOHYD	122	122	
50	SEQUENCE	257 AA	27419 MW	BY SIMILARITY, N-LINKED (GLCNAC... ) (POTENTIAL), 2EN9320918AE505B CRC64

CC	EMBL: 230090; CAAB2906.1; -	
DR	HSP: JH0400; JH0400.	
DR	HSP: P34130; 1898.	
DR	InterPro: IPR002072; NGF.	
DR	PIfam: PF00243; NGF; 1.	
DR	Prints: PR00268; NGF.	
DR	ProDom: PD002052; NGF; 1.	
DR	SMART: SM00140; NGF; 1.	
DR	ProSITE: PS00248; NGF_1; 1.	
DR	ProSITE: PS50270; NGF_2; 1.	
KM	Growth factor; Signal.	
FT	Signal	1 18
FT	PROPEP	19 113
FT	CHAIN	114 236
FT	DISULEID	131 196
FT	DISULEID	174 225
FT	DISULEID	184 227
FT	CARBOHYD	47 106
FT	CARBOHYD	106 106
FO	SEQUENCE	236 AA; 26213 MW; A210F7F2010357D CRC64;

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DR EMBL: M83378; AAA68880.1; -  
 DR HSP: P20783; 188K;  
 DR InterPro: IPR002400; GF\_cytnot.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF\_1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF\_1.  
 DR SMART: SM00140; NGF\_1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS00270; NGF\_2; 1.  
 DR Growth factor; Signal.  
 RM SIGNAL 1 16  
 FT PROPEP 17 138 POTENTIAL.  
 FT CHAIN 139 257 NEUROTROPHIN-3.  
 FT DISULFID 152 217 BY SIMILARITY.  
 FT DISULFID 195 246 BY SIMILARITY.  
 FT DISULFID 205 248 BY SIMILARITY.  
 FT CARBOHYD 131 131 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SO SEQUENCE 257 AA; 29701 MW; E043BA2A005C1E7 CRC64;

Query Match 51.3%; Score 358; DB 1; Length 257;  
 Best Local Similarity 55.4%; Pred. No. 8, 6e-28;  
 Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;

OY 9 SRRELAVCPAGSGWTDRATVDLNGREVEVGEVPAAGSGPLNGPFFETCKADNME 68  
 DB 144 SHRGYVCSSESLMTDKASLIDIRHOVTYVGEI-KTGNSPVQYFETCK-----E 197  
 OY 69 GGPAGGGGCGRVDNRHVSSECKAKOSYVALTAHAQNGVMWRIRIDTACVCTLLSTRG 128  
 DB 198 AKPVK--NGCRGIDDKHMSOCKTSQYVALTSENNKLVGNMWRIDTSCVCAISRIG 255  
 OY 129 R 129  
 DB 256 R 256

RESULT 8  
 NT3\_HUMAN STANDARD; PRT; 257 AA.  
 AC P20783;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neutrophin-3 precursor (NP-3) (Neutrophilic factor) (HNF)  
 DE (Nerve growth factor 2) (NGF-2).  
 GN NT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:90062727; PubMed-2344409;  
 RA Rosethal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,  
 RT "Primary structure and biological activity of a novel human  
 RT neurotrophic factor.";  
 RL Neuron 4:767-773(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91045937; PubMed-2236018;  
 RA Jones K.R., Reichardt L.F.;  
 RT "Molecular cloning of a human gene that is a member of the nerve  
 RT growth factor family.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90306351; PubMed-2365067;  
 RA Kishino Y., Yoshimura K., Nakahama K.;  
 RT "Cloning and expression of a cDNA encoding a novel human neurotrophic  
 RT factor.";  
 RL FEBS Lett. 266:187-191(1990).

RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91365361; PubMed-1889806;  
 RA Maisongier P.C., Le Beau M.N., Espinosa R. III, Ip N.Y.,  
 RA Belluscio L., de la Monte S.M., Squinto S., Furth M.E.,  
 RA Yancopoulos G.D.;  
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:  
 RT gene structures, distributions, and chromosomal localizations.";  
 RL Genomics 10:558-568(1991).

RN [5]  
 RP SEQUENCE OF 194-236 FROM N.A.  
 RC TISSUE-Deukocyte;  
 RX MEDLINE-9122573; PubMed-2025430;  
 RA Halboeck F., Ibanez C.F., Persson H.;  
 RT "Evolutionary studies of the nerve growth factor family reveal a  
 RT novel member abundantly expressed in Xenopus ovary.";  
 RL Neuron 6:845-858(1991).

RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE-95217877; PubMed-7703225;  
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.;  
 RT "Structure of the brain-derived neurotrophic factor/neurotrophin 3  
 RT heterodimer.";  
 RL Biochemistry 34:4139-4146(1995).

RN [7]  
 RP VARIANT Glu-76.  
 RX MEDLINE-95251647; PubMed-7733919;  
 RA Hattori M., Nanko S.;  
 RT "Association of neurotrophin-3 gene variant with severe forms of  
 RT schizophrenia.";  
 RL Biochem. Biophys. Res. Commun. 209:513-518(1995).

RN [8]  
 RP VARIANT Glu-76.  
 RX MEDLINE-96253892; PubMed-8925252;  
 RA Arinami T., Takekoshi K., Itokawa M., Hamaguchi H., Toru M.;  
 RT "Failure to find associations of the CA repeat polymorphism in the  
 RT first intron and the Glu-63/Glu-63 polymorphism of the neurotrophin-3  
 RT gene with schizophrenia.";  
 RL Psychiatr. Genet. 6:113-15(1996).

CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND  
 CC PROPRIOCEPTIVE SENSORY NEURONS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.  
 CC -1- POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was  
 CC thought to be associated with severe forms of schizophrenia. This  
 CC does not seem to be the case.

CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC  
 DR EMBL: X53655; CAA37703.1; -  
 DR EMBL: M37763; AAA59553.1; -  
 DR EMBL: M61180; AAA63231.1; -  
 DR PIR: JH0141; JH0141.  
 DR PIR: A36208; A36208.  
 DR PIR: S10719; S10719.  
 DR PIR: C40304; C40304.  
 DR PIR: IBDN; 04-APR-96.  
 DR PDB: 1B8K; 09-FEB-99.

```

DR Genev: HGNC:8023: NTF3.
DR MIM: 162660: -.
DR InterPro: IPR002400: GF_cysknob.
DR InterPro: IPR002072: NGF.
DR Pfam: PF00243: NGF.1.
DR PRINTS: PR00438: GFCYSKNOT.
DR PRINTS: PR00268: NGF.
DR ProDom: PD002052: NGF.1.
DR SMART: SM00140: NGF.1.
DR PROSITE: PS00248: NGF_1; 1.
DR PROSITE: PS50270: NGF_2; 1.
DR Growth factor: Signal; Polymorphism: 3D-structure.
KW SIGNAL 1 16
FT PROPEP 17 138
FT CHAIN 139 257
FT DISULFID 152 217
FT DISULFID 195 246
FT DISULFID 205 248
FT CARBOHD 131 131
FT VARIANT 76 76
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT G->E.
FT /FTID=VAR.012084.
SQ SEQUENCE 257 AA; 29354 MW; 39A5B83B25E03 CRC64:

Query Match 51.3%; Score 358; DB 1; Length 257;
Best Local Similarity 55.4%; Pred. No. 8.6e-28;
Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;

OY 9 SRRGELAVCDVAGVTRTRAVDLRGREVEVLGEVPAAGSPPLRQYFEETRCKADNAEE 68
DB 144 SHRGELVCDSESLVMTWTKSSAIDIRGHQVTLGEI-KTGNSPVQYETRCK-----E 197
OY 69 GGGPAGGCGRGVDRRWVSECKAKSYRALTAAAGRGVGRWIRIDTACVCTLLSRFG 128
DB 198 ARPVK--NGCRIDDKHNMNSCKTSQTYVALTSENKMLVGMWRIRIDTSCVCLSRKIG 255
OY 129 R 129
DB 256 R 256

RESULT 9
NT3_MOUSE STANDARD: PRT: 258 AA.
ID NT3_MOUSE
AC P20181;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
DE NTF3 OR NTF-3.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90190865; PubMed=2314473;
RA Hohn A., Leebrock J., Bailey K., Barde Y.-A.;
RT Identification and characterization of a novel member of the nerve
RT growth factor/brain-derived neurotrophic factor family.*;
RL Nature 344:339-341(1990).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSOR NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC EMBL: X53257; CA37348.1; -.
DR PIR: S09155; S09155.
DR HSSP: P20783; 1B8K.
DR MGD: MG1:97380; NTF3.
DR InterPro: IPR002400: GF_cysknob.
DR InterPro: IPR002072: NGF.
DR Pfam: PF00243: NGF.1.
DR PRINTS: PR00438: GFCYSKNOT.
DR ProDom: PD002052: NGF.1.
DR SMART: SM00140: NGF.1.
DR PROSITE: PS00248: NGF_1; 1.
DR PROSITE: PS50270: NGF_2; 1.
DR Growth factor: Signal; POTENTIAL.
KW SIGNAL 1 16
FT PROPEP 17 139
FT CHAIN 140 258
FT DISULFID 153 218
FT DISULFID 196 247
FT DISULFID 206 249
FT CARBOHD 131 131
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 258 AA; 29587 MW; 7180064E8AE042 CRC64:

Query Match 51.3%; Score 358; DB 1; Length 258;
Best Local Similarity 55.4%; Pred. No. 8.6e-28;
Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;

OY 9 SRRGELAVCDVAGVTRTRAVDLRGREVEVLGEVPAAGSPPLRQYFEETRCKADNAEE 68
DB 145 SHRGELVCDSESLVMTWTKSSAIDIRGHQVTLGEI-KTGNSPVQYETRCK-----E 198
OY 69 GGGPAGGCGRGVDRRWVSECKAKSYRALTAAAGRGVGRWIRIDTACVCTLLSRFG 128
DB 199 ARPVK--NGCRIDDKHNMNSCKTSQTYVALTSENKMLVGMWRIRIDTSCVCLSRKIG 256
OY 129 R 129
DB 257 R 257

RESULT 10
NT3_RAT STANDARD: PRT: 258 AA.
ID NT3_RAT
AC P18280;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
DE NTF3 OR NTF-3.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319130; PubMed=2164684;
RA Ernforts P., Ibanez C.F., Ebendal T., Olson L., Persson H.;
RT Molecular cloning and neurotrophic activities of a protein with
RT structural similarities to nerve growth factor: developmental and
RT topographical expression in the brain.*;
RL Proc. Natl. Acad. Sci. U.S.A. 87:5454-5458(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90208301; PubMed=2321006;
RA Maisonnierre P.C., Belluscio L., Squinto S., Ip N.Y., Furch M.E.,
RA Lindsay R.M., Yancopoulos G.D.;
RT "Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.*";
RL Science 247:1446-1451(1990).
RN [3]
RP SEQUENCE FROM N.A.

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```

RX MEDLINE-91365361; PubMed-1889806;
RA Maisompierre P.C., Le Beau M., Esplinoza R. III, IP N.Y.,
RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
RA Yancopoulos G.D.,
RA "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
RT gene structures, distributions, and chromosomal localizations.",
RL Genomics 10:558-568(1991).
RN
RP [4]
RP SEQUENCE OF 195-237 FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Liver;
RX MEDLINE-9122573; PubMed-2035430;
RA Hallboeck F., Ibanez C.F., Persson H.,
RA "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in xenopus ovary.",
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: M34643; AAA4313.1; -
DR EMBL: M33968; AAA41727.1; -
DR EMBL: M61179; AAA63497.1; -
DR PIR: A35781; A35781.
DR PIR: A40094; A40094.
DR HSSP: P20783; 1B8K.
DR InterPro: IPR002400; GE_cysknot.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00438; GFCTSKNOT.
DR PRODOM: PD00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
KM Growth factor; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 139
FT CHAIN 140 258 NEUROTROPHIN-3.
FT DISULFID 153 218 BY SIMILARITY.
FT DISULFID 195 247 BY SIMILARITY.
FT DISULFID 205 249 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 258 AA; 29644 MW; 74D557CF8518A1CE CRC64;

Query Match 51.3%; Score 358; DB 1; Length 258;
Best Local Similarity 35.4%; Pred. No. 8; 6e-28;
Matches 67; Conservative 18; Mismatches 28; Indels 8; Gaps 3;

OY 9 SRGELAVCDVAGWVTRRTAVDLRGREVEVLGEVPAGSGPRLQVFFETRCADNAEE 68
DB 145 SHRGESVCDSESLWVTRSHIDIRGHQVYLGEI-KTGNSPVKQVFEYTRCK-----E 198
OY 69 GGRGAGGCGGRCVDRRHVSECKAKQSYRALTAAAGRVGMWRIRIDTACVCTLSRTG 128
DB 199 ARPVK--NGCRGIDDKHNSOCKTSQTYVRLATSENKLVGMWRIRIDTSCVCALEKIG 256
OY 129 R 129
DB 257 R 257

RESULT 11
NT3_FEICA

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ID NT3_FEICA STANDARD: PRT; 257 AA.
AC 09T5T2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDMF)
DE (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-20211727; PubMed-10745216;
RA Lein E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system
RT development.",
RL J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: AF192538; AAF03424.1; -
DR HSSP: P20783; 1B8K.
DR InterPro: IPR002400; GE_cysknot.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
DR Growth factor; Signal.
KM Growth factor; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 138
FT CHAIN 139 257 NEUROTROPHIN-3.
FT DISULFID 152 217 BY SIMILARITY.
FT DISULFID 195 246 BY SIMILARITY.
FT DISULFID 205 248 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 257 AA; 29403 MW; EB53FE59C5113E4 CRC64;

Query Match 51.0%; Score 356; DB 1; Length 257;
Best Local Similarity 54.5%; Pred. No. 1.3e-27;
Matches 66; Conservative 20; Mismatches 27; Indels 8; Gaps 3;

OY 9 SRGELAVCDVAGWVTRRTAVDLRGREVEVLGEVPAGSGPRLQVFFETRCADNAEE 68
DB 144 SHRGESVCDSESLWVTRSHIDIRGHQVYLGEI-KSGNSPVKQVFEYTRCK-----E 197
OY 69 GGRGAGGCGGRCVDRRHVSECKAKQSYRALTAAAGRVGMWRIRIDTACVCTLSRTG 128
DB 198 ARPVK--NGCRGIDDKHNSOCKTSQTYVRLATSENKLVGMWRIRIDTSCVCALEKIG 255
OY 129 R 129
DB 256 R 256

RESULT 12
NT3_XENLA
ID NT3_XENLA STANDARD: PRT; 260 AA.
AC P25435;
DT 01-MAY-1992 (Rel. 22, Created)

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01-NOV-1997 (Rel. 35, last sequence update)  
 30-MAY-2000 (Rel. 39, last annotation update)  
 Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HNF) (Nerve growth factor 2) (NGF-2)  
 Xenopus laevis (African clawed frog).  
 Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodidae; Xenopus.  
 NCBI\_Taxid=8355;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Brain;  
 MEDLINE=97252639; PubMed=9096131;  
 Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;  
 "Activity-dependent expression of NT-3 in muscle cells in culture: implications in the development of neuromuscular junctions.";  
 J. Neurosci. 17:2947-2958(1997).  
 [2]  
 SEQUENCE OF 197-217 FROM N.A.  
 TISSUE=Liver;  
 MEDLINE=9122573; PubMed=2025430;  
 Hallboeck F., Idanez C.F., Petsson H.;  
 "Evolutionary studies of the nerve growth factor family reveal a novel member abundantly expressed in Xenopus ovary.";  
 Neuron 6:845-858(1991).  
 -1- FUNCTION: SEEMS TO PROMOTE THE SURVIVAL OF VISCERAL AND PROPRIOCEPTIVE SENSORY NEURONS.  
 -1- SUBCELLULAR LOCATION: Secreted.  
 -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
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 EMBL: U27576; AB017723.1; -  
 HSSP: P20783; 188K.  
 DR InterPro: IPR002400; GF\_cysknoc.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRINTS: PR00438; GFCSKNOT.  
 DR PRODOM: PD00268; NGF.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT PROPEP 17 141 NEUTROPHIN-3.  
 FT CHAIN 142 260 BY SIMILARITY.  
 FT DISULFID 155 220 BY SIMILARITY.  
 FT DISULFID 198 249 BY SIMILARITY.  
 FT DISULFID 208 251 BY SIMILARITY.  
 FT CARBOHYD 114 134 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5E8A93C5 CRC64;  
 Query Match 50.9%; Score 355; DB 1; Length 260;  
 Best Local Similarity 55.0%; Pred. No. 1,7e-27;  
 Matches 66; Conservative 18; Mismatches 28; Indels 8; Gaps 3;  
 Oy 11 RGEIACVADAGSGWTDRTAVDLRGREVEVLEGPANAGSGPLRQYFFETRCADNAEEGG 70  
 Db 149 RGEISVDSSESLWTDKMAHIDIRGHQTVLGEI-KTGNSEVVKQYFFETRCCK-----EAR 202  
 Oy 71 PGAGGGCGRCGRVRRHNVSECKAKOSYVRLTAHAAGRGVGRMIRIDTACVCTLIISRTGRA 130  
 Db 203 PVK--NGCRGIDDKHNSCKTSQTVYRALTSENNKAVGMIMRIDISCVCAISRKIGRS 260  
 RESULT 13

BDNF\_CAVPO STANDARD; PRT; 255 AA.  
 ID BDNF\_CAVPO  
 AC 070183;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Brain-derived neurotrophic factor precursor (BDNF).  
 GN BDNF.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.  
 OX NCBI\_Taxid=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Hartley white; TISSUE=Liver;  
 RA Inoue K., Nakayama C., Noyuchi H.;  
 Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RL FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE ALL LOCATED TO IT (BY SIMILARITY).  
 CC CONNECTED TO IT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
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 EMBL: AB012097; BA025176.1; -  
 HSSP: P23560; 188M.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF. 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF. 1.  
 DR SMART: SM00140; NGF. 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 135 BY SIMILARITY.  
 FT CHAIN 137 255 BRAIN-DERIVED NEUROTROPHIC FACTOR.  
 FT SITE 57 58 CLEAVAGE (BY SIP) (BY SIMILARITY).  
 FT DISULFID 149 216 BY SIMILARITY.  
 FT DISULFID 194 245 BY SIMILARITY.  
 FT DISULFID 204 247 BY SIMILARITY.  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 255 AA; 28308 MW; BA05BA3EBB88FA04 CRC64;  
 Query Match 49.6%; Score 346; DB 1; Length 255;  
 Best Local Similarity 54.5%; Pred. No. 1,2e-26;  
 Matches 67; Conservative 21; Mismatches 25; Indels 10; Gaps 3;  
 Oy 9 SRRGELAVCDVAGSGWT--DRTAVDLRGREVEVLEGPANAGSGPLRQYFFETRCADNA 66  
 Db 141 ARRGELSVCDVSGVSMVTAADKRTAVDMSCGTVLEKVPNSGO-LQYFFETRCNDP--- 196  
 Oy 67 EBGPGAGGGCGGRVRRHNVSECKAKOSYVRLTAHAAGRGVGRMIRIDTACVCTLIISR 126  
 Db 197 ---MGTRKRCRQIDKRNHNSCKRTQSYVRLTMDSKRKRGMRIRIDISCVCTLIK 252  
 Oy 127 TGR 129  
 Db 253 RGR 255  
 RESULT 14  
 BDNF\_HUMAN STANDARD; PRT; 247 AA.  
 ID BDNF\_HUMAN  
 AC P23560; Q9UC24; Q9BY17;  
 DT 01-NOV-1991 (Rel. 20, Created)



Db 245 RGR 247

Job time : 5.33411 secs

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RESULT 15
ID BDNF_PROLO STANDARD: PRT: 247 AA.
AC 018755;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-derived neurotrophic factor precursor (BDNF).
OS BDNF.
OS Procyon lotor (Raccoon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Procyon.
OX NCBI_TaxID=9654;
RN [1]
RP SEQUENCE FROM N.A.
RA Ltn F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS THAT ARE
CC ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRECTLY
CC CONNECTED TO IT (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF003188; AAB71654.1; -.
DR HSSP: P23560; 188M.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00288; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 128 POTENTIAL.
FT CHAIN 129 247 BRAIN-DERIVED NEUROTROPHIC FACTOR.
FT SITE 57 58 CLEAVAGE (BY SLP) (BY SIMILARITY).
FT DISULFID 141 208 BY SIMILARITY.
FT DISULFID 186 237 BY SIMILARITY.
FT DISULFID 196 239 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SROUENCE 247 AA: 27834 MW: 58377EAFEF1F52A0 CRC64;

Query Match 49.4%; Score 345; DB 1; Length 247;
Best Local Similarity 53.7%; Pred. No. 1.5e-26;
Matches 66; Conservative 22; Mismatches 25; Indels 10; Gaps 3;

OY 9 SRGELAVCDVAGVWT--DRRTAVDLGRREVLYGEVPAAGSPLRQYFEETCKADNA 66
DB 133 ARRGELSTVCSISEWTAADKTAIVDMGSGTVLEKVPVSKGO-LKQYFEETKCNP--- 188
OY 67 EEGGPGAGGGCGRGVDRRHVSECKAKOSYVRALTAHAGRGVGRWIRITDACYCTILSR 126
DB 189 ---MGYTKEGCGIDKIRHMNSQCHTQSYVRALTMDSKRIGWRFIRIDTSCVCTLTIR 244
OY 127 TGR 129
DB 245 RGR 247
```

Search completed: December 2, 2002, 15:12:44



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 2, 2002, 15:05:42 : Search time 20.1172 seconds  
(without alignments)  
1331.501 Million cell updates/sec

Title: US-10-072-681-6  
Perfect score: 698  
Sequence: 1 GVSEFAPASRGEALVCDV.....RWIRIDTACVCTLLSRGTA 130

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.21:\*  
1: SP\_Archea:\*  
2: SP\_Bacteria:\*  
3: SP\_Fungi:\*  
4: SP\_Human:\*  
5: SP\_Invertebrate:\*  
6: SP\_Mammal:\*  
7: SP\_mhc:\*  
8: SP\_Organelle:\*  
9: SP\_Phage:\*  
10: SP\_Plant:\*  
11: SP\_Protozoa:\*  
12: SP\_Virus:\*  
13: SP\_Vertebrate:\*  
14: SP\_Unclassified:\*  
15: SP\_Virus:\*  
16: SP\_Bacteriophage:\*  
17: SP\_Archeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	49.4	153	11 09CYL3	09CYL3 mus musculu
2	345	49.4	247	6 097759	097759 allurus ful
3	345	49.4	249	11 08VNH4	08VNH4 mus musculu
4	336	48.1	177	13 091BL2	091BL2 poephilla gu
5	334	47.9	246	13 080C74	080C74 cyclophilops
6	332	47.6	246	13 080G75	080G75 phytocepha
7	328	47.0	246	13 080G76	080G76 japalura sp
8	327	46.8	270	13 09VH42	09VH42 brachydania
9	323.5	46.3	324	13 09X985	09X985 lampetra fl
10	322	46.1	241	6 09N182	09N182 macaca fusc
11	317.5	45.5	247	13 080G77	080G77 cytotriclo
12	297.5	42.6	241	4 09P260	09P260 homo sapien
13	297.5	42.6	241	4 09P260	09P260 homo sapien
14	297.5	42.6	241	4 09P260	09P260 homo sapien
15	297.5	42.6	241	6 09N2P1	09N2P1 pan troglod
16	297.5	42.6	241	6 09N2P0	09N2P0 gorilla gor

17	297.5	42.6	241	6 09N2E9	09N2E9 pongo pygma
18	296	42.4	101	6 09PT22	09PT22 macaca fusc
19	277.5	39.8	294	11 091XB4	091XB4 mus musculu
20	265.5	38.2	217	6 09N183	09N183 macaca fusc
21	265.5	38.0	241	13 090W38	090W38 bothrops ja
22	262.5	37.6	241	13 090E29	090E29 crocalus du
23	228.5	32.7	286	13 091988	091988 xiphophorus
24	216	30.9	85	6 002792	002792 notoryctes
25	215	30.9	87	4 09P224	09P224 homo sapien
26	213	30.5	85	6 013114	013114 leiodon mac
27	213	30.5	85	6 013122	013122 tarsipes ro
28	213	30.5	85	6 002795	002795 ornithorhyn
29	213	30.5	85	6 002798	002798 petaurus br
30	213	30.5	85	6 013104	013104 cercartacus
31	213	30.5	85	6 002790	002790 macroopus fu
32	213	30.5	85	6 013105	013105 daayuroides
33	213	30.5	85	6 002801	002801 techylosasu
34	212.5	30.4	87	6 09TMC3	09TMC3 cervus elap
35	212	30.4	85	6 002803	002803 trichosurus
36	178	25.5	186	12 0905D9	0915d9 fowipox vir
37	162	23.2	185	6 09BFK7	09BFK7 erinaceus c
38	162	23.2	186	6 09BFK0	09BFK0 chaetophrac
39	160	22.9	185	11 099NV9	099NV9 pedetes cap
40	159	22.8	184	6 09BRJ5	09BRJ5 tupia alai
41	159	22.8	185	6 09BRK5	09BRK5 condylura c
42	159	22.8	185	6 09BRK5	09BRK5 condylura c
43	159	22.8	186	6 09BFJ3	09BFJ3 choleopus d
44	159	22.8	186	6 09BFJ2	09BFJ2 choleopus d
45	159	22.8	186	6 09BFK9	09BFK9 tamandua te

## ALIGNMENTS

RESULT 1  
ID 09CYL3 PRELIMINARY: PRT; 153 AA.  
AC 09CYL3;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Brain derived neurotrophic factor.  
GN BDNF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID-10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J; TISSUE-EMBRYO;  
RX MEDLINE-21083660; PubMed-11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana H.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochila H.,  
RA Rehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quakebush J.,  
RA Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Orido T., Furuno M., Aono H., Baldarelli R., Barch G.,  
RA Blake J., Boilell D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombashta P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch R.-F.,  
RA Suzuki H., Toyo-oka K., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Watanabe-Boriss A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK017559; BAB30805.1; -  
HSSP; P23560; 1B8M.

DR MCD: MGI:88145; Bdnf.  
DR Interpro: IPRO02072; NCF.  
DR Pfam: PF00243; NCF: 1.  
DR PRINTS: PR00268; NCF.  
DR ProDom: PD002052; NCF: 1.  
DR SMART: SM00140; NCF: 1.  
DR PROSITE: PS00248; NCF\_2: 1.  
DR PROSITE: PS0270; NCF\_2: 1.  
DR SEQUENCE 153 AA: 17519 MW: CA8EBB944CE5B37 CRC6;

Query Match	49.48;	Score 345;	DB 11;	Length 153;
Best Local Similarity	53.78;	Pred. No. 1.3e-26;		
Matches 66;	Conservative 22;	Mismatches 25;	Indels 10;	Gaps 3;

```

0y  9  SRGELAVCDAAAGVNT--DRTTAVDGRGEVEVLEAVPAAGSPLDROFFETTRCKDNA  66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  39  ARGELSTVCDSTSEVNTAADKRTAVDMSGSTVYVLEKVPVSKGO-LKQFYETKCNP---  94

0y  67  EEKGPPAGGGCGRGVDRRHAWYSECKAKOSVYRALTAAGRGVHRIRIRIDPACVCTLLSR  126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  95  ----AGTTEGGRGDKDKNHNSGCRQTQSVYRALTDMSKRRKGRIRIRIDISCVCTLLIK  150

```

Qy	127	TGR	129
Db	151	RGR	153

RESULT 2	
097759	
ID 097759	PRELIMINARY; PRT; 247 AA

```
DT 01-MAY-1999 (TREMblurel. 10, Created)
DT 01-MAY-1999 (TREMblurel. 10, last sequence update)
DT 01-JUN-2001 (TREMblurel. 17, last annotation update)
DE Brain derived neurotrophic factor.
```

OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.  
OX NCBI\_TaxID=9649;

RT deduced amino acid sequences."  
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.

```
DR      HSSP; P23560; 1B94.
DR      InterPro; IPR002072; NCF.
DR      Pfam; PF00243; NCF. 1.
DR      PRINTS; PR00268; NCF.
DR      ProDom; PD002052; NCF. 1.
DR      SMART; SM00140; NCF. 1.
DR      ProSITE; PS00248; NCF_1. 1.
DR      ProSITE; PS50270; NCF_2. 1.
DR      PROSITE 247 AA; 278-70 MM;
SQ      FE86C2C71AC03EE CRC644
```

Query Match	49.4%;	Score 345;	DB 6;	Length 247;
Best Local Similarity	53.7%;	Pred. No. 2.2e-26;		
Matches 66;	Conservative 22;	Mismatches 25;	Indels 10;	Gaps 3;

```

Qy      9  SRGELAVCDVAGSWMT--DRRTAVDLGRREVEVLGEVPAAGSPLEIROYFFETRCCKADNA 66
      :||||:||||:| | | :|||:| | | | | :| | :| | :|||:| | :|
Db     133  ARGELSYCDSTSEMTAAADKKTAVDMSGTVTYLEKVPVSKGQ-LKQYFYERKCNP---- 186

```

```

0y      67  EGGPGAGGGCGCVCVDRHHVSECKAKOSYVALTAHAOCRGVGMWIRIDTACVCTLSR 120
          |  ||||:||||:|:  |||||  ::|||:||||:||||:
Db      189  ---KGTTEGGCGIDKRHHNSQCRTGSYVALTMDSKKRIGMRFRIIDTSCVCTLTIR 240

```

QY	127	TGR	129
Db	245	RGR	247

RESULT 3	
Q8VHH4	
ID Q8VHH4	PRELIMINARY;
	PRT; 249 AA

DT	01-MAR-2002 (TREMblrel. 20. Created)
DT	01-MAR-2002 (TREMblrel. 20. Last sequence update)
DT	01-JUN-2002 (TREMblrel. 21. Last annotation update)
DE	Anorexia BDNF.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;	
px	[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-B6C3FE-A/J-ANXA+/A;  
RA Kim S.-J., Kim C.-S., Cha Y.-J., Song K.-Y., Yeo M.-G.;  
RT "Anorexia mouse ORE BDNF. "  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBD databases

DR PFAM; PF00243; NCF; 1.  
DR PRINTS; PRO0268; NCF.  
DR PRODOM; PD002052; NCF; 1.  
DR SWISS-PROT; S000140; NCF; 1.

DR PROSITE; PS00248; NGF\_1; UNKNOWN\_1  
DR PROSITE; PS50270; NGF\_2; 1.  
SQ SEQUENCE 249 AA; 28109 MW; 21C1

Query Match	49.48;	Score 345;	DB 11;	Length 249;
Best Local Similarity	53.78;	Pred. No. 2.2e-26;		
Matches 66;	Conservative 22;	Mismatches 25;	Indels 10;	Gaps 3.

```
Oy      9  SRRGELAVCDAYSGWNT--DRRTAVDLKRGREVEVGEVPAAGGSPLRQYFEETCRCKADNA 66
          |||||:||||:| | | :|||:| | | :| | | :|||:| | |
Db     135  ARGELSTVDCDSISEWNTAADKKTAVDMGCGTVLVEKVPVSKGQ-DKQYFETKCNP--- 190D
```

```

OY      67  EGGPGAGGGCGCRGVDRHHVSECKAKOSYVRLTAHOGVGMNRIRIDTACVCTLSR 126
          |  |||::|||::|: |||||::: |||::|||::|||:::
Db      191  ---MGTYKEGCRGIDKRHMNSGCRITQSYVRLTMDSKRRIIGREFRIDPSVCVCTLIK 246

```

QY	127	TGR	129
		11	
Db	247	RGR	249

RESULT 4		
Q918L2		
ID Q918L2	PRELIMINARY;	PRT; 177 AA

DT 01-MAR-2001 (TIREBLRel, 16, last sequence update)  
DT 01-DEC-2001 (TIREBLRel, 19, last annotation update)  
DE BDNF (Fragment).

03 *Reptalia guttata* (Lacépède, 1799) (*Reptalia* - *guttata*)  
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
0C Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
0C Estrildinae; Taeniopygia.

RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20193595,

RL Brain Res. Dev. Brain Res. 120:113-123(2000).

DR HSSP; P23560; 1B8M.  
DR InterPro; IPR002072; NGF.  
DR Pfam; PF00243; NGF; 1.

DR PRINTS; PRO0268; NGF.  
DR PRODOM; PD002052; NGF; 1.  
DR SMART; SM00140; NGF; 1.

SQ SEQUENCE 249 AA; 28109 MW; 21CEAE60A235D97 CRC64;

Query Match	49.48;	Score 345;	DB 11;	Length 249;
Best Local Similarity	53.78;	Pred. No. 2.2e-26;		
Matches 66;	Conservative 22;	Mismatches 25;	Indels 10;	Gaps 3.

```
Oy      9  SRRGELAVCDAYSGWNT--DRRTAVDLKRGREVEVGEVPAAGGSPLRQYFEETCRCKADNA 66
          ||||:||||: || |::|||: | ||: | ||:||||:|
Db     135 ARGELSVCDSTISEMTAADKKTAVDMGCGTVLEKVPVSKGQ-DKQYFETKCNP--- 190D
```

```

OY      67  EGGPGAGGGCGCRGVDRHHVSECKAKOSYVRLTAHOGVGMNRIRIDTACVCTLSR 126
          |  |||::|||::|: |||||::: |||::|||::|||:::
Db      191  ---MGTYKEGCRGIDKRHMNSGCRITQSYVRLTMDSKRRIIGREFRIDPSVCVCTLIK 246

```

QY	127	TGR	129
		11	
Db	247	RGR	249

RESULT 4	
Q918L2	
ID Q918L2	PRELIMINARY; PRT; 177 AA

DT 01-MAR-2001 (TIREBLRel, 16, last sequence update)  
DT 01-DEC-2001 (TIREBLRel, 19, last annotation update)  
DE BDNF (Fragment).

03 *Reptalia guttata* (Lacépède, 1799) (*Reptalia* - *guttata*)  
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
0C Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;  
0C Estrildinae; Taeniopygia.

RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20193595,

RL Brain Res. Dev. Brain Res. 120:113-123(2000).

DR HSSP; P23560; 1B8M.  
DR InterPro; IPR002072; NGF.  
DR Pfam; PF00243; NGF; 1.

DR PRINTS; PRO0268; NGF.  
DR PRODOM; PD002052; NGF; 1.  
DR SMART; SM00140; NGF; 1.



OY 127 TGR 129  
DB 244 RGR 246

## RESULT 8

OY942 PRELIMINARY; PRT: 270 AA.

AC OY942: 01-MAY-1999 (TREMELREL. 10, Created)

DT 01-MAY-1999 (TREMELREL. 10, Last sequence update)

DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)

DE Brain-derived neurotrophic factor.

OS Brachydanio rerio (zebrafish) (zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

NCBI\_TaxID=7955;

RM [1]

RP SEQUENCE FROM N.A.

RA Hashimoto M., Heinrich G.;

RL Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.

DR HSSP: U42489; AAD00016.1;

DR HSSP: P23560; 188M.

DR 2FIN: 2DB-GENE-000412-1; bdnf.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF\_1; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

RL J. Neurosci. 18:8700-8711(1998).

DR EMBL: AF071432; AAD22744.1; -.

DR HSSP: P20783; 188K.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

DR PROSITE: PS50270; NGF\_2; 1.

Query Match 46.3%; Score 323.5; DB 13; Length 324;  
Best Local Similarity 44.5%; Pred. No. 4e-24;  
Matches 69; Conservative 14; Mismatches 41; Indels 31; Gaps 4;

OY 7 PASR--RGELAVCDVAVSGVTRRAVLRGVEVLAEPVPAAGS-----50

DB 170 PSRRPRGEPVPCDSESRVSDRDYAFDTGMRVRLGELSLSSSSSSSSSSSSQ9 229

OY 51 -PLRQVFEETRCADNAEEG-----GCGAC-GCGCGVDRRHVSECKAKOS 95

DB 230 STSVKQVFEETRCADNAEEG-----GCGAC-GCGCGVDRRHVSECKAKOS 289

OY 96 YRALTAHAGRGVGRVIRIDTACVCTLSRTGTA 130

DB 290 EVRLTEDAGRLAWRMIRLDTACVCTLSRTGTA 324

## RESULT 10

OY9N182 PRELIMINARY; PRT: 241 AA.

AC OY9N182: 01-OCT-2000 (TREMELREL. 15, Created)

DT 01-OCT-2000 (TREMELREL. 15, Last sequence update)

DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)

DE Neurotrophin-3 (Fragment).

OS Macaca fasciata (Japanese macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

NCBI\_TaxID=9542;

RM [1]

RP SEQUENCE FROM N.A.

RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;

RL MEDLINE-99270338; PubMed-10340513;

RT Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in

RT visual and limbic areas along the occipito-temporo-hippocampal pathway

RT in adult macaque monkeys.";

RT J. Comp. Neurol. 408:378-398(1999).

RM [2]

RP SEQUENCE FROM N.A.

RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;

RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and

RT their receptor messenger RNAs in monkey rhinal cortex.";

RL Neurosci. 21:1000-1010(1998).

DR EMBL: AF222683; AAF33791.1; -.

DR HSSP: P20783; 188K.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF.1.

DR PRINTS: PR00268; NGF.

DR PRODOM: PD002052; NGF.1.

DR SMART: SM00140; NGF.1.

DR PROSITE: PS00248; NGF\_1; 1.

Query Match 46.1%; Score 322; DB 6; Length 241;  
Best Local Similarity 56.0%; Pred. No. 4e-24;  
Matches 61; Conservative 16; Mismatches 24; Indels 8; Gaps 3;

OY 241 PASR--RGELAVCDVAVSGVTRRAVLRGVEVLAEPVPAAGS-----50

DB 170 PSRRPRGEPVPCDSESRVSDRDYAFDTGMRVRLGELSLSSSSSSSSSSSSQ9 229

OY 51 -PLRQVFEETRCADNAEEG-----GCGAC-GCGCGVDRRHVSECKAKOS 95

DB 230 STSVKQVFEETRCADNAEEG-----GCGAC-GCGCGVDRRHVSECKAKOS 289

OY 96 YRALTAHAGRGVGRVIRIDTACVCTLSRTGTA 130

DB 290 EVRLTEDAGRLAWRMIRLDTACVCTLSRTGTA 324

OY 9 SRGELAYCDVAGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCKADNAEE 58  
 DB 141 SRRELSVCSSESUWTDSSAIDIRGHQVYVLEGEI-KTGNSPVQYETRECK-----E 194  
 OY 69 GGRGAGGCGRCVDRRRHVSSECKAKOSYVALTAHAGRCVNRIRIDT 117  
 DB 195 ARPVK--NGCRGIDRKHNSQCKTSQTYVALTSNNKLVGWRIRIDT 241

## RESULT 11

OY 080G77 PRELIMINARY: PRT: 247 AA.  
 AC 080G77:  
 DT 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Brain derived neurotrophic factor.  
 OS Tylocitron taliaensis.  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;  
 CC Tylocitron.  
 CC NCBI\_TaxID=129885;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cao M., Yang Y.H., Zhang Y.Z.:  
 RT "Cloning and sequence analysis of brain derived neurotrophic factor  
 (BDNF) gene from Sichuan Newt (Tylocitron taliaensis)".  
 RL Yang Yung Yu Huan Ching Sheng Wu Hsueh Pao 8:0-0(2002).  
 DR EMBL: AF97712; AM18078.1;  
 SO SEQUENCE 247 AA; 27841 MW; FFCB5F28A7620DED CRC64;

Query Match 45.58; Score 317.5; DB 13; Length 247;  
 Best Local Similarity 51.28; Pred. No. 1.2e-23;  
 Matches 63; Conservative 23; Mismatches 23; Indels 11; Gaps 4;  
 OY 5 TAPASRGELAYCDVAGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 62  
 DB 130 SGPA-RRELSVCSSESUWTDSSAIDIRGHQVYVLEGEI-KTGNSPVQYETRECK-- 185  
 OY 63 ADNAEEGCGRCVDRRRHVSSECKAKOSYVALTAHAGRCVNRIRIDTACT 122  
 DB 186 -----RRPMGIMKRGCKIDRKHNSQCKTSQTYVALTSNNKLVGWRIRIDTSCVT 240  
 OY 123 LLSRTGR 129  
 DB 241 LTIKGR 247

## RESULT 12

OY 09P208 PRELIMINARY: PRT: 241 AA.  
 AC 09P208:  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Beta-nerve growth factor (Fragment).  
 GN BETA-NGF  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kilian T., Kobayakawa H., Saltou N.:  
 RT "Silver Project."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB07517; BA90437.1;  
 DR HSSP: P01135; 1DET.  
 DR InterPro: IPR02072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR ProDom: PD002052; NGF; 1.

DR SMART: SM00140; NGF\_1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 FT MONTER 241  
 SO SEQUENCE 241 AA; 26998 MW; D531ED825D96C14 CRC64;

Query Match 42.68; Score 297.5; DB 4; Length 241;  
 Best Local Similarity 46.58; Pred. No. 1.1e-21;  
 Matches 59; Conservative 20; Mismatches 39; Indels 9; Gaps 3;

OY 3 SETAPASRGELAYCDVAGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 62  
 DB 122 SSSHPFIRGGEFSYCDVSVMGDKTATDICKREYVNLGEV-NINNSVFKQYFEETRCK 180  
 OY 63 ADNAEEGCGRCVDRRRHVSSECKAKOSYVALTAHAGRCVNRIRIDTACT 122  
 DB 181 DPNPVD-----SGCRGIDRKHNSICTTTHFVALTMDGR-QAAMRFIRIDTACV 232  
 OY 123 LLSRTGR 129  
 DB 233 LSRKAVR 239

## RESULT 13

OY 09P60 PRELIMINARY: PRT: 241 AA.  
 AC 09P60:  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Nerve growth factor beta.  
 GN NGF.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.:  
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF411536; AA05874.1;  
 DR InterPro: IPR02072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR ProDom: PD002052; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS0270; NGF\_2; 1.  
 SO SEQUENCE 241 AA; 26964 MW; 745216485C21E558 CRC64;

Query Match 42.68; Score 297.5; DB 4; Length 241;  
 Best Local Similarity 45.78; Pred. No. 1.1e-21;  
 Matches 58; Conservative 22; Mismatches 38; Indels 9; Gaps 3;

OY 3 SETAPASRGELAYCDVAGVTDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETRCK 62  
 DB 122 SSSHPFIRGGEFSYCDVSVMGDKTATDICKREYVNLGEV-SINNSVFKQYFEETRCK 180  
 OY 63 ADNAEEGCGRCVDRRRHVSSECKAKOSYVALTAHAGRCVNRIRIDTACT 122  
 DB 181 DPNPVD-----SGCRGIDRKHNSICTTTHFVALTMDGR-QAAMRFIRIDTACV 232  
 OY 123 LLSRTGR 129  
 DB 233 LSRKAVR 239

## RESULT 14

OY 09UKL8 PRELIMINARY: PRT: 241 AA.  
 AC 09UKL8:  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Nerve growth factor B.

GN NGFB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9256269; PubMed=10322959;  
RA Tong Y., Wang H., Chen M.;  
RT cloning and sequencing of the gene for premature beta nerve growth  
RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tong Y., Wang H.;  
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF150960; A055975.1; -.  
DR HSSP; P01139; 1BET.  
DR InterPro; IPR002072; NGF.  
DR Pfam; PF00243; NGF; 1.  
DR PRINTS; PR00268; NGF.  
DR PRODOM; PD002052; NGF; 1.  
DR SMART; SM00140; NGF; 1.  
DR PROSITE; PS00248; NGF\_1; 1.  
DR PROSITE; PS0270; NGF\_2; 1.  
SO SEQUENCE 241 AA; 26959 MW; 619DFC65FB3BD671 CRC64;

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Query Match          42.6%; Score 297.5; DB 4; Length 241;
Best Local Similarity 46.5%; Pred. No. 1.1e-21;
Matches    59; Conservative    20; Mismatches   39; Indels     9; Gaps      3;

OY      3 SETAPASRRELAVCAVSGHYTDRTAYDLRGREVEVLGEVPAAAGSPULROYFFETACK 62
           | : ||| ||||| : || : ||| : ||| ||| | : ||||| : |
DB      122 SSSPHRIHKEFSDSVSWMGDKRTTATIDGKEMVNLGEV-NINNSVFROYFFETACKR 180
           | : ||| ||||| : || : ||| : ||| ||| | : ||||| : |
OY      63 ADNAEECGPAGGGCGNGVDNRHMWSECCAKOSYVRALTAHAGRVGRMTRIDTACTCT 122
           ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
DB      181 DPNVD-----SGCRGIDSKHMNSYCTTHTFVKALLDQCK-QAAMRFTRIDTACVCY 232
           | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      123 LLSRTGR 129
           | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      233 LSRAVR 239

RESULT 15
OQN2FL ID OQN2FL PRELIMINARY: PRT: 241 AA.
AC OQN2FL:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OC Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHMP-220;
RA Milano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL EMBL: AB037518; BAA90438.1; -
DR HSSP: P01139; IBBT.
DR InterPro: IPRO02072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PSS0270; NGF_2; 1.
FT NON_TER 241 241
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[illegible]

Search completed: December 2, 2002, 15:12:03  
Job time : 21.1172 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: December 2, 2002, 15:05:42 ; Search time 8.99179 Seconds  
(without alignments)  
425.386 Million cell updates/sec

Title: US-10-072-681-6

Perfect score: 698

Sequence: 1 GVSETPASRGLAVCAV.....RMIRIDPACVCTLSRTGRA 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/p/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/p/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/p/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/p/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/p/ptodata/1/1aa/6C.COMB.pep:\*
- 6: /cgn2\_6/p/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	698	100.0	130	3	US-08-970-865-6
2	698	100.0	130	3	US-08-581-662-1
3	698	100.0	130	4	US-09-363-573-6
4	698	100.0	130	4	US-09-675-503-6
5	698	100.0	130	4	US-09-664-293-1
6	689	98.7	130	1	US-08-440-049-5
7	689	98.7	130	2	US-08-441-513A-5
8	689	98.7	130	5	PCT-US91-06918-6
9	689	98.7	168	1	US-08-451-947-6
10	689	98.7	168	2	US-08-424-826A-6
11	689	98.7	168	3	US-08-928-694-6
12	689	98.7	168	5	PCT-US91-06950-6
13	689	98.7	210	1	US-08-451-947-2
14	689	98.7	210	1	US-08-424-826A-2
15	689	98.7	210	3	US-08-928-694-2
16	689	98.7	210	5	PCT-US91-06950-2
17	689	98.7	215	1	US-07-796-106-23
18	689	98.7	130	1	US-08-451-947-62
19	689	98.7	130	1	US-08-451-947-68
20	689	98.7	130	2	US-08-424-826A-62
21	689	98.7	130	2	US-08-424-826A-68
22	689	98.7	130	3	US-08-928-694-62
23	689	98.7	130	3	US-08-928-694-68
24	689	98.7	130	5	PCT-US91-06950-62
25	689	98.7	130	5	PCT-US91-06950-68
26	689	98.7	130	1	US-08-451-947-22
27	689	98.7	130	1	US-08-451-947-59

28	684	98.0	130	1	US-08-451-947-61	Sequence 61, Appl
29	684	98.0	130	1	US-08-451-947-63	Sequence 63, Appl
30	684	98.0	130	1	US-08-451-947-64	Sequence 64, Appl
31	684	98.0	130	1	US-08-451-947-69	Sequence 69, Appl
32	684	98.0	130	2	US-08-424-826A-22	Sequence 22, Appl
33	684	98.0	130	2	US-08-424-826A-59	Sequence 59, Appl
34	684	98.0	130	2	US-08-424-826A-61	Sequence 61, Appl
35	684	98.0	130	2	US-08-424-826A-63	Sequence 63, Appl
36	684	98.0	130	2	US-08-424-826A-64	Sequence 64, Appl
37	684	98.0	130	2	US-08-424-826A-69	Sequence 69, Appl
38	684	98.0	130	3	US-08-928-694-22	Sequence 22, Appl
39	684	98.0	130	3	US-08-928-694-59	Sequence 59, Appl
40	684	98.0	130	3	US-08-928-694-61	Sequence 61, Appl
41	684	98.0	130	3	US-08-928-694-63	Sequence 63, Appl
42	684	98.0	130	3	US-08-928-694-64	Sequence 64, Appl
43	684	98.0	130	3	US-08-928-694-69	Sequence 69, Appl
44	684	98.0	130	5	PCT-US91-06950-22	Sequence 22, Appl
45	684	98.0	130	5	PCT-US91-06950-59	Sequence 59, Appl

## ALIGNMENTS

RESULT 1  
US-08-970-865-6  
Sequence 6, Application US/08970865  
Patent No. 6005081  
GENERAL INFORMATION:  
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck  
TITLE OF INVENTION: Purification of NGR  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970, 865  
FILING DATE: 14-NO. 6005081-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030838  
FILING DATE: 11/15/1996  
PRIOR APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P106382  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/952-8674  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-970-865-6  
Query Match 100.0%, Score 698, DB 3, Length 130;  
Best Local Similarity 100.0%, Pred. No. 5.2e-73;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GVSETPASRGLAVCAVGVGTRPAVDLRREVEVGEPVAGGSPLEPFETR 60  
|||||

Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
QY 61 CKADNAEEGPGAGGGCGGVDRRHMYSECKAKOSYVALTAHACRGVGMIRIDTACY 120  
Db 61 CKADNAEEGPGAGGGCGGVDRRHMYSECKAKOSYVALTAHACRGVGMIRIDTACY 120  
QY 121 CTLLSRTGRA 130  
Db 121 CTLLSRTGRA 130

## RESULT 2

US-08-581-662-1  
Sequence 1, Application US/08581662  
Patent No. 6121235  
GENERAL INFORMATION:  
APPLICANT: Geo. Wei-Qiang  
TITLE OF INVENTION: Treatment of Balance Impairments  
FILE REFERENCE: P0981  
CURRENT APPLICATION NUMBER: US/08/581,662  
CURRENT FILING DATE: 1995-12-29  
NUMBER OF SEQ ID NOS: 36  
SEQ ID NO 1  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-581-662-1

## Query Match

Best Local Similarity 100.0%; Score 698; DB 3; Length 130;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
QY 61 CKADNAEEGPGAGGGCGGVDRRHMYSECKAKOSYVALTAHACRGVGMIRIDTACY 120  
Db 61 CKADNAEEGPGAGGGCGGVDRRHMYSECKAKOSYVALTAHACRGVGMIRIDTACY 120  
QY 121 CTLLSRTGRA 130  
Db 121 CTLLSRTGRA 130

## RESULT 3

US-09-363-573-6  
Sequence 6, Application US/09363573  
Patent No. 6184360

GENERAL INFORMATION:  
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck  
TITLE OF INVENTION: Purification of NCF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: WinPatln (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,573  
FILING DATE:

CLASSIFICATION: DATA:  
PRIOR APPLICATION NUMBER: US/08/970,865  
FILING DATE: 14-NO. 6184360-1997  
APPLICATION NUMBER: 60/030838

FILING DATE: 11/15/1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047855  
FILING DATE: 5/29/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1063R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-363-573-6

Query Match 100.0%; Score 698; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
QY 61 CKADNAEEGPGAGGGCGGVDRRHMYSECKAKOSYVALTAHACRGVGMIRIDTACY 120  
Db 61 CKADNAEEGPGAGGGCGGVDRRHMYSECKAKOSYVALTAHACRGVGMIRIDTACY 120  
QY 121 CTLLSRTGRA 130  
Db 121 CTLLSRTGRA 130

## RESULT 4

US-09-675-503-6  
Sequence 6, Application US/09675503  
Patent No. 6421831

GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Beck, Joanne T.  
TITLE OF INVENTION: ISOLATION OF NEUTROPHILS FROM A  
MIXTURE CONTAINING OTHER PROTEINS AND NEUTROPHIL VARIANTS  
TITLE OF INVENTION: USING HYDROPHOBIC INTERACTION CHROMATOGRAPHY  
FILE REFERENCE: GENENT 03/02  
CURRENT APPLICATION NUMBER: US/09/675,503  
CURRENT FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6

LENGTH: 130  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-675-503-6

Query Match 100.0%; Score 698; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
Db 1 GVSETAPASRGEALVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60



OY 61 CKADNAEBCGGAGCGCGVDRRHVSECKAKOSYVRLTAHAQGVGRMIRIDTACY 120  
|||||  
DB 61 CKADNAEBCGGAGCGCGVDRRHVSECKAKOSYVRLTAHAQGVGRMIRIDTACY 120  
OY 121 CTLISRTGRA 130  
|||||  
DB 121 CTLISRTGRA 130

## RESULT 5

US-09-664-295-1  
; Sequence 1, Application US/09664295  
; Patent No. 6429196  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Wei-Oiang  
; TITLE OF INVENTION: Treatment of Balance Impairments  
; FILE REFERENCE: GENENT.051C1  
; CURRENT APPLICATION NUMBER: US/09/664,295  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/08/581,662  
; PRIOR FILING DATE: 1995-12-29  
; NUMBER OF SEQ ID NOS: 37  
; SEQ ID NO 1  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-664-295-1

Query Match 100.0%; Score 698; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 5,2e-73;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEVPAAGSPLRQFFETR 60  
|||||  
DB 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEVPAAGSPLRQFFETR 60  
OY 61 CKADNAEBCGGAGCGCGVDRRHVSECKAKOSYVRLTAHAQGVGRMIRIDTACY 120  
|||||  
DB 61 CKADNAEBCGGAGCGCGVDRRHVSECKAKOSYVRLTAHAQGVGRMIRIDTACY 120  
OY 121 CTLISRTGRA 130  
|||||  
DB 121 CTLISRTGRA 130

## RESULT 6

US-08-440-049-5  
; Sequence 5, Application US/08440049  
; Patent No. 5728803  
; GENERAL INFORMATION:  
; APPLICANT: Uffer, Roman  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: PANTROPIC NEUROTROPHIC FACTORS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,049  
; FILING DATE: 12-May-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/253937

FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P0905C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8674  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 130 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-440-049-5

Query Match 98.7%; Score 689; DB 1; Length 130;  
Best Local Similarity 99.2%; Pred. No. 5,7e-72;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEVPAAGSPLRQFFETR 60  
|||||  
DB 1 GVSETAPASRGELAVCDVSGWTDRTAVDLRGREVLGEVPAAGSPLRQFFETR 60  
OY 61 CKADNAEBCGGAGCGCGVDRRHVSECKAKOSYVRLTAHAQGVGRMIRIDTACY 120  
|||||  
DB 61 CKADNAEBCGGAGCGCGVDRRHVSECKAKOSYVRLTAHAQGVGRMIRIDTACY 120  
OY 121 CTLISRTGRA 130  
|||||  
DB 121 CTLISRTGRA 130

## RESULT 7

US-08-441-513A-5  
; Sequence 5, Application US/08441513A  
; Patent No. 5981480  
; GENERAL INFORMATION:  
; APPLICANT: Uffer, Roman  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: Pantropic Neurotrophic Factors  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,513A  
; FILING DATE: 15-May-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/253937  
; FILING DATE: 03-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, Ph.D., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P0905C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 130 amino acids  
; TYPE: Amino Acid

TOPOLOGY: Linear  
US-08-441-513A-5

Query Match 98.7%: Score 689; DB 2; Length 130;  
Best Local Similarity 99.2%: Pred. No. 5.7e-72;  
Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
DB 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
QY 61 CADNAEEGGPGAGGCGRGVDRRHVYSECKAKOSYVRALTAAOGRVGMRIIDTACV 120  
DB 61 CADNAEEGGPGAGGCGRGVDRRHVYSECKAKOSYVRALTAAOGRVGMRIIDTACV 120  
QY 121 CTLLSRTGRA 130  
DB 121 CTLLSRTGRA 130

## RESULT 8

PCT-US95-06918-6  
Sequence 6, Application PC/TUS9506918  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: ANTROPIC NEUTROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06918  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 905PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US95-06918-6

Query Match 98.7%: Score 689; DB 5; Length 130;  
Best Local Similarity 99.2%: Pred. No. 5.7e-72;  
Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
DB 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
QY 61 CADNAEEGGPGAGGCGRGVDRRHVYSECKAKOSYVRALTAAOGRVGMRIIDTACV 120  
DB 61 CADNAEEGGPGAGGCGRGVDRRHVYSECKAKOSYVRALTAAOGRVGMRIIDTACV 120

QY 121 CTLLSRTGRA 130  
DB 121 CTLLSRTGRA 130

RESULT 9  
US-08-451-947-6  
Sequence 6, Application US/08451947  
Patent No. 5702906  
GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUTROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,947  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-947-6

Query Match 98.7%: Score 689; DB 1; Length 168;  
Best Local Similarity 99.2%: Pred. No. 7.3e-72;  
Matches 129: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 60  
DB 39 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQYFFETR 98  
QY 61 CADNAEEGGPGAGGCGRGVDRRHVYSECKAKOSYVRALTAAOGRVGMRIIDTACV 120  
DB 99 CADNAEEGGPGAGGCGRGVDRRHVYSECKAKOSYVRALTAAOGRVGMRIIDTACV 158  
QY 121 CTLLSRTGRA 130  
DB 159 CTLLSRTGRA 168

RESULT 10  
US-08-424-826A-6  
Sequence 6, Application US/08424826A  
Patent No. 5830858  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,826A  
FILING DATE: 19-Apr-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240387  
FILING DATE: 10-May-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0666P1C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-424-826A-6

Query Match 98.7%: Score 689; DB 2; Length 168;  
Best Local Similarity 99.2%: Pred. No. 7.9e-72;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSETAPASRGEGLAVCAVSGWYTDRTAYDLRGREVEVLGEVPAAGSPLEQYFFETR 60  
DB 39 GSETAPASRGEGLAVCAVSGWYTDRTAYDLRGREVEVLGEVPAAGSPLEQYFFETR 98  
QY 61 CKADNAEEGPGAGGGCGGVDRRHWSSECKAKOSYVRAITAHAGRGVGRWIRITDACY 120  
DB 99 CKADNAEEGPGAGGGCGGVDRRHWSSECKAKOSYVRAITAHAGRGVGRWIRITDACY 158  
QY 121 CTLLSRTGRA 130  
DB 159 CTLLSRTGRA 168

RESULT 11  
US-08-928-694-6  
Sequence 6, Application US/08928694  
Patent No. 6037320  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,694  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/451947  
FILING DATE: 26-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-928-694-6

Query Match 98.7%: Score 689; DB 3; Length 168;  
Best Local Similarity 99.2%: Pred. No. 7.9e-72;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSETAPASRGEGLAVCAVSGWYTDRTAYDLRGREVEVLGEVPAAGSPLEQYFFETR 60  
DB 39 GSETAPASRGEGLAVCAVSGWYTDRTAYDLRGREVEVLGEVPAAGSPLEQYFFETR 98  
QY 61 CKADNAEEGPGAGGGCGGVDRRHWSSECKAKOSYVRAITAHAGRGVGRWIRITDACY 120  
DB 99 CKADNAEEGPGAGGGCGGVDRRHWSSECKAKOSYVRAITAHAGRGVGRWIRITDACY 158  
QY 121 CTLLSRTGRA 130  
DB 159 CTLLSRTGRA 168

RESULT 12  
PCT-us91-06950-6  
Sequence 6, Application PC/TUS9106950  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06950  
FILING DATE: 19910924  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
ATTORNEY/AGENT INFORMATION:  
NAME: Hensley, Max D.  
REGISTRATION NUMBER: 27,043  
REFERENCE/DOCKET NUMBER: 666P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US91-06950-6

Query Match 98.7% Score 689; DB 5; Length 168;  
Best Local Similarity 99.2% Pred. No. 7,9e-72;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREYVGEVPAAAGSFLRQYFEETR 60  
DB 39 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREYVGEVPAAAGSFLRQYFEETR 96  
QY 61 CKADNAEEGGPGAGGGCGGCRGVDRRHVSCEKAKOSYVALTAHAGRGVGMIRIDTACY 120  
DB 99 CKADNAEEGGPGAGGGCGGCRGVDRRHVSCEKAKOSYVALTAHAGRGVGMIRIDTACY 158  
QY 121 CTLISRTGRA 130  
DB 159 CTLISRTGRA 168

RESULT 13  
US-08-451-947-2  
Sequence 2, Application US/08451947  
Patent No. 5702906  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,947

FILING DATE: 514  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-451-947-2

Query Match 98.7% Score 689; DB 1; Length 210;  
Best Local Similarity 99.2% Pred. No. 1e-71;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREYVGEVPAAAGSFLRQYFEETR 60  
DB 81 GVSETAPASRRGELAVCDVSGWYDRTAVDLRGREYVGEVPAAAGSFLRQYFEETR 140  
QY 61 CKADNAEEGGPGAGGGCGGCRGVDRRHVSCEKAKOSYVALTAHAGRGVGMIRIDTACY 120  
DB 141 CKADNAEEGGPGAGGGCGGCRGVDRRHVSCEKAKOSYVALTAHAGRGVGMIRIDTACY 200  
QY 121 CTLISRTGRA 130  
DB 201 CTLISRTGRA 210

RESULT 14  
US-08-424-826A-2  
Sequence 2, Application US/08424826A  
Patent No. 5830858  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
APPLICANT: GENENTECH, INC.  
TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,826A  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240387  
FILING DATE: 10-MAY-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchla, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0666PIC2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-424-826A-2

Query Match 98.7%; Score 689; DB 2; Length 210;  
Best Local Similarity 99.2%; Pred. No. 1e-71;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPILROYFFETR 60  
DB 81 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPILROYFFETR 140  
QY 61 CKADNAEEGGPGAGGGCGGVDRRHVYSECKAKQSYVRLTAHAGRGVGMIRIDTACY 120  
DB 141 CKADNAEEGGPGAGGGCGGVDRRHVYSECKAKQSYVRLTAHAGRGVGMIRIDTACY 200  
QY 121 CTLSRTGRA 130  
DB 201 CTLSRTGRA 210

RESULT 15  
US-08-928-694-2  
Sequence 2, Application US/08928694  
Patent No. 6037320  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipalin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,694  
FILING DATE: 12-SEP-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/451947  
FILING DATE: 26-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchla, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-928-694-2

Query Match 98.7%; Score 689; DB 3; Length 210;  
Best Local Similarity 99.2%; Pred. No. 1e-71;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPILROYFFETR 60  
DB 81 GVSETAPASRSGELAYCDVAVSGWTDRTAVDLRGREVEVLGEVPAAGSPILROYFFETR 140  
QY 61 CKADNAEEGGPGAGGGCGGVDRRHVYSECKAKQSYVRLTAHAGRGVGMIRIDTACY 120  
DB 141 CKADNAEEGGPGAGGGCGGVDRRHVYSECKAKQSYVRLTAHAGRGVGMIRIDTACY 200  
QY 121 CTLSRTGRA 130  
DB 201 CTLSRTGRA 210

Search completed: December 2, 2002, 15:09:45  
Job time: 9.99179 secs

```

: Sequence 60, Application US/08450842
: Patent No. US20020045576A1
: GENERAL INFORMATION:
: APPLICANT: GENENTECH, INC.
: APPLICANT: ROSENTHAL, ARNON
: TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
: NUMBER OF SEQUENCES: 100
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/450,842
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/426419
: FILING DATE: 19-APR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/030013
: FILING DATE: 22-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/648482
: FILING DATE: 31-JAN
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/587707
: FILING DATE: 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: 666P2C1D3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-8674
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 60:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 130 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-450-842-60

```

```

Query Match      97.9%  Score 683; DB 8; Length 130;
Best Local Similarity 98.5%  Pred. No. 2.3e-60;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSETPAPSRKGLAVCAVSGMTDRTAVDLRGREVEYLGVPAAAGSGPLQYFFETR 60
Db 1 GYSETPAPSRKGLAVCAVSGMTDRTAVDLRGREVEYLGVPAAAGSGPLQYFFETR 60

QY 61 CKADNAEEGPGAGCGGCGVDRRHVYSECKAKOSYVRLTAHAQGRVGRMIRIDTACY 120
Db 61 CKADNAEEGPGAGCGGCGVDRRHVYSECKAKOSYVRLTAHAQGRVGRMIRIDTACY 120

QY 121 CTLLSRTGRA 130
Db 121 CTLLSRTGRA 130

```

Search completed: December 2, 2002, 15:14:35  
 Job time : 4.5721 secs

QY 121 CTLSTRGRA 130  
DB 121 CTLSTRGRA 130

RESULT 13  
US-08-450-842-20

Sequence 20, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-20

Query Match 97.9%; Score 683; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 2.3e-60;

Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSSTAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAAGSPLRQYFEETR 60  
DB 1 GVSSTAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAAGSPLRQYFEETR 60  
QY 61 CKADNAEEGGPGAGGCGCGVDRRHVSECKAKOSYVRALTAHAGRVGMIRITDACY 120  
DB 61 CKADNAEEGGPGAGGCGCGVDRRHVSECKAKOSYVRALTAHAGRVGMIRITDACY 120  
QY 121 CTLSTRGRA 130  
DB 121 CTLSTRGRA 130

RESULT 14  
US-08-450-842-23

Sequence 23, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-23

Query Match 97.9%; Score 683; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 2.3e-60;

Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSSTAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAAGSPLRQYFEETR 60  
DB 1 GVSSTAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAAGSPLRQYFEETR 60  
QY 61 CKADNAEEGGPGAGGCGCGVDRRHVSECKAKOSYVRALTAHAGRVGMIRITDACY 120  
DB 61 CKADNAEEGGPGAGGCGCGVDRRHVSECKAKOSYVRALTAHAGRVGMIRITDACY 120  
QY 121 CTLSTRGRA 130  
DB 121 CTLSTRGRA 130

RESULT 15  
US-08-450-842-60

OY 1 GVSFAPASRGGELAVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60  
DB 1 GVSFAPASRGGELAVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60  
OY 61 CKADNAEEGCGPAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRCVGRWIRIDTACV 120  
DB 61 CKADNAEEGCGPAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRCVGRWIRIDTACV 120  
OY 121 CTLLSRTGRA 130  
DB 121 CTLLSRTGRA 130

RESULT 11  
US-08-450-842-64  
Sequence 64, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patln (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
ATTORNEY/AGENT INFORMATION:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-64

Query Match 98.0%; Score 684; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.8e-60;  
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 GVSFAPASRGGELAVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60  
DB 1 GVSFAPASRGGELAVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60

OY 61 CKADNAEEGCGPAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRCVGRWIRIDTACV 120  
DB 61 CKADNAEEGCGPAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRCVGRWIRIDTACV 120  
OY 121 CTLLSRTGRA 130  
DB 121 CTLLSRTGRA 130

RESULT 12  
US-08-450-842-69  
Sequence 69, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patln (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
ATTORNEY/AGENT INFORMATION:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-69

Query Match 98.0%; Score 684; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.8e-60;  
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GVSFAPASRGGELAVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60  
DB 1 GVSFAPASRGGELAVCDVAVSGWYTDRTAVDLRGREVEVLGEVPAAGSPPLRQYFFETR 60  
OY 61 CKADNAEEGCGPAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRCVGRWIRIDTACV 120  
DB 61 CKADNAEEGCGPAGGCGCGVDRRHVWSECKAKOSYVRLTAHAGRCVGRWIRIDTACV 120



LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-59

Query Match 98.0%; Score 684; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.8e-60;  
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGGSPILROYFEETR 60  
DB 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGGSPILROYFEETR 60  
QY 61 CKADNAEKGPGAGGGGCGYDRHRHWSCKAKOSYVRLTAHAGRGVGRMIRIDTACV 120  
DB 61 CKADNAEKGPGAGGGGCGYDRHRHWSCKAKOSYVRLTAHAGRGVGRMIRIDTACV 120  
QY 121 CTLSRTGRA 130  
DB 121 CTLSRTGRA 130

RESULT 9

US-08-450-842-61  
Sequence 61, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELETYPE: 910/371-7168  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-61

Query Match 98.0%; Score 684; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.8e-60;  
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGGSPILROYFEETR 60  
DB 1 GVSETAPASRGEIACVAVSGWYTDRTAVDLRGREVEVLGEVPAAGGSPILROYFEETR 60  
QY 61 CKADNAEKGPGAGGGGCGYDRHRHWSCKAKOSYVRLTAHAGRGVGRMIRIDTACV 120  
DB 61 CKADNAEKGPGAGGGGCGYDRHRHWSCKAKOSYVRLTAHAGRGVGRMIRIDTACV 120  
QY 121 CTLSRTGRA 130  
DB 121 CTLSRTGRA 130

RESULT 10

US-08-450-842-63  
Sequence 63, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELETYPE: 910/371-7168  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-63

Query Match 98.0%; Score 684; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.8e-60;  
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-68

Query Match 98.1%; Score 685; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.4e-60;

Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPPLQYFEETR 60  
DB 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPPLQYFEETR 60  
QY 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRVGWRIRIDTACY 120  
DB 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRVGWRIRIDTACY 120  
QY 121 CTLLSRTGRA 130  
DB 121 CTLLSRTGRA 130

## RESULT 7

US-08-450-842-22  
Sequence 22, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-22

Query Match 98.0%; Score 684; DB 8; Length 130;  
Best Local Similarity 98.5%; Pred. No. 1.4e-60;

Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPPLQYFEETR 60  
DB 1 GVSETAPASRGEIACVDAVSGVTDRTAVDLRGREVEVLGEVPAAGSPPLQYFEETR 60  
QY 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRVGWRIRIDTACY 120  
DB 61 CKADNAEEGPGAGGCGCGVDRRHMYSECKAKOSYVRLTAAGRVGWRIRIDTACY 120  
QY 121 CTLLSRTGRA 130  
DB 121 CTLLSRTGRA 130

## RESULT 8

US-08-450-842-59  
Sequence 59, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: TORCHIA, TIMOTHY E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-2

Query Match  
Best Local Similarity 98.7%; Score 689; DB 8; Length 210;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQFFETR 60  
DB 81 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQFFETR 140  
QY 61 CKADNAEEGPGAGGGCGGCVDRHRWVSECKAKOSYVRLTAHAQGRVGRWIRIDTACV 120  
DB 141 CKADNAEEGPGAGGGCGGCVDRHRWVSECKAKOSYVRLTAHAQGRVGRWIRIDTACV 200  
QY 121 CTLSTRGRA 130  
DB 201 CTLSTRGRA 210

RESULT 5  
US-08-450-842-62  
Sequence 62, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: TORCHIA, TIMOTHY E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: 666P2C1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-450-842-62

Query Match  
Best Local Similarity 98.1%; Score 685; DB 8; Length 130;  
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQFFETR 60  
DB 1 GVSETAPASRRGELAVCDVSGWYTDRTAVDLRGREVEVLGEVPAAGSPLRQFFETR 60  
QY 61 CKADNAEEGPGAGGGCGGCVDRHRWVSECKAKOSYVRLTAHAQGRVGRWIRIDTACV 120  
DB 61 CKADNAEEGPGAGGGCGGCVDRHRWVSECKAKOSYVRLTAHAQGRVGRWIRIDTACV 120  
QY 121 CTLSTRGRA 130  
DB 121 CTLSTRGRA 130

RESULT 6  
US-08-450-842-68  
Sequence 68, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.

OY 121 CILLSTRGRA 130  
Db 121 CILLSTRGRA 130

## RESULT 2

US-09-813-398-12  
Sequence 12, Application US/09813398  
Patent No. US20020169292A1  
GENERAL INFORMATION:  
APPLICANT: Bruce D. Weintraub  
APPLICANT: Mariusz W. Szudlinski  
TITLE OF INVENTION: CISTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: UOPMD.003C1  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US98/19772  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 131  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-09-813-398-12

## Query Match

Best Local Similarity 98.7%; Score 689; DB 9; Length 131;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSSTAPASRSGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60  
Db 2 GVSSTAPASRSGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 61

OY 61 CKADNAEEGGPGAGGGCGGVDRRHVVSECKAKOSYVRLTAHAGRGVGMIRITDACY 120  
Db 62 CKADNAEEGGPGAGGGCGGVDRRHVVSECKAKOSYVRLTAHAGRGVGMIRITDACY 121

OY 121 CILLSTRGRA 130  
Db 122 CILLSTRGRA 131

## RESULT 3

US-08-450-842-6  
Sequence 6, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/030013

FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 666P2C1D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-842-6

## Query Match

Best Local Similarity 98.7%; Score 689; DB 8; Length 168;  
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GVSSTAPASRSGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 60  
Db 39 GVSSTAPASRSGELAVCDVSGWYDRTAVDLRGREVEVLGEVPAAGSPLRQYFEETR 98

OY 61 CKADNAEEGGPGAGGGCGGVDRRHVVSECKAKOSYVRLTAHAGRGVGMIRITDACY 120  
Db 99 CKADNAEEGGPGAGGGCGGVDRRHVVSECKAKOSYVRLTAHAGRGVGMIRITDACY 158

OY 121 CILLSTRGRA 130  
Db 159 CILLSTRGRA 168

## RESULT 4

US-08-450-842-2  
Sequence 2, Application US/08450842  
Patent No. US20020045576A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,842  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/030013  
FILING DATE: 22-MAR-1993

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 15:08:47 ; Search time 4.5721 Seconds  
(without alignments)  
452.778 Million cell updates/sec

Title: US-10-072-681-6  
Perfect score: 698  
Sequence: 1 GVSTFAPASRSGELAVCDV.....RWIRIDYACVTLISRTGRA 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCRTUS\_PUBCOMB pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698	100.0	130	12	US-10-072-681-6
2	689	98.7	131	9	US-03-813-398-12
3	689	98.7	168	8	US-08-450-842-6
4	689	98.7	210	8	US-08-450-842-2
5	685	96.1	130	8	US-08-450-842-62
6	685	96.1	130	8	US-08-450-842-62
7	684	98.0	130	8	US-08-450-842-22
8	684	98.0	130	8	US-08-450-842-22
9	684	98.0	130	8	US-08-450-842-61
10	684	98.0	130	8	US-08-450-842-63
11	684	98.0	130	8	US-08-450-842-63
12	684	98.0	130	8	US-08-450-842-69
13	683	97.9	130	8	US-08-450-842-20
14	683	97.9	130	8	US-08-450-842-23
15	683	97.9	130	8	US-08-450-842-60
16	683	97.9	130	8	US-08-450-842-65
17	683	97.9	130	8	US-08-450-842-70
18	683	97.9	130	8	US-08-450-842-72
19	682	97.7	130	8	US-08-450-842-66

20	682	97.7	130	8	US-08-450-842-73	Sequence 73, Appl
21	681	97.6	130	8	US-08-450-842-17	Sequence 17, Appl
22	681	97.6	130	8	US-08-450-842-67	Sequence 67, Appl
23	680	97.4	130	8	US-08-450-842-18	Sequence 18, Appl
24	680	97.4	130	8	US-08-450-842-71	Sequence 71, Appl
25	679	97.3	130	8	US-08-450-842-19	Sequence 19, Appl
26	679	97.3	130	8	US-08-450-842-21	Sequence 21, Appl
27	677	97.0	130	8	US-08-450-842-13	Sequence 13, Appl
28	677	97.0	130	8	US-08-450-842-14	Sequence 14, Appl
29	677	97.0	130	8	US-08-450-842-15	Sequence 15, Appl
30	677	97.0	130	8	US-08-450-842-16	Sequence 16, Appl
31	669.5	95.9	129	8	US-08-450-842-53	Sequence 53, Appl
32	669.5	95.9	129	8	US-08-450-842-54	Sequence 54, Appl
33	651	93.3	130	8	US-08-450-842-47	Sequence 47, Appl
34	650	93.1	126	8	US-08-450-842-57	Sequence 57, Appl
35	642	92.0	124	8	US-08-450-842-55	Sequence 55, Appl
36	586	84.0	114	8	US-08-450-842-58	Sequence 58, Appl
37	571	81.8	105	8	US-08-450-842-31	Sequence 31, Appl
38	558	79.9	103	8	US-08-450-842-30	Sequence 30, Appl
39	540	77.4	142	8	US-08-450-842-52	Sequence 52, Appl
40	535.5	76.7	107	8	US-08-450-842-56	Sequence 56, Appl
41	535.5	76.7	132	8	US-08-450-842-51	Sequence 51, Appl
42	501.5	71.8	185	8	US-08-450-842-12	Sequence 12, Appl
43	494.5	70.8	215	8	US-08-450-842-8	Sequence 8, Appl
44	478.5	68.6	257	8	US-08-450-842-10	Sequence 10, Appl
45	468	67.0	92	8	US-08-450-842-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1  
US-10-072-681-6  
Sequence 6, Application US/10072681  
Patent No. US20020137893A1  
GENERAL INFORMATION:  
APPLICANT: Burton, Louis E.  
APPLICANT: Schmelzer, Charles H.  
TITLE OF INVENTION: PURIFICATION OF NGF  
FILE REFERENCE: GENENT.037C3  
CURRENT APPLICATION NUMBER: US/10/072,681  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: 60/030838  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/047855  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: 08/970865  
PRIOR FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 09/363573  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/675,503  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-072-681-6

Query Match 100.0% Score 698 DB 12 Length 130:  
Best Local Similarity 100.0% Pred. No. 7,7e-62:  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GVSTFAPASRSGELAVCDVSGVTRRANVYDLRGREVEYAGVPAAGSPLROYFEETR 60  
Db 1 GVSTFAPASRSGELAVCDVAVSGVTRRANVYDLRGREVEYAGVPAAGSPLROYFEETR 60  
Oy 61 CKADNAEEGGPGAGGGCGGVRHRRVNSECKAKOSYVATLTAHAGRGVNRWIRIDYACV 120  
Db 61 CKADNAEEGGPGAGGGCGGVRHRRVNSECKAKOSYVATLTAHAGRGVNRWIRIDYACV 120